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OM protein - protein search, using sw model

Run on: June 18, 2004, 10:49:07 ; Search time 23 Seconds
(without alignments)
482.591 Million cell updates/sec

Title: US-09-819-371-6

Perfect score: 1173
Sequence: 1 IAVEYVDDTQFLRFDSDAAI.....QRDGEQTDTELVTETPAG 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	940	80.1	274	1	US-08-222-851-1
2	857	73.1	365	2	US-08-484-905-104
3	857	73.1	365	3	US-08-481-985B-104
4	857	73.1	365	3	US-08-370-476-104
5	856	73.0	365	2	US-08-484-905-100
6	856	73.0	365	3	US-08-481-985B-100
7	856	73.0	365	3	US-08-370-476-100
8	853	72.7	365	2	US-08-484-905-99
9	853	72.7	365	3	US-08-481-985B-99
10	853	72.7	365	3	US-08-370-476-99
11	852	72.6	274	2	US-08-484-905-107
12	852	72.6	274	2	US-08-484-905-108
13	852	72.6	274	3	US-08-481-985B-107
14	852	72.6	274	3	US-08-481-985B-108
15	852	72.6	274	3	US-08-370-476-107
16	852	72.6	274	3	US-08-370-476-108
17	851	72.5	365	2	US-08-484-905-103
18	851	72.5	365	3	US-08-481-985B-103
19	851	72.5	365	3	US-08-370-476-103
20	850	72.5	365	2	US-08-484-905-102
21	850	72.5	365	3	US-08-481-985B-102
22	850	72.5	365	3	US-08-370-476-102
23	849	72.4	365	2	US-08-484-905-97
24	849	72.4	365	2	US-08-484-905-98
25	849	72.4	365	3	US-08-481-985B-97
26	849	72.4	365	3	US-08-481-985B-98
27	849	72.4	365	3	US-08-652-265-23

Sequence 23, Appl
Sequence 97, Appl
Sequence 98, Appl
Sequence 23, Appl
Sequence 105, App
Sequence 105, App
Sequence 105, App
Sequence 105, App
Sequence 38, Appl
Sequence 106, App
Sequence 106, App
Sequence 106, App
Sequence 101, App
Sequence 101, App
Sequence 101, App
Sequence 22, Appl
Sequence 22, Appl
Sequence 37, Appl

28 849 72.4 365 3 US-08-834-497A-23
29 849 72.4 365 3 US-08-370-476-97
30 849 72.4 365 3 US-08-370-476-98
31 849 72.4 365 3 US-09-503-444A-23
32 848 72.3 274 2 US-08-484-905-105
33 848 72.3 274 2 US-08-481-985B-105
34 848 72.3 274 3 US-08-370-476-105
35 848 72.3 341 3 US-08-890-719-38
36 844 72.0 274 2 US-08-484-905-106
37 844 72.0 274 3 US-08-481-985B-106
38 844 72.0 274 3 US-08-370-476-106
39 835 71.2 365 2 US-08-484-905-101
40 835 71.2 365 3 US-08-481-985B-101
41 835 71.2 365 3 US-08-370-476-101
42 809 69.0 361 3 US-08-652-265-22
43 809 69.0 361 3 US-08-834-497A-22
44 809 69.0 361 3 US-09-503-444A-22
45 805 68.6 363 4 US-08-914-372C-37

ALIGNMENTS

RESULT 1
US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRSNFORSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-222-851-1

Query Match 80.1%; Score 940; DB 1; Length 274;

Best Local Similarity 80.5%; Pred. No. 9.2e-90;
Matches 173; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPEPVVEGGQYWEWTTGYAKANACTORVALRNLL 60

DB 23 IAVEYVDDTQFLRFDSDAAIPRMEPEPVVEGGQYWEWTTGYAKANACTORVALRNLL 82

QY 61 RRYNSEAGSHTLQNMNGCDMGDPGRLLRGYHQAHDGKDYISLNEDLRSWTAADTVAQI 120
DB 83 GYNNQSEAGSHTLQNMNGCDMGDPGRLLRGYHQAHDGKDYISLNEDLRSWTAADTVAQI 142
QY 121 TORFYAEAEYAEFRYLEGECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
DB 143 TQKWEAARVAEQRLAYLEGTCEVWLRRLYLENGKETLQADPPKAAHVAHPISDHEATLR 202
QY 181 CWALGFYPAEITLWQDGEQOTDTLWETRPAG 215
DB 203 CWALGFYPAEITLWQDGEQOTDTLWETRPAG 237

RESULT 2
US-08-484-905-104
; Sequence 104, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-104

Query Match 73.1%; Score 857; DB 2; Length 365;
Best Local Similarity 73.5%; Pred. No. 6e-81;
Matches 158; Conservative 18; Mismatches 39; Indels 0; Gaps 0;
QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPFWVEQEGPYWETWTGYAKANAQTDRLVALNLL 60
DB 47 IAVGYVDDTQFLRFDSDAAIPRMEPRPFWVEQEGPYWETWTGYAKANAQTDRLVALNLL 106

QY 61 RRYNSEAGSHTLQNMNGCDMGDPGRLLRGYHQAHDGKDYISLNEDLRSWTAADTVAQI 120
DB 107 GYNNQSEAGSHTLQNMNGCDMGDPGRLLRGYHQAHDGKDYISLNEDLRSWTAADTVAQI 166
QY 121 TORFYAEAEYAEFRYLEGECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
DB 167 TQKWEAARVAEQRLAYLEGTCEVWLRRLYLENGKETLQADPPKAAHVAHPISDHEATLR 226
QY 181 CWALGFYPAEITLWQDGEQOTDTLWETRPAG 215
DB 227 CWALGFYPAEITLWQDGEQOTDTLWETRPAG 261

RESULT 3
US-08-481-985B-104
; Sequence 104, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-104

Query Match 73.1%; Score 857; DB 3; Length 365;
Best Local Similarity 73.5%; Pred. No. 6e-81;
Matches 158; Conservative 18; Mismatches 39; Indels 0; Gaps 0;
QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPFWVEQEGPYWETWTGYAKANAQTDRLVALNLL 60
DB 47 IAVGYVDDTQFLRFDSDAAIPRMEPRPFWVEQEGPYWETWTGYAKANAQTDRLVALNLL 106
QY 61 RRYNSEAGSHTLQNMNGCDMGDPGRLLRGYHQAHDGKDYISLNEDLRSWTAADTVAQI 120

47	I	A	V	G	V	D	T	Q	F	R	F	S	D	A	A	S	O	R	M	E	P	R	A	P	I	E	Q	E	G	P	E	Y	D	F	N	T	R	N	V	K	A	Q	S	O	T	O	R	V	L	S	T	I	R	100
51	P	R	N	O	S	E	A	G	S	H	T	L	O	M	N	G	C	D	M	G	P	D	R	L	L	G	H	Y	O	H	A	W	D	G	K	Y	I	S	L	N	E	D	L	S	T	A	A	D	V	A	O	I	120	
107	G	Y	N	O	S	E	A	G	S	H	T	I	O	M	N	G	C	D	M	G	P	D	R	L	L	G	H	Y	O	H	A	W	D	G	K	Y	I	S	L	N	E	D	L	S	T	A	A	D	V	A	O	I	166	
121	T	O	R	P	E	A	E	V	A	B	E	P	T	I	L	O	E	C	T	E	L	L	R	Y	L	E	N	G	K	E	T	L	O	R	A	D	P	K	A	H	V	A	H	P	I	S	D	H	E	A	T	I	R	180
167	T	K	H	K	E	A	H	A	B	O	E	R	A	L	E	G	T	C	V	E	M	U	R	R	Y	L	E	N	G	K	E	T	L	O	R	D	A	P	K	T	H	T	H	A	V	S	D	H	E	A	T	I	R	226
181	C	W	A	L	G	F	P	A	E	I	L	T	W	O	R	D	G	B	E	O	T	D	E	L	V	E	T	R	P	A	G	215																						
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RESULT 5
US-08-484-905-100
; Sequence 100, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilesky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.

```

Query Match      73.0%; Score 856; DB 2; Length 365;
Best Local Similarity 73.5%; Fred. No. 7.6e-51;
Matches 158; Conservative 39; Indels 0; Gaps 0;

Qy 1 IAVEYVDDTQFLRFDSDAALPERPEPWPVEQSGPQWENTTGAKAKANAQTDRAVALNNLL 60
Db 47 IAVGYVDDTQFLRFDSDAASQRMPEAPMTWEGQPEYWDGKETRKVAKHSQTHRVLDLSTLR 106

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QY 61 RRYNQSEAGSHTLQGMNCGMDGDFGRLLRGYHQHAWDGKDYISLNEEDLSRWSWTAADTVAQI 120
Db 107 GYTNQSEAGSHTVQRMFGCDVSGDFLGRGYHAYDGDYIALKEDLSWTAADMAAQT 166
QY 121 TQRFYAEAEYAEFRFYLEGECLELLRRYLENGKETLQADPPKAVHHPISDHEATLR 180
Db 167 TKHWEAAHVAEQRLAYLEGTVCWEMLRRYLENGKETLQRTDAPKTHMTTHAVSDHEATLR 226
QY 181 CWALGFYPAEITLITWQDGEQQTDELVELVETRPAG 215
Db 227 CWALSFYPAEITLITWQDGEDQTDDELVELVETRPAG 261

RESULT 6
US-08-481-985B-100
; Sequence 100, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-100

Query Match 73.0%; Score 856; DB 3; Length 365;
Best Local Similarity 73.5%; Pred. No. 7.6e-81;
Matches 159; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAIPRMEPRFVWEQEGPQYWTGTGYAKANAQTDRAVALRNL 60
Db 47 IAVEYVDDTQFLRFDSDAIPRMEPRFVWEQEGPQYWTGTGYAKANAQTDRAVALRNL 106
QY 61 RRYNQSEAGSHTLQGMNCGMDGDFGRLLRGYHQHAWDGKDYISLNEEDLSRWSWTAADTVAQI 120

Db 107 GYTNQSEAGSHTVQRMFGCDVSGDFLGRGYHAYDGDYIALKEDLSWTAADMAAQT 166
QY 121 TQRFYAEAEYAEFRFYLEGECLELLRRYLENGKETLQADPPKAVHHPISDHEATLR 180
Db 167 TKHWEAAHVAEQRLAYLEGTVCWEMLRRYLENGKETLQRTDAPKTHMTTHAVSDHEATLR 226
QY 181 CWALGFYPAEITLITWQDGEQQTDELVELVETRPAG 215
Db 227 CWALSFYPAEITLITWQDGEDQTDDELVELVETRPAG 261

RESULT 7
US-08-370-476-100
; Sequence 100, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Casrouge, Amanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-100

Query Match 73.0%; Score 856; DB 3; Length 365;
Best Local Similarity 73.5%; Pred. No. 7.6e-81;
Matches 159; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAIPRMEPRFVWEQEGPQYWTGTGYAKANAQTDRAVALRNL 60

Db 47 IAVGVDDTQFVRPDSDAASQRMPEAPWIEQSGPEYWDGTRKVKAHQSOTHRVDLSTLR 106
 QY 61 RRYNSEAGSHTLQGMNCGDMGPDGRLRGVGHQHWGDKYISLNEEDLRSWTAADTVAQI 120
 Db 107 GYINQSEAGSHTVORMFGCDVSGDGRFLRGVHQYAYDGRDYIALKEDLRSWTAADMAAQT 166
 QY 121 TQRFYEAEBEFTYLEGCELELLRRYLENGKETLQRADPPKARVAHPHPSDHEATLR 180
 Db 167 TKHWEAHHVQLRAYLGTCTVEWLRRLYLENGKETLQRTDAPKTHTHHVAHSDHEATLR 226
 QY 181 CWALGFYPAEITLTWQDGEOTQDTLVELVETPAG 215
 Db 227 CWALSFYPAEITLTWQDGEDQDTLVELVETPAG 261

RESULT 8
 US-08-484-905-99
 ; Sequence 99, Application US/08484905
 ; Patent No. 5976551
 ; GENERAL INFORMATION:
 ; APPLICANT: Mottez, Estelle
 ; APPLICANT: Abastado, Jean-Pierre
 ; APPLICANT: Kourilsky, Philippe
 ; TITLE OF INVENTION: An Altered Major Histocompatibility
 ; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
 ; TITLE OF INVENTION: Determinant
 ; NUMBER OF SEQUENCES: 127
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/484,905
 ; FILING DATE: 07-JUNE-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION NUMBER: US 07/801,818
 ; FILING DATE: 05-DEC-1991
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION NUMBER: US 07/792,473
 ; FILING DATE: 15-NOV-1991
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Potter, Jane E. R.
 ; REGISTRATION NUMBER: 33,332
 ; REFERENCE/DOCKET NUMBER: 03495.0106-03000
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 99:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 365 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-484-905-99

Query Match 72.7%; Score 853; DB 2; Length 365;
 Best Local Similarity 73.0%; Pred. No. 1.6e-80;
 Matches 157; Conservative 19; Mismatches 39; Indels 0; Gaps 0;
 QY 1 IAVEYDDTQFLRFDSDAAIPRMEPREPWEQEGPQYWEWTTGYAKANAQTDRLVALNLL 60

Db 47 IAVGVDDTQFVRPDSDAASQRMPEAPWIEQSGPEYWDGTRKVKAHQSOTHRVDLSTLR 106
 QY 61 RRYNSEAGSHTLQGMNCGDMGPDGRLRGVGHQHWGDKYISLNEEDLRSWTAADTVAQI 120
 Db 107 GYINQSEAGSHTVORMFGCDVSGDGRFLRGVHQYAYDGRDYIALKEDLRSWTAADMAAQT 166
 QY 121 TQRFYEAEBEFTYLEGCELELLRRYLENGKETLQRADPPKARVAHPHPSDHEATLR 180
 Db 167 TKHWEAHHVQLRAYLGTCTVEWLRRLYLENGKETLQRTDAPKTHTHHVAHSDHEATLR 226
 QY 181 CWALGFYPAEITLTWQDGEOTQDTLVELVETPAG 215
 Db 227 CWALSFYPAEITLTWQDGEDQDTLVELVETPAG 261

RESULT 9
 US-08-481-985B-99
 ; Sequence 99, Application US/08481985B
 ; Patent No. 6011146
 ; GENERAL INFORMATION:
 ; APPLICANT: Mottez, Estelle
 ; APPLICANT: Abastado, Jean-Pierre
 ; APPLICANT: Kourilsky, Philippe
 ; TITLE OF INVENTION: An Altered Major Histocompatibility Complex
 ; TITLE OF INVENTION:
 ; NUMBER OF SEQUENCES: 148
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/481,985B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER: US 07/801,818
 ; FILING DATE: 05-DEC-1991
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER: US 07/792,473
 ; FILING DATE: 15-NOV-1991
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Kenneth J.
 ; REGISTRATION NUMBER: 25,146
 ; REFERENCE/DOCKET NUMBER: 03495.0106-04000
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 99:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 365 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-481-985B-99

Query Match 72.7%; Score 853; DB 3; Length 365;
 Best Local Similarity 73.0%; Pred. No. 1.6e-80;
 Matches 157; Conservative 19; Mismatches 39; Indels 0; Gaps 0;
 QY 1 IAVEYDDTQFLRFDSDAAIPRMEPREPWEQEGPQYWEWTTGYAKANAQTDRLVALNLL 60
 Db 47 IAVGVDDTQFVRPDSDAASQRMPEAPWIEQSGPEYWDGTRKVKAHQSOTHRVDLSTLR 106

QY 61 RRYNQEAGSHLTQGMNCGDMPGRLRLRGYHQAHDGKDYISLNEDLRSWTAADTVAQI 120
DB 107 GYNYQSEAGSHTVQRMYGCDVSGDRFLRGYHQAHDGKDYIALKEDLRSWTAADMAAQT 166
QY 121 TORFYEAEBEAFRTYLEGCELELLRRYLENGKETLQADPPKARVAHHPISDHEATLR 180
DB 167 TKHKWETAHEAQBWRAYLEGTCTVWMLRRYLENGKETLQADPTKTHMTHAVSDHEATLR 226
QY 181 CWALGFYPAEITLTWQDGEBOQTDELVELTRPAG 215
DB 227 CWALSFYPAEITLTWQDGEDQTDDELVELTRPAG 261
RESULT 10
US-08-370-476-99
; Sequence 99, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Casrouge, Amanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-99

Query Match 72.78; Score 853; DB 3; Length 365;
Best Local Similarity 73.0%; Pred. No. 1.6e-80;
Matches 157; Conservative 19; Mismatches 39; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYWEWTTGYAKANAQTDRAVALRNLL 60
DB 47 IAVGYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYWEWTTGYAKANAQTDRAVALRNLL 106
QY 61 RRYNQEAGSHLTQGMNCGDMPGRLRLRGYHQAHDGKDYISLNEDLRSWTAADTVAQI 120
DB 107 GYNYQSEAGSHTVQRMYGCDVSGDRFLRGYHQAHDGKDYIALKEDLRSWTAADMAAQT 166
QY 121 TORFYEAEBEAFRTYLEGCELELLRRYLENGKETLQADPPKARVAHHPISDHEATLR 180
DB 167 TKHKWETAHEAQBWRAYLEGTCTVWMLRRYLENGKETLQADPTKTHMTHAVSDHEATLR 226
QY 181 CWALGFYPAEITLTWQDGEBOQTDELVELTRPAG 215
DB 227 CWALSFYPAEITLTWQDGEDQTDDELVELTRPAG 261
RESULT 11
US-08-484-905-107
; Sequence 107, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-107

Query Match 72.6%; Score 852; DB 2; Length 274;
Best Local Similarity 73.5%; Pred. No. 1.3e-80;
Matches 158; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYWEWTTGYAKANAQTDRAVALRNLL 60

Db 23 IAVGYDDTQFVRFDSDAASRRMEPRAPWIEQSGPEYWDGETRNVKAHSQTHRVLDLSTLR 82
QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLRLRGYHQHAWDGKDYISLNEDLRSWTAADTVAQI 120
Db 83 GYYNQSEAGSHTLQRMYGCDVGSDFWFLRGYHQYAYDGKDYALKEDLSWTAADWAAQT 142
QY 121 TORFYPAEYAEFRYVLEGCLELLRRLYENGKETLQRADPPKHAHVHPIISDHEATLR 180
Db 143 TKHWEAAHVAEQWRAVLEGTCTVEWLRRLYENGKETLQRTDAPKTHMTHHVSDEATLR 202
QY 181 CWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAG 215
Db 203 CWALSFYPAEITLTWQDGEDQDTQDTLVEVTRPAG 237

RESULT 12
US-08-484-905-108
; Sequence 108, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-108

Query Match 72.6%; Score 852; DB 2; Length 274;
Best Local Similarity 73.5%; Pred. No. 1.3e-80;
Matches 158; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAIPRMEPRPWEQSGPQYEWNTGAKANAQTDRAVLRNLL 60

Db 23 IAVGYDDTQFVRFDSDAASRRMEPRAPWIEQSGPEYWDGETRNVKAHSQTHRVLDLSTLR 82
QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLRLRGYHQHAWDGKDYISLNEDLRSWTAADTVAQI 120
Db 83 GYYNQSEAGSHTLQRMYGCDVGSDFWFLRGYHQYAYDGKDYALKEDLSWTAADWAAQT 142
QY 121 TORFYPAEYAEFRYVLEGCLELLRRLYENGKETLQRADPPKHAHVHPIISDHEATLR 180
Db 143 TKHWEAAHVAEQWRAVLEGTCTVEWLRRLYENGKETLQRTDAPKTHMTHHVSDEATLR 202
QY 181 CWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAG 215
Db 203 CWALSFYPAEITLTWQDGEDQDTQDTLVEVTRPAG 237

RESULT 13
US-08-481-985B-107
; Sequence 107, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-107

Query Match 72.6%; Score 852; DB 3; Length 274;
Best Local Similarity 73.5%; Pred. No. 1.3e-80;
Matches 158; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAIPRMEPRPWEQSGPQYEWNTGAKANAQTDRAVLRNLL 60

Db 23 IAVGYDDTQFVRFDSDAASRRMEPRAPWIEQSGPEYWDGETRNVKAHSQTHRVLDLSTLR 82

QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLLRGVHQHAWDGKDYISLNEDLSRNTAADTVAAQI 120
Db 83 GYVYQSEAGSHTLQRMVYCDVGSDFLGRGYHAYDGDYIALKEDLSRNTAADMAAQT 142
QY 121 TORFYBAEYAEFRYLEGECELELLRRLRYLNGKETLQADPPKHAHVAHPISDHEATLR 180
Db 143 TKHWEAAHVAEQRAYLEGTCEVWLRLRYLNGKETLQRTDAPKTHMTHHVAHSDHEATLR 202
QY 181 CWALGFYPAEITLTWQDGEQOTQDTVELVETRPAG 215
Db 203 CWALSFYPAEITLTWQDGEDQDTQDTVELVETRPAG 237

RESULT 14
US-08-481-985B-108
; Sequence 108, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Casrouge, Armand
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-108

Query Match 72.6%; Score 852; DB 3; Length 274;
Best Local Similarity 73.5%; Pred. No. 1.3e-80;
Matches 158; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRPSDAAPRMEPRFWQEGPQYWEWTTGYAKANAQTRVALRNLL 60
Db 23 IAVGVDDTQFVRDSDAASRRMEPRAPWIEQEGPEYWDGETRNVKAHSQTHRVLDLSTLR 82
QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLLRGVHQHAWDGKDYISLNEDLSRNTAADTVAAQI 120

Db 83 GYVYQSEAGSHTLQRMVYCDVGSDFLGRGYHAYDGDYIALKEDLSRNTAADMAAQT 142
QY 121 TORFYBAEYAEFRYLEGECELELLRRLRYLNGKETLQADPPKHAHVAHPISDHEATLR 180
Db 143 TKHWEAAHVAEQRAYLEGTCEVWLRLRYLNGKETLQRTDAPKTHMTHHVAHSDHEATLR 202
QY 181 CWALGFYPAEITLTWQDGEQOTQDTVELVETRPAG 215
Db 203 CWALSFYPAEITLTWQDGEDQDTQDTVELVETRPAG 237

RESULT 15
US-08-370-476-107
; Sequence 107, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Casrouge, Armand
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-107

Query Match 72.6%; Score 852; DB 3; Length 274;
Best Local Similarity 73.5%; Pred. No. 1.3e-80;
Matches 158; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRPSDAAPRMEPRFWQEGPQYWEWTTGYAKANAQTRVALRNLL 60

Db	23	IAVGVDOTQFVRFDSDAASRRMEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVLDLSTLR	82
Qy	61	RYNQSEAGSHTLQMGNGCDMGDGLLRGYHQHAWDGKDYISLNEDLRSWTAADTVAQI	120
Db	83	GYNQSEAGSHTLQRMYGCDVGSQWFLRGYHQYAYDGYALXEDLRSWTAADMAAQT	142
Qy	121	TORFYAEAEFPTYLEGECELELRRYLENGKETLQADPPKAVAHHPISDHEATLR	180
Db	143	TXKWEAAHVABQWRAYLEGTCVEWLRYLENGKETLQRTDAPKTHMTHHAVSDHEATLR	202
Qy	181	CWALGFYPAEITLTWORDGEQOTQDELVEITRPAG	215
Db	203	CWALSFYPAEITLTWORDGEDQOTDELVEITRPAG	237

Search completed: June 18, 2004, 10:52:55
Job time : 23 secs

16	848	72.3	510	12	US-10-108-511-5	Sequence 5, Appli
17	832	70.9	371	12	US-10-210-172-156	Sequence 156, App
18	832	70.9	371	12	US-10-085-198-72	Sequence 72, Appli
19	828.5	70.6	389	12	US-10-108-511-2	Sequence 2, Appli
20	822	70.1	256	16	US-10-408-765A-247	Sequence 247, App
21	809	69.0	361	14	US-10-138-888-22	Sequence 22, Appl
22	792.5	67.6	452	12	US-10-210-172-152	Sequence 152, App
23	792.5	67.6	452	15	US-10-085-198-70	Sequence 70, Appl
24	766.5	65.3	389	15	US-10-085-198-70	Sequence 174, App
25	766	65.3	421	12	US-10-210-172-174	Sequence 32, Appl
26	766	65.3	421	15	US-10-138-588-32	Sequence 30, Appl
27	739	63.0	540	14	US-10-015-535-22	Sequence 22, Appl
28	733	62.5	541	14	US-10-015-535-28	Sequence 28, Appl
29	733	62.5	541	14	US-10-015-535-24	Sequence 24, Appl
30	733	62.5	542	14	US-10-015-535-26	Sequence 26, Appl
31	733	62.5	542	14	US-10-015-535-32	Sequence 32, Appl
32	733	62.5	542	14	US-10-015-535-34	Sequence 34, Appl
33	733	62.5	542	14	US-10-015-535-36	Sequence 36, Appl
34	728	62.1	542	14	US-10-264-049-4199	Sequence 4199, Ap
35	665	56.7	201	15	US-10-104-047-3648	Sequence 3648, Ap
36	624	53.2	284	15	US-09-858-580-21	Sequence 21, Appl
37	616	52.5	184	9	US-09-858-580-21	Sequence 21, Appl
38	616	52.5	184	10	US-09-847-172-21	Sequence 21, Appl
39	581	49.5	181	10	US-09-013-077A-13	Sequence 13, Appl
40	488	41.6	110	9	US-09-796-692-799	Sequence 799, App
41	488	41.6	110	9	US-09-796-692-799	Sequence 2139, Ap
42	488	41.6	110	14	US-10-040-862-799	Sequence 799, App
43	488	41.6	110	14	US-10-040-862-799	Sequence 2139, Ap
44	488	41.6	110	15	US-10-057-475B-799	Sequence 799, App
45	488	41.6	110	15	US-10-057-475B-2139	Sequence 2139, Ap

ALIGNMENTS

RESULT 1
US-09-819-371-6
; Sequence 6, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-6

Query Match 100.0%; Score 1173; DB 12; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-112;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	I AVEVDDTQFLRFDSDAAI PRMEPRPWPVQEGPOYWEWTTGYAKANAQTDRAVRNLL	60
DB	1	I AVEVDDTQFLRFDSDAAI PRMEPRPWPVQEGPOYWEWTTGYAKANAQTDRAVRNLL	60
QY	61	RRYNQSEAGSHTLQGMNGCDMGPDGRLRLRGYHQHAWDGKDYISLNEDLSRWTAAADTVAQI	120
DB	61	RRYNQSEAGSHTLQGMNGCDMGPDGRLRLRGYHQHAWDGKDYISLNEDLSRWTAAADTVAQI	120
QY	121	TQRFYEAEYAEFFTYLEGECLLELLRRYLENGKETLQRAADPPPKAHVAHPHSDHEATLR	180
DB	121	TQRFYEAEYAEFFTYLEGECLLELLRRYLENGKETLQRAADPPPKAHVAHPHSDHEATLR	180
QY	181	CWALGFYPAEITLTWQDGEQEQDTDELVEVTRPAG	215
DB	181	CWALGFYPAEITLTWQDGEQEQDTDELVEVTRPAG	215

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 10:51:58 ; Search time 67 Seconds
(without alignments)
905.932 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 1173
Sequence: 1 IAVEVDDTQFLRFDSDAAI.....QRDGEQQTDELVEVTRPAG 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTU5_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1173	100.0	215	12	US-09-819-371-6
2	1164	99.2	271	9	US-09-925-301-1431
3	1164	99.2	274	12	US-09-819-371-5
4	1164	99.2	362	12	US-10-257-021-82
5	1164	99.2	442	16	US-10-408-765A-1887
6	1157	98.6	362	12	US-09-819-371-4
7	869	74.1	326	12	US-10-380-880-7
8	859.5	73.3	379	12	US-10-210-172-160
9	859.5	73.3	379	15	US-10-093-463-78
10	852	72.6	364	15	US-10-093-463-80
11	849	72.4	365	14	US-10-138-888-23
12	848	72.3	280	14	US-10-073-300-6
13	848	72.3	280	16	US-10-075-257-6
14	848	72.3	415	14	US-10-073-300-5
15	848	72.3	415	16	US-10-075-257-5

Db 83 RRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDVGKDYISLNEDLRSWTAADTVAQI 142
Qy 121 TORFYAEAYAEPRFYLEGECELELLRRYLENGKETLQADPPKARVAHPISDHEATLR 180
Db 143 TORFYAEAYAEPRFYLEGECELELLRRYLENGKETLQADPPKARVAHPISDHEATLR 202
Qy 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 203 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 237

RESULT 4
US-10-257-021-82
; Sequence 82, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-021-82

Query Match 99.2%; Score 1164; DB 12; Length 362;
Best Local Similarity 99.5%; Pred. No. 2.5e-111; Indels 0; Gaps 0;
Matches 214; Conservative 1; Mismatches 0;
Qy 1 IAVEYVDDTQFLRFSDAAIPRMEPRPWEQEGPOYWEWTTGYAKANAQTDVALRNLL 60
Db 44 IAVEYVDDTQFLRFSDAAIPRMEPRPWEQEGPOYWEWTTGYAKANAQTDVALRNLL 103
Qy 61 RRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDVGKDYISLNEDLRSWTAADTVAQI 120
Db 104 RRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDVGKDYISLNEDLRSWTAADTVAQI 163
Qy 121 TORFYAEAYAEPRFYLEGECELELLRRYLENGKETLQADPPKARVAHPISDHEATLR 180
Db 164 TORFYAEAYAEPRFYLEGECELELLRRYLENGKETLQADPPKARVAHPISDHEATLR 223
Qy 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 224 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 258

RESULT 5
US-10-408-765A-1887
; Sequence 1887, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465

Db 83 RRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDVGKDYISLNEDLRSWTAADTVAQI 142
Qy 121 TORFYAEAYAEPRFYLEGECELELLRRYLENGKETLQADPPKARVAHPISDHEATLR 180
Db 143 TORFYAEAYAEPRFYLEGECELELLRRYLENGKETLQADPPKARVAHPISDHEATLR 202
Qy 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 203 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 237

RESULT 4
US-10-257-021-82
; Sequence 82, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-021-82

Query Match 99.2%; Score 1164; DB 9; Length 271;
Best Local Similarity 99.5%; Pred. No. 1.7e-111; Indels 0; Gaps 0;
Matches 214; Conservative 1; Mismatches 0;
Qy 1 IAVEYVDDTQFLRFSDAAIPRMEPRPWEQEGPOYWEWTTGYAKANAQTDVALRNLL 60
Db 50 IAVEYVDDTQFLRFSDAAIPRMEPRPWEQEGPOYWEWTTGYAKANAQTDVALRNLL 109
Qy 61 RRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDVGKDYISLNEDLRSWTAADTVAQI 120
Db 110 RRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDVGKDYISLNEDLRSWTAADTVAQI 169
Qy 121 TORFYAEAYAEPRFYLEGECELELLRRYLENGKETLQADPPKARVAHPISDHEATLR 180
Db 170 TORFYAEAYAEPRFYLEGECELELLRRYLENGKETLQADPPKARVAHPISDHEATLR 229
Qy 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 230 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 264

RESULT 5
US-10-408-765A-1887
; Sequence 1887, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408, 765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1887
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1887

Query Match 99.2%; Score 1164; DB 16; Length 442;
Best Local Similarity 99.5%; Pred. No. 3.3e-111;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 60
DB 44 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 103
QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 120
DB 104 RRYNQSEAGSHTLQGMNGCDMGDPGLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 163
QY 121 TORFYAEYAEFRTYLGECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
DB 164 TORFYAEYAEFRTYLGECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 223
QY 181 CWALGFYPAEITLTWQDGEQTDTELVEPTRAG 215
DB 224 CWALGFYPAEITLTWQDGEQTDTELVEPTRAG 258

RESULT 6

US-09-819-371-4

; Sequence 4, Application US/09819371

; Publication No. US2004005344A1

; GENERAL INFORMATION:

; APPLICANT: Egawa, Kohji

; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can

; FILE REFERENCE: 30815

; CURRENT APPLICATION NUMBER: US/09/819, 371

; CURRENT FILING DATE: 2002-03-15

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 362

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-819-371-4

Query Match 98.6%; Score 1157; DB 12; Length 362;
Best Local Similarity 99.1%; Pred. No. 1.3e-110;
Matches 213; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 60
DB 44 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 103
QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 120
DB 104 RRYNQSEAGSHTLQGMNGCDMGDPGLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 163
QY 121 TORFYAEYAEFRTYLGECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
DB 164 TORFYAEYAEFRTYLGECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 223
QY 181 CWALGFYPAEITLTWQDGEQTDTELVEPTRAG 215
DB 224 CWALGFYPAEITLTWQDGEQTDTELVEPTRAG 258

RESULT 7

US-10-380-880-7

; Sequence 7, Application US/10380880
; Publication No. US20040044182A1
; GENERAL INFORMATION:
; APPLICANT: Hunt, Joan S.
; APPLICANT: Morales, Pedro J.
; APPLICANT: Petroff, Margaret G.
; TITLE OF INVENTION: EXPRESSION, PREPARATION, USES, AND SEQUENCE OF RECOMBINANTLY-DERI
; FILE REFERENCE: Docket No. US20040044182A1 30772
; CURRENT APPLICATION NUMBER: US/10/380,880
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/232,761
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-880-7

Query Match 74.1%; Score 869; DB 12; Length 326;

Best Local Similarity 74.9%; Pred. No. 5.7e-81;

Matches 161; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 60
DB 54 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 113
QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 120
DB 114 RRYNQSEAGSHTLQGMNGCDMGDPGLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 173
QY 121 TORFYAEYAEFRTYLGECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
DB 174 TORFYAEYAEFRTYLGECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 233
QY 181 CWALGFYPAEITLTWQDGEQTDTELVEPTRAG 215
DB 234 CWALGFYPAEITLTWQDGEQTDTELVEPTRAG 268

RESULT 8

US-10-210-172-160

; Sequence 160, Application US/10210172

; Publication No. US20040043928A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Miller, Charles

; APPLICANT: Patturajan, Meera

; APPLICANT: Pena, Carol

; APPLICANT: Rieger, Daniel

; APPLICANT: Shimkets, Richard

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Li, Li

; APPLICANT: Ji, Weizhen

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Casman, Stacie

; APPLICANT: Voss, Edward

; APPLICANT: Boldog, Ferenc

; APPLICANT: Gorman, Linda

; APPLICANT: Leite, Mario

; APPLICANT: Vernet, Corine

; APPLICANT: Anderson, David

; APPLICANT: Guo, Xiaojia

; APPLICANT: Zhong, Mei

; APPLICANT: Gerlach, Valerie

; APPLICANT: Hjal, Tord

; APPLICANT: Rastelli, Luca

; APPLICANT: Spytek, Kimberly

; APPLICANT: Edinger, Shalomit

; APPLICANT: Ellerman, Karen

; APPLICANT: Malyankar, Uriel


```

; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 160
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-160

Query Match 73.3%; Score 859.5; DB 12; Length 379;
Best Local Similarity 73.9%; Pred. No. 6.7e-80;
Matches 161; Conservative 19; Mismatches 35; Indels 3; Gaps 1;

QY 1 IAVEYDDTQFLRFDSDAIPRMEPRVWVEQSGPYWTTGAYAKANAQTRVALRNLL 60
DB 47 IANGYVDDTQFLRFDSDAIPRMEPRVWVEQSGPYWTTGAYAKANAQTRVALRNLL 106
QY 61 RRVNQESEA--GSHTLQGNKCDMGDPGRLLRGYHOHAWDGDYISLNEDLSWTAADTV 117
DB 107 GYTNQSGVGPQSGHTLQWMIQCDLGDGDRLLRGYEQYAYDGDYIALNEDLSWTAADTA 166
QY 118 AQITQRYFAEYAEFFRTYLEGECLELLRRYLENGKETLQADPPKAAVHHPISDHBA 177
DB 167 AQISKKCEANVAEQRRAYLEGTCTVEWHLRYLENGKEMQLQADPPKTHVTHHPVFDYEA 226
QY 178 TLRWALGFYPAEITITWQDGEEOQDTELVEVTRAG 215
DB 227 TLRWALGFYPAEITITWQDGEEOQDTELVEVTRAG 264

RESULT 9
US-10-093-463-78
; Sequence 78, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Pena, Carol
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gorman, Linda
; APPLICANT: Spaderna, Steven
; APPLICANT: Voss, Edward
; APPLICANT: Malyankar, Uriel
; APPLICANT: Anderson, David
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; TITLE OF INVENTION: No. US20030208039A1 Antibodies that Bind to Antigenic Polypeptide
; TITLE OF INVENTION: Encoding the Antigens, and Methods of Use.
; FILE REFERENCE: 21402-290A (Cura 590AT)
; CURRENT APPLICATION NUMBER: US/10/093,463
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/283,675
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,101
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 78
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-78

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Query Match 73.3%; Score 859.5; DB 15; Length 379;
Best Local Similarity 73.9%; Pred. No. 6.7e-80;
Matches 161; Conservative 19; Mismatches 35; Indels 3; Gaps 1;

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Db	47	I	A	M	Y	V	D	D	T	Q	F	V	R	F	S	D	S	A	C	P	M	E	P	R	A	P	W	E	Q	E	G	P	E	Y	W	E	E	T	R	T	K	A	H	A	O	T	D	S	M	T	Q	T	L	R	106				
Qy	61	R	R	N	O	S	E	A	-	-	G	S	H	T	L	Q	M	N	G	C	D	M	P	G	D	R	L	L	G	R	Y	G	H	A	W	G	K	O	V	I	S	N	E	D	L	R	S	W	T	A	D	T	V	117					
Db	107	G	Y	N	O	S	E	G	V	G	P	S	H	T	L	Q	M	I	G	D	L	S	D	R	L	G	R	Y	G	V	A	I	D	G	K	O	V	I	A	N	E	D	L	R	S	W	T	A	D	T	A	166							
Qy	118	A	Q	I	T	Q	F	E	A	E	Y	A	B	E	F	T	L	E	G	E	C	L	E	L	L	R	Y	L	E	N	G	K	E	T	L	Q	R	A	D	P	P	K	A	H	A	H	P	I	S	D	E	A	177						
Db	167	A	Q	I	S	K	E	C	E	A	N	V	E	O	R	R	A	L	L	E	G	T	C	V	E	W	L	H	R	Y	L	E	N	G	K	E	M	L	Q	R	A	D	P	P	K	T	H	T	H	P	V	P	D	E	A	226			
Qy	178	T	L	R	C	W	A	L	G	P	P	A	E	I	L	T	W	O	R	D	E	E	B	O	T	Q	T	E	L	V	E	T	R	P	A	G	215																						
Db	227	T	L	R	C	W	A	L	G	P	P	A	E	I	L	T	W	O	R	D	E	D	O	T	Q	V	E	L	V	E	T	R	P	A	G	264																							

RESULT 10

US-10-093-463-80
Sequence 80, Application US/10093463
Publication No. US20030208039A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Gusev, Vladimir
APPLICANT: Pochart, Pascal
APPLICANT: Zhong, Mei
APPLICANT: Rastelli, Luca
APPLICANT: Mezes, Peter
APPLICANT: Smithson, Glennnda
APPLICANT: Guo, Xiaojia
APPLICANT: Gerlach, Valerie
APPLICANT: Casman, Stacie
APPLICANT: Boldos, Ferenc
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan
APPLICANT: Tchernev, Velizar
APPLICANT: Gangolli, Esha
APPLICANT: Vernet, Corine
APPLICANT: Pena, Carol
APPLICANT: Burgess, Catherine
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly
APPLICANT: Gorman, Linda
APPLICANT: Spaderna, Steven
APPLICANT: Voss, Edward
APPLICANT: Malyankar, Uriel
APPLICANT: Anderson, David
APPLICANT: Patturajan, Meera
APPLICANT: Miller, Charles
APPLICANT: Taupier, Raymond J. Jr.
TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypeptides
TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.
FILE REFERENCE: 21402-290A (Cura 590AT)
CURRENT APPLICATION NUMBER: US/10/093,463
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/283,675
PRIOR FILING DATE: 2001-04-14
PRIOR APPLICATION NUMBER: 60/338,092
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/274,101
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/325,681
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/304,354
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/279,995
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/294,899
PRIOR FILING DATE: 2001-05-31

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; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-80

Query March 72.6%; Score 852; DB 15; Length 364;
Best Local Similarity 73.5%; Pred. No. 3.8e-79;
Matches 158; Conservative 23; Mismatches 34; Indels 0; Gaps 0

Qy 1 IAVEYVDVDTQFLRPDSDAALPRMEPRFPWVEQEGPQYWEWTGYAKANAQTDRAVALNLL 60
Db 47 IAVGVDDTFVRPDSVSUSPRMERRAPWVEQEGLEYWDQETRAKGAHQIVRVNIRILL 106
Qy 61 RRYNQSEAGSHITLQMMGNCMDGPPDRLLRGVHQHAWDGKQYISINEDLRSTADTVAQI 120
Db 107 RYTNQSEHGSHITIQKHGCDVGPDRLLRRRYEQFAYDGKDYIALNEDLHSWTAANTAAQI 166
Qy 121 TORVEAEVEAEERTYLEGCELLRRYLKNGKETIQRADPPKAAHVAHPISDEATLR 180
Db 167 SQHKWEADKYSQEVAYLEGKCMWLRRHLNGKETIQHADPPKAAHVTOHPISDEATLR 226
Qy 181 CWALGFYPAEITLTWQDGBEQTDQTELVEPRPAG 215
Db 227 CWALGLYPAEITLTWQDGEDQTDQTELVEPRPAG 261

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RESULT 11

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US-10-138-888-23
; Sequence 23, Application US/10138888
; Publication NO. US20030148972A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchinashi, Zenta
; Wolff, Roger K.
;
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;
; NUMBER OF SEQUENCES: 79
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brian M. Poissant
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-095-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..365
; OTHER INFORMATION: /note= "Human Major Histocompatibility
; Class I (MHC) protein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-138-888-23

Query Match 72.4%; Score 849; DB 14; Length 365;
Best Local Similarity 73.5%; Pred. No. 7.7e-79;
Matches 158; Conservative 17; Mismatches 40; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFSDAAIPRMEPEPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNL 60
Db 47 IAVGVYDDTQFVRFDSDAASQRMPEAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLR 106
QY 61 RRYNQSAGSHTLQGMNGCDMGDPGRLRGYHQHAWDGKDYISLNEDLSRWTAAQTVAQI 120
Db 107 GYNNQSEAGSHTLQMMFGDVGSDWFLRGYHQYAYDGKDYIALKEDLSRWTAAQMAAQT 166
QY 121 TORFYEAEYAEFFRTYLEGECLELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
Db 167 TKHKEAAHVAEQRLAYLGTCVWELRRYLENGKETLQRTDAPKTHMTHAVSDHEATLR 226
QY 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 227 CWALSFYPAEITLTWQDGEDQTDTELVTETPAG 261

RESULT 12
US-10-073-300-6
; Sequence 6, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT

; ORGANISM: Homo sapiens
Query Match 72.3%; Score 848; DB 16; Length 280;
Best Local Similarity 73.0%; Pred. No. 6.8e-79;
Matches 157; Conservative 18; Mismatches 40; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFSDAAIPRMEPEPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNL 60
Db 23 IAVGVYDDTQFVRFDSDAASQRMPEAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLR 82
QY 61 RRYNQSAGSHTLQGMNGCDMGDPGRLRGYHQHAWDGKDYISLNEDLSRWTAAQTVAQI 120
Db 83 GYNNQSEAGSHTVQRMYGCDVGSDWFLRGYHQYAYDGKDYIALKEDLSRWTAAQMAAQT 142
QY 121 TORFYEAEYAEFFRTYLEGECLELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
Db 143 TKHKEAAHVAEQRLAYLGTCVWELRRYLENGKETLQRTDAPKTHMTHAVSDHEATLR 202
QY 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 203 CWALSFYPAEITLTWQDGEDQTDTELVTETPAG 237

RESULT 13
US-10-075-257-6
; Sequence 6, Application US/10075257
; Publication No. US20040086960A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES,
; FILE REFERENCE: 02/23338
; CURRENT APPLICATION NUMBER: US/10/075,257
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-075-257-6

Query Match 72.3%; Score 848; DB 16; Length 280;
Best Local Similarity 73.0%; Pred. No. 6.8e-79;
Matches 157; Conservative 18; Mismatches 40; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFSDAAIPRMEPEPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNL 60
Db 23 IAVGVYDDTQFVRFDSDAASQRMPEAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLR 82
QY 61 RRYNQSAGSHTLQGMNGCDMGDPGRLRGYHQHAWDGKDYISLNEDLSRWTAAQTVAQI 120
Db 83 GYNNQSEAGSHTVQRMYGCDVGSDWFLRGYHQYAYDGKDYIALKEDLSRWTAAQMAAQT 142
QY 121 TORFYEAEYAEFFRTYLEGECLELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
Db 143 TKHKEAAHVAEQRLAYLGTCVWELRRYLENGKETLQRTDAPKTHMTHAVSDHEATLR 202
QY 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 203 CWALSFYPAEITLTWQDGEDQTDTELVTETPAG 237

RESULT 14
US-10-073-300-5
; Sequence 5, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
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Search completed: June 18, 2004, 10:57:38
Job time : 68 secs

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; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human beta2 microglobulin linked to MHC class I heavy chain
US-10-073-300-5

Query Match      72.3%; Score 848; DB 14; Length 415;
Best Local Similarity 73.0%; Pred. No. 1.2e-78;
Matches 157; Conservative 18; Mismatches 40; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPEPWVEQEGPOYEWTTGYAKANAQTDRAVALRNLL 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 138 IAVGYVDDTQFVRPDSDAASQRMPEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLR 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 RRYNQSEAGSHTLQGNMGCDMGDGRLLRGYHGHAWDKDYISINEDLRSWTAADTVAQI 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 198 GYINQSEAGSHTVQRYMGCDVGSDFRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQT 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 TQRYEAEYAEFRFYLEGECLELRLRYLNGKETLQRADPPKHAHVHHPISDHEATLR 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 258 TKHKWEAAHVAEQRLAYLEGTCEVWLRRLRYLNGKETLQRTDAPKTHHTHVAHSDHEATLR 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 CWALGFYPAEITLTWQDDGEEQTDTELVEVPAG 215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 318 CWALSFPAEITLTWQDDGEDQTDTELVEVPAG 352
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-10-075-257-5
; Sequence 5, Application US/10075257
; Publication No. US2004008690A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
; FILE REFERENCE: 02/23338
; CURRENT APPLICATION NUMBER: US/10/075,257
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human beta2 microglobulin linked to MHC class I heavy chain
US-10-075-257-5

Query Match      72.3%; Score 848; DB 16; Length 415;
Best Local Similarity 73.0%; Pred. No. 1.2e-78;
Matches 157; Conservative 18; Mismatches 40; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPEPWVEQEGPOYEWTTGYAKANAQTDRAVALRNLL 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 138 IAVGYVDDTQFVRPDSDAASQRMPEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLR 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 RRYNQSEAGSHTLQGNMGCDMGDGRLLRGYHGHAWDKDYISINEDLRSWTAADTVAQI 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 198 GYINQSEAGSHTVQRYMGCDVGSDFRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQT 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 TQRYEAEYAEFRFYLEGECLELRLRYLNGKETLQRADPPKHAHVHHPISDHEATLR 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 258 TKHKWEAAHVAEQRLAYLEGTCEVWLRRLRYLNGKETLQRTDAPKTHHTHVAHSDHEATLR 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 CWALGFYPAEITLTWQDDGEEQTDTELVEVPAG 215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 318 CWALSFPAEITLTWQDDGEDQTDTELVEVPAG 352
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 07:47:45 ; Search time 3729 Seconds
(without alignments)
2498.995 Million cell updates/sec

US-09-819-371-6

Title: 1173
Sequence: 1 IAVEYVDDTQFLRDSDAI.....ORDGEBQTDTELVTETRPAG 215

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -SPART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DICALIGN=200 -THE SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09819371@cgn_1_1_3731@runat_16062004_170027_7846 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

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2: gb_htg.*
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11: gb_sts.*
12: gb_sv.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mtl.*
20: em_on.*
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22: em_ov.*
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29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rdt.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1164	99.2	645	6	E63815	E63815 Cancer cell
2	1164	99.2	645	6	AX552557	AX552557 Sequence
3	1164	99.2	645	6	BD187423	BD187423 Cancer pr
4	1164	99.2	822	6	E63814	E63814 Cancer cell
5	1164	99.2	822	6	AX552556	AX552556 Sequence
6	1164	99.2	822	6	BD187422	BD187422 Cancer pr
7	1164	99.2	972	9	AY216682	AY216682 Homo sapi
8	1164	99.2	972	9	AY221102	AY221102 Homo sapi
9	1164	99.2	1041	9	AY2533269	AY2533269 Homo sapi
10	1164	99.2	1041	9	AY2533270	AY2533270 Homo sapi
11	1164	99.2	1089	6	E63813	E63813 Cancer cell
12	1164	99.2	1089	6	AX552555	AX552555 Sequence
13	1164	99.2	1089	6	BD187421	BD187421 Cancer pr
14	1164	99.2	1167	9	BC062991	BC062991 Homo sapi
15	1164	99.2	1523	9	BC009260	BC009260 Homo sapi
16	1164	99.2	2598	9	AK096962	AK096962 Homo sapi
17	1164	99.2	2598	9	CHPVHCAD	M30685 Pan Troglod
18	1100	93.8	1056	9	MMHLAFHOM	Z21819 M.mulatta H
19	993.5	84.7	4316	6	AX302563	AX302563 Sequence
20	993.5	84.7	4316	6	AX411069	AX411069 Sequence
21	993.5	84.7	4316	6	AX795667	AX795667 Sequence
22	993.5	84.7	4316	6	AX822118	AX822118 Sequence
23	993.5	84.7	4316	6	AX825758	AX825758 Sequence
24	993.5	84.7	4316	9	HSILAF	X17093 Human HLA-F
25	992	84.6	5161	9	AF338355	AF338355 Pan trogl
26	992	84.6	250601	9	AB100087	AB100087 Pan trogl
27	987	84.1	6367	9	AF523294	AF523294 Homo sapi
28	987	84.1	130934	9	EX005428	EX005428 Human DNA
29	982.5	83.8	6530	9	AB080802	AB080802 Homo sapi
30	982.5	83.8	6993	9	AF523285	AF523285 Homo sapi
31	982.5	83.8	6993	9	AF523286	AF523286 Homo sapi
32	982.5	83.8	6993	9	AF523289	AF523289 Homo sapi
33	982.5	83.8	6993	9	AF523290	AF523290 Homo sapi
34	982.5	83.8	6993	9	AF523293	AF523293 Homo sapi
35	982.5	83.8	6993	9	AF523296	AF523296 Homo sapi
36	982.5	83.8	6993	9	AF523297	AF523297 Homo sapi
37	982.5	83.8	6998	9	AF523284	AF523284 Homo sapi
38	982.5	83.8	6998	9	AF523291	AF523291 Homo sapi
39	982.5	83.8	6998	9	AF523292	AF523292 Homo sapi
40	982.5	83.8	7000	9	AF523292	AF523292 Homo sapi
41	982.5	83.8	7000	9	AF523288	AF523288 Homo sapi
42	982.5	83.8	7000	9	AF523295	AF523295 Homo sapi
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44	982.5	83.8	41617	9	AC004213	AC004213 Homo sapi
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ALIGNMENTS

RESULT 1

E63815
LOCUS
DEFINITION
Cancer cell-specific HLA-F antigen and method for diagnosing cancer
using the same.
E63815
ACCESSION
E63815.1 GI:22553653
VERSION
JP 2001095584-A/3.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 645)
Egawa,K.
Cancer cell-specific HLA-F antigen and method for diagnosing cancer
using the same
Patent: JP 2001095584-A 3 10-APR-2001;
KOJI EGAWA,KK MEDINET,KEIJI KIMURA
OS Homo sapiens (human)
COMMENT
PN JP 2001095584-A/3
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279566
PI KOJI EGAWA
PC
C12N15/09,C07K14/82,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/PC
C12N15/09,C07K14/82,C12N1/15,C12N1/19,C12N1/21,C12R1:19),(C12P21/02,PC
G01N33/53,G01N33/574,G01N33/68)/(C12N1/21,C12R1:19),(C12P21/02,PC
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PC C12N15/00,C12N5/00
CC
PH Key Location/Qualifiers.
1..645 Location/Qualifiers.
/organism="Homo sapiens"
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1..645
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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ORIGIN
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Pred. No.: 3,64e-106 Length: 645
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
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DB 61 CCGAGGATGGAGCGCGGAGCGCGTGGTGGAGCAAGAGCGCGCGGATTTGGAGTGG 120
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60
DB 121 ACCACAGGTACGCCAAGGCCAACGACAGACTGACCGAGTGCGCTGAGGAACCTGCTC 180
QY 61 ArgArgTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 181 CGCCGCTACACACAGCGAGGCTGGTCTTCACACCTCCAGGGAATGAATGGCTGCAC 240
QY 81 MetGlyProAspGlyArgLeuLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 100
DB 301 TACATCTCCCTGAACAGGACCTCGCTCCTCGACCGCGCGACACCGCTGCATC 360
QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluPheArgThrTyrLeuGluGly 140

361 ACCCAGCGCTTCTATGAGGACAGGAATATGCAGAGAGTTTCAGGACCTACCTGGAGGGC 420
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 421 GAGTGCCTGGAGTTGCTCCGACATATCTTGGAGATGGGAGGAGACGCTACAGCGGCA 480
QY 161 AspProProLysAlaHisValAlaHisHisProLysSerAspHisGluAlaThrLeuArg 180
DB 481 GATCCTCCAAAGGCACACGTTGGCCACCACCCCTCTCTGACCATGAGGCCACCTTAGG 540
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 200
DB 541 TGTGGGCCCTTGGCTTCTACCTTGGGAGATACGCTGACCTGGGACGCGGATGGGAG 600
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
DB 601 GAACAGACCCAGGACACAGAGCTTGTGGACACGAGGCTGCAGGG 645
RESULT 2
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LOCUS
DEFINITION
Sequence 3 from Patent EP1245675.
AX552557
ACCESSION
AX552557.1 GI:25896577
VERSION
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Egawa,K.
Cancer cell-specific hla-f antigen and a diagnostic method of
cancer by using thereof
Patent: EP 1245675-A 3 02-OCT-2002;
Egawa, Kohji (JP); Medinet Co., Ltd. (JP); Kimura, Yoshiji (JP)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 3,64e-106 Length: 645
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 6 Gaps: 0
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DB 61 CCGAGGATGGAGCGCGGAGCGCGTGGTGGAGCAAGAGCGCGCGGATTTGGAGTGG 120
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60
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QY 61 ArgArgTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 181 CGCCGCTACACACAGCGAGGCTGGTCTTCACACCTCCAGGGAATGAATGGCTGCAC 240
QY 81 MetGlyProAspGlyArgLeuLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 100
DB 241 ATGGGGCCCGAGCGCGCTCCTCGGGGTATCACCAGCACGCGGTACGCGGCAAGAT 300

QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
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QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 361 ACCAGCGCTTCTATGAGCAGAGGAATATGAGAGGAGTTCAGGACCTTACCTGAGGCGC 420
QY 141 GluCysLeuGluLeuLeuArgTyrTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 421 GAGTGCTCGAGTGTCTCCGAGATCTTGGAGATGGAGAGACGCTACAGCGCGCA 480
QY 161 AspProPLeuAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 481 GATCTCTCCAAAGGCACACGCTTGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 540
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 541 TGTCTGGCCCTGGGCTTCTACCTCGGAGATCACCTGAGGAGTTCAGGCGGATGGGGAG 600
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCTGCAGGG 645
RESULT 3
LOCUS BD187423 645 bp DNA linear PAT 17-JUL-2003
DEFINITION Cancer prophylactic/treatment agent.
ACCESSION BD187423
VERSION BD187423.1 GI:32997162
KEYWORDS JP 2003012544-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 645)
AUTHORS Egawa,K.
TITLE Cancer prophylactic/treatment agent.
JOURNAL Patent: JP 2003012544-A 3 15-JAN-2003;
K EGAWA et al
COMMENT OS human
PN JP 2003012544-A/3
PD 15-JAN-2003
PF 27-MAR-2002 JP 2002088991
PI Koji egawa
CC
FH Key Location/Qualifiers.
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/mol_type="genomic DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 3.64e-106 Length: 645
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: Gaps: 0
US-09-819-371-6 (1-215) x BD187423 (1-645)
QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
Db 1 ATCCCGCTGGAGTACGTAGACGACACGCAATCTCTCGGTTCTGACAGCGCGCGGAT 60
QY 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 61 CCGAGGATGAGCCGCGGAGCCCTGGGTGGAGCAAGAGGGCGCGAGTATGGAGTGG 120
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60

Db 121 ACCACAGGTACGCCAAGGCCAACGCACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 180
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 181 GCGCCCTACAAACAGACGAGGCTGGGTCTCACACCTCCAGGAATGATGGCTGGCAC 240
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Db 241 ATGGGGCCCGACGAGCGCTCTCTCGCGGGTATCACACGACGCGGTACGACGCAAGGAT 300
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 301 TACATCTCCCTGACGAGACCTGGCTCTCTGGACCGCGCGGACACCGTGGCTCAGATC 360
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 361 ACCAGCGCTTCTATGAGCAGAGGAATATGAGAGGAGTTCAGGACCTTACCTGAGGCGC 420
QY 141 GluCysLeuGluLeuLeuArgTyrTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 421 GAGTGCTCGAGTGTCTCCGAGATCTTGGAGATGGAGAGACGCTACAGCGCGCA 480
QY 161 AspProPLeuAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 481 GATCTCTCCAAAGGCACACGCTTGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 540
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 541 TGTCTGGCCCTGGGCTTCTACCTCGGAGATCACCTGAGGAGTTCAGGCGGATGGGGAG 600
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCTGCAGGG 645
RESULT 4
LOCUS E63814 822 bp DNA linear PAT 27-AUG-2002
DEFINITION Cancer cell-specific HLA-F antigen and method for diagnosing cancer using the same.
ACCESSION E63814
VERSION E63814.1 GI:22553652
KEYWORDS JP 2001095584-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 822)
AUTHORS Egawa,K.
TITLE Cancer cell-specific HLA-F antigen and method for diagnosing cancer using the same
JOURNAL Patent: JP 2001095584-A 2 10-APR-2001;
KOJI EGAWA,KK MEDINET,KIJI KIMURA
COMMENT OS Homo sapiens (human)
PN JP 2001095584-A/2
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279566
PI KOJI EGAWA
PC
C12N15/09,C07K14/82,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/PC
02,
PC
G01N33/53,G01N33/574,G01N33/68// (C12N1/21,C12R1:19), (C12P21/02,PC
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/mol_type="genomic DNA"
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FEATURES
source
ORIGIN

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Pred. No.: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 6 Gaps: 0

US-09-819-371-6 (1-215) x E63914 (1-822)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaIle 20
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QY 21 ProArgMetGluProArgGluProTropValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 127 CCGAGGATGGAGCCCGGAGCGCGTGGTGGAGAGGGCGCGCAGTATTGGGAGTGG 186
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 187 ACCACAGGTTACGCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 246
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 247 CGCGCGTACCAACACGAGCGAGGCTGCTCCCGGGTATCACCAGCAGCGGTACGACGGCAGGAT 306
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 307 ATGGGGCCCGACGAGCGCTCTCCGCGGTATCACCAGCAGCGGTACGACGGCAGGAT 366
QY 101 TyrIleSerLeuAsnGlnAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
DB 367 TACATCTCCCTGAACGAGGACCTCGCTCTCGAGCGCGGACACCGCTGGCTCAGATC 426
QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluPheArgThrTyrLeuGluGly 140
DB 427 ACCACGCGCTTCTATGAGGACAGGAAATATGACAGAGTTCAGGACCTACCTGGAGGGC 486
QY 141 GluCysLeuGluLeuLeuLeuArgTyrTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 487 GAGTGCCTCGAGTGTCTCCGAGATACTTGGAGAAATGGAGAGACGCTACAGCGCGCA 546
QY 161 AspProProlLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
DB 547 GATCCTCCAAAGGACACAGTTCGCCACCAACCCCATCTCTGACCATGAGGCCACCTGAGG 606
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
DB 607 TGTGGGCGCTGGGCTTCTACCTTCGGAGATCAGCTGACCTGGCAGCGGATGGGGAG 666

RESULT 5
AX52556 822 bp DNA linear PAT 27-NOV-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Egawa, K.
Cancer cell-specific hla-f antigen and a diagnostic method of
cancer by using thereof
Patent: EP 1245675-A 2 02-OCT-2002;
Egawa, Kohji (JP); Medinet Co., Ltd. (JP); Kimura, Yoshiji (JP)
Location/Qualifiers

US-09-819-371-6 (1-215) x AX52556 (1-822)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaIle 20
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QY 21 ProArgMetGluProArgGluProTropValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 127 CCGAGGATGGAGCCCGGAGCGCGTGGTGGAGAGGGCGCGCAGTATTGGGAGTGG 186
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 187 ACCACAGGTTACGCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 246
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 247 CGCGCGTACCAACACGAGCGAGGCTGCTCCCGGGTATCACCAGCAGCGGTACGACGGCAGGAT 306
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 307 ATGGGGCCCGACGAGCGCTCTCCGCGGTATCACCAGCAGCGGTACGACGGCAGGAT 366
QY 101 TyrIleSerLeuAsnGlnAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
DB 367 TACATCTCCCTGAACGAGGACCTCGCTCTCGAGCGCGGACACCGCTGGCTCAGATC 426
QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluPheArgThrTyrLeuGluGly 140
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QY 161 AspProProlLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
DB 547 GATCCTCCAAAGGACACAGTTCGCCACCAACCCCATCTCTGACCATGAGGCCACCTGAGG 606
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
DB 607 TGTGGGCGCTGGGCTTCTACCTTCGGAGATCAGCTGACCTGGCAGCGGATGGGGAG 666

RESULT 6
AX52556 822 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Egawa, K.
Cancer prophylactic/treatment agent.
Patent: EP 1245675-A 2 02-OCT-2002;
Egawa, Kohji (JP); Medinet Co., Ltd. (JP); Kimura, Yoshiji (JP)
Location/Qualifiers
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TITLE      Cancer prophylactic/treatment agent
JOURNAL    Patent: JP 2003012544-A 2 15-JAN-2003;
COMMENT    K EGAWA et al
           OS human
           PN JP 2003012544-A/2
           PD 15-JAN-2003
           PP 27-MAR-2002 JP 2002088991
           PI Koji egawa
           CC
           FH Key Location/Qualifiers.

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Pred. No.: 4.83e-106 Length: 822
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 6 Gaps: 0

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Db 127 CCGAGGATGGCGCGGGGCGCGTGGTGGAGCAGAGGGCGCGCAGTATTGGAGTGG 186
Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 187 ACCACAGGATACGCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 246
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Db 367 TACATCTCCCTGAACGAGACCTGCGCTCTGACCGCGGCGACACCGTGGCTCAGATC 426
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Db 547 GATCTCCAAAGGCACACGTTGGCCACCCACCCCATCTCTGACATGAGGCCACCTGAGG 606
Qy 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 607 TGTGGGCGCTGGGCTTCTACCTCGCGGAGATCACGCTGACCTGGCAGCGGATGGGAG 666
Qy 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 667 GAACAGACCCAGACACAGAGCTTGTGGAGACCGAGCGCTGCAGGG 711

RESULT 7
AY216682

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LOCUS      AY216682 972 bp mRNA linear PRI 10-FEB-2003
DEFINITION Homo sapiens nonclassical MHC class I antigen (HLA-F) mRNA,
            HLA-F*0101 variant allele, partial cds.
ACCESSION  AY216682
VERSION    AY216682.1 GI:28300437
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 972)
AUTHORS    He X., Xu, L., Liu, Y. and Zeng, Y.
TITLE      Nonclassical MHC class I HLA-F
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 972)
AUTHORS    He X., Xu, L., Liu, Y. and Zeng, Y.
TITLE      Direct Submission
JOURNAL    Submitted (10-JAN-2003) Key Laboratory of Ministry of Education for
            Tissue Transplantation and Immunology, Jinan University, Shipai,
            Guangzhou, Guangdong 510632, China
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ORIGIN
Alignment Scores:
Pred. No.: 5.87e-106 Length: 972
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Percent Similarity: 100.00% Conservative: 1
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Query Match: 99.23% Indels: 0
DB: 9 Gaps: 0

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Db 178 CCGAGGATGGAGCGCGGAGCGCGTGGTGGAGCAAGAGGGCGCGCAGTATTGGGAGTGG 237
Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 238 ACCACAGGATACGCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 297
Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 298 CGCGCTACCAACGACGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAATGGCTGGCAC 357
Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 358 ATGGGGCCCGACGAGCGCTCTCCGCGGATATCACAGCAGCGTACGACGCGCAAGGAT 417
Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120

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418 TACATCTCCCTGAACAGAGACCTGGCGCTCTGGACCCGGCGGACACCGTGGCTCAGATC 477
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121 ThrGlnArgPheTyxGluAlaGluGluTyxAlaGluGluPheArgThrTyxLeuGluGly 140
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478 ACCCAGCGCTTCTATGAGGAGAGAGATATGACAGAGGAGTTTCAAGACCTACCTGGAGGC 537
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141 GluCysLeuGluLeuLeuArgArgTyxLeuGluAlaGluGluGluGluGluGluGluGluGlu 160
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538 GAGTCCCTGGAGTGTCTCCGAGATCTTGGAGATGAGAGAGACCTACAGCGCGCA 597
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161 AspProPolyAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
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598 GATCTCTCCAAAGCACACGTTGGCCACACCCCTCTCTGACCATGAGGCCACCTGAGG 657
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181 CysTrpAlaLeuGluPheTyxProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 200
|||
658 TGCTGGGCGCTGGGCTTCTACCTCGGAGATCACTGACCTGCGACGGGATGGGGAG 717
|||
201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
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718 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAGGCTGCAGGG 762
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RESULT 8
AY221102 972 bp mRNA linear PRI 08-FEB-2003
LOCUS Homo sapiens MHC class I antigen (HLA-F) mRNA, partial cds.
DEFINITION
ACCESSION AY221102
VERSION AY221102.1 GI:28274639
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 972)
AUTHORS Liu,Y., Xu,L., Zeng,Y. and He,X.
TITLE A new polymorphism in non-classical MHC class I HLA-F
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 972)
AUTHORS Liu,Y., Xu,L., Zeng,Y. and He,X.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-2003) Key Laboratory of Ministry of Education for
Tissue Transplantation and Immunology, Jinan University, Shipai,
Guangzhou, Guangdong 510632, China
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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/note="non-classical; similar to HLA-F*0101"
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QRFYAEVYEFRTYLEGCLELLRRLRYLNGKETLORADPPKARVHHHPISDHEATL
RCWALGFPAETLTWQDGERQTDTELVEPTRPADGTFOKWAAVVPSGEEQRYTC
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variation
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/gene="HLA-F"
/note="compared to HLA-F*0101"
/replace="C"

ORIGIN
Alignment Scores: 5.87e-106 Length: 972
Pred. No.: 1164.00 Matches: 214
Score:

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Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 9 Gaps: 0
US-09-819-371-6 (1-215) x AY221102 (1-972)

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Db 118 ATCCCGCTGGATGCTAGACGACGACGATTCCTCGGCTTCGACAGCGACGCCGCGATT 177
QY 21 ProArgMetGluProArgGluProTrpValGluGluGluGluGluGluGluGluGlu 40
Db 178 CCGAGGATGAGCGCGCGGAGCGCTGGTGGTGGAGCAGAGGGGCGCGAGTATTGGGAGTGG 237
QY 41 ThrThrGlyTyxAlaValAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 238 ACCACAGGGTACCGGAAGGCCAACCGACAGACTGACCGAGTGGCCCTGAGGAACTGCTCT 297
QY 61 ArgArgTyxAsnGlnSerGluAlaGlySerHisThrLeuGlnGlnGlyMetAsnGlyCysAsp 80
Db 298 CGCGGCTACAACACAGAGCGAGGCTGGGTCTCACCCCTCCAGGGAATGAATGGCTCGGAC 357
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyxHisGlnHisAlaTrpAspGlyLysAsp 100
Db 358 ATGGGCGCCGACGACGCTCTCCCGGGGTATCACACGACCGCTGACGCGGACGACGAGAT 417
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 418 TACATCTCCCTGAACAGGACCTGCGCTCTGAGCGCGCGACACACCGCTGAGTCTCAGATC 477
QY 121 ThrGlnArgPheTyxGluAlaGluGluTyxAlaGluGluPheArgThrTyxLeuGluGly 140
Db 478 ACCCAGCGCTTCTATGAGGACGAGGATATGACAGAGGATTCAGGACCTACCTGGAGGGC 537
QY 141 GluCysLeuGluLeuLeuArgArgTyxLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
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QY 161 AspProPolyAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
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QY 181 CysTrpAlaLeuGluPheTyxProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 200
Db 658 TGCTGGGCGCTGGGCTTCTACCTCGGAGATCACCTGACCTGAGCGAGCGGATGGGGAG 717
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 718 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAGGCTGCAGGG 762

RESULT 9
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LOCUS Homo sapiens MHC class Ib antigen (HLA-F) mRNA, HLA-F*0101 variant
DEFINITION
1 allele, complete cds.
ACCESSION AY253269
VERSION AY253269.1 GI:29650890
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1041)
AUTHORS He,X., Liu,Y., Xu,L. and Zeng,Y.
TITLE Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 1041)
AUTHORS He,X., Liu,Y., Xu,L. and Zeng,Y.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-2003) Key Laboratory of Ministry of Education for
Tissue Transplantation and Immunology, Jinan University, Shipai,
Guangzhou, Guangdong 510632, China

```

QY	161	AspProProLysAlaHisValAlaHisHisProLysSerAspHisGluAlaThrLeuArg	180
Db	610	GATCCTCCAAAGGCACACGTTGGCCACCCCATCTCTGACCATGGCCACCTTGAGG	669
QY	181	CysTrpAlaLeuGlyPheTyProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu	200
Db	670	TGCTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGACGCGGATGGGAG	729
QY	201	GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	215
Db	730	GAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTCGAGGG	774
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
gene			
CDS			
Alignment Scores:			
Pred. No.:	6,36e-106	Length:	1041
Score:	1164.00	Matches:	214
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.53%	Mismatches:	0
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QY	21	ProArgMetGluProArgGluProValGluGlnGluGlyProGlnTyTrpGluTrp	40
Db	190	CCGAGATGAGCGCGGAGCGCTGGTGGTGGAGAGGGCGCCATATTTGGAGTGG	249
QY	41	ThrThrGlyTyAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu	60
Db	250	ACCACAGGTATCCCAAGCCCAACGACACAGATGACCGAGTGGCCCTGAGGAACCTGTC	309
QY	61	ArgArgTyAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp	80
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QY	81	MetGlyProAspGlyArgLeuLeuArgGlyTyTrpHisGlnHisAlaTrpAspGlyAsp	100
Db	370	ATGGGCGCGAGCGACGCTCTCCGCGGTATCACCAGCAGCGCTACGCGCAAGGAT	429
QY	101	TyrIleSerLeuAsnGlnAspLeuArgSerTrpThrAlaAlaAspThrValaGlnIle	120
Db	430	TACATCTCCCTGACAGGACCTTCGCTCTCCGCGCGGCGGACACCGTGGCTCAGATC	489
QY	121	ThrGlnArgPheTyGluAlaGluGluTyTrpAlaGluGluPheArgThrTyTrpLeuGluGly	140
Db	490	ACCCAGCGCTTCTATGAGGACAGAGATATGACAGGAGCTTCAGGACCTACCTGGAGGC	549
QY	141	GluCysLeuGluLeuLeuArgArgTyTrpLeuGluAsnGlyGlyGluThrLeuGlnArgAla	160
Db	550	GAGTGGCTGGAGTTGCTCCGACATATCTGGAGATGGAGAGAGACGCTACAGCGCA	609

Db	130	ATCGCCGTGGAGTACGTAGACGACGCAATTCCTCGGTTTCGACGACGCGCGGATT	189
Qy	21	ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr	40
Db	190	CCGAGGATGGAGCCCGCGGAGCCGTGGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGG	249
Qy	41	ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu	60
Db	250	ACCACAGGTTACGCCCAAGCCCAACGACAGACTGACGAGTGGCCCTGAGGAACCTGCTC	309
Qy	61	ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp	80
Db	310	CGCGCTCAACACGAGCGAGCGTGGGTCTCACACCTCTCCAGGGAATGAATGGCTGGAC	369
Qy	81	MetGlyProAspGlyValArgLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp	100
Db	370	ATGGGCGCCGACGCGCTCTCTCGCGGTATCACACGACGCGTACGAGCGCAAGAT	429
Qy	101	TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle	120
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Qy	121	ThrGlnArgPheTyrGluAlaGluGlnTyrAlaGluGlnPheArgThrTyrLeuGluGly	140
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Qy	141	GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla	160
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Qy	161	AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg	180
Db	610	GATCTCCAAAGGACACGTTGGCCACCCACCTCTTGACCATGAGCCACCTGAGG	669
Qy	181	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu	200
Db	670	TGCTGGCGCCCTGGCTTCTACCTCGCGAGATCACGCTGACCTGCGGAGCGGAGTGGG	729
Qy	201	GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	215
Db	730	GAACAGACCCGACACAGAGCTTGTGGAGACGAGCGCTGCAGGG	774
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LOCUS	Cancer cell-specific HLA-F antigen and method for diagnosing cancer		
DEFINITION	using the same.		
ACCESSION	E63813		
VERSION	E63813.1 GI:22553651		
KEYWORDS	JP 2001095584-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1089)		
JOURNAL	Cancer cell-specific HLA-F antigen and method for diagnosing cancer		
COMMENT	using the same		
	Patent: JP 2001095584-A 1 10-APR-2001;		
	KOJI EGAWA, KK MEDINET, KEIJI KIMURA		
	OS Homo sapiens (human)		
	PN JP 2001095584-A/1		
	PD 10-APR-2001		
	PF 30-SEP-1999 JP 1999279566		
	PI KOJI EGAWA		
	PC		
	C12N15/09, C07K14/82, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/ PC		
	02,		
	PC		
	G01N33/53, G01N33/574, G01N33/68// (C12N1/21, C12R1:19), (C12P21/02, PC		
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source		/db_xref="taxon:9606"
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Alignment Scores:		
Pred. No.:	6.7e-106	Length: 1089
Score:	1164.00	Matches: 214
Percent Similarity:	100.00%	Conservative: 1
Best Local Similarity:	99.53%	Mismatches: 0
Query Match:	99.23%	Indels: 0
DB:	6	Gaps: 0
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Qy	1	IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
Db	130	ATCGCGGTGGAGTACGTAGACGACGCAATTCCTCGGTTTCGACGACGCGCGGATT 189
Qy	21	ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr 40
Db	190	CCGAGGATGGAGCCCGCGGAGCCGTGGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGG 249
Qy	41	ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db	250	ACCACAGGTTACGCCCAAGCCCAACGACAGACTGACGAGTGGCCCTGAGGAACCTGCTC 309
Qy	61	ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db	310	CGCGCTCAACACGAGCGAGCGTGGGTCTCACACCTCTCCAGGGAATGAATGGCTGGAC 369
Qy	81	MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 100
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Qy	101	TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
Db	430	TACATCTCCCTGAACGAGGACCTGCGCTCTCGAGAGGATTCAGACGCGGACCGCTCAGATC 489
Qy	121	ThrGlnArgPheTyrGluAlaGluGlnTyrAlaGluGlnPheArgThrTyrLeuGluGly 140
Db	490	ACCCAGCGCTTCTATGAGCGAGAGGATTCAGAGGAGTTCAGACCTACCTGGAGGGC 549
Qy	141	GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db	550	GAGTGGCTGGAGTTGCTCCGACATCTTGGAGATGGGAAGAGACGCTACAGCGCGCA 609
Qy	161	AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
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Qy	181	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db	670	TGCTGGCGCCCTGGCTTCTACCTCGCGAGATCACGCTGACCTGCGGAGCGGAGTGGG 729
Qy	201	GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db	730	GAACAGACCCGACACAGAGCTTGTGGAGACGAGCGCTGCAGGG 774
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ACCESSION	AX552555	
VERSION	AX552555.1 GI:25896575	
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 6.7e-106 Length: 1089
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 6 Gaps: 0
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QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 190 CCGAGGATGGAGCGCGGGAGCGTGGTGGAGCAAGAGGGCGCGAGTATTGGAGTGG 249
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 250 ACCACAGGTTACGCCAAGGCCACGACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 309
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 310 CGCGGCTACACACAGAGCGAGGCTGCTCCCGGGGTATCCACAGCAGCGTACCGCGAGGAT 369
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DB 370 ATGGGGCCCGACGAGCGCTCTCCGCGGTATCCACAGCAGCGCTACGACGCAAGGAT 429
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAspThrValAlaGlnIle 120
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QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
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QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 550 GAGTGCTGGAGTTGCTCCGAGATACCTTGGAGAAATGGAGAGGAGAGCGCTACAGCGCGCA 609
QY 161 AspProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
DB 610 GATCCTCCAAAGGCACACGTTGGCCACCCCATCTCTGACCATGAGGCCACCTGAGG 669
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 200
DB 670 TGTGGGCGCTGGGCTTCTACCTCGGGAGATCACGCTGACCTGGCAGCGGATGGGGAG 729
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
DB 730 GAACAGACCCAGGACACAGAGCTTGGAGACCAGCGCTGCAGG 774
RESULT 13
BD187421
LOCUS
DEFINITION
ACCESSION
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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Egawa, K.
Cancer cell-specific hla-f antigen and a diagnostic method of
cancer by using thereof
Patent: EP 1245675-A 1 02-OCT-2002;
Egawa, Kohji (JP); Medinet Co., Ltd. (JP); Kimura, Yoshiji (JP)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Euteleostomi;
Eukaryota; Euthera; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1089)
Egawa, K.
Cancer prophylactic/treatment agent
K EGAWA et al
OS human
PN JP 2003012544-A/1
PD 15-JAN-2003
PF 27-MAR-2002 JP 2002088991
PI koji egawa
CC
FH
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1. .1089
/organism="Homo sapiens"
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 6.7e-106 Length: 1089
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 6 Gaps: 0
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QY 1 IleAlaValGluTyrValAspSerThrGlnPheLeuArgPheAspSerAspAlaAla 20
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QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 190 CCGAGGATGGAGCGCGGGAGCGTGGTGGAGCAAGAGGGCGCGAGTATTGGAGTGG 249
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 250 ACCACAGGTTACGCCAAGGCCACGACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 309
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
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QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
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DB 610 GATCCTCCAAAGGCACACGTTGGCCACCCCATCTCTGACCATGAGGCCACCTGAGG 669
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Db      670 TGCTGGGCGCTTCTACCTCGGAGATCAGCTGACCTGCAGCGGGATGGGAG 729
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DEFINITION      BC062991
ACCESSION      BC062991.1 GI:38649062
VERSION      MGC.
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Strausberg, R.L., Feingold, F.A., Grouse, L.H., Derge, J.G.,
      Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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      Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
      Saheer, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
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      Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smalusz, D.E.,
      Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
      Generation and initial analysis of more than 15,000 full-length
      human and mouse cDNA sequences
      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
      12477932
JOURNAL      2 (bases 1 to 1167)
PUBMED
AUTHORS      Strausberg, R.
REFERENCE
TITLE      Direct Submission
JOURNAL      Submitted (01-DEC-2003) National Institutes of Health, Mammalian
      Gene Collection (MGC), Cancer Genomics Office, National Cancer
      Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
      USA
REMARK
COMMENT      NIH-MGC Project URL: http://mgc.nci.nih.gov
      Contact: MGC help desk
      Email: cgabs-remail.nih.gov
      Tissue Procurement: Lou Staudt
      CDNA Library Preparation: Life Technologies, Inc.
      CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLN)
      DNA Sequencing by: National Institutes of Health Intramural
      Sequencing Center (NISC),
      Gaithersburg, Maryland;
      Web site: http://www.nisc.nih.gov/
      Contact: nisc.mgc@nih.gov
      Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
      Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
      Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P.,
      Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
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(cDNA clone IMAGE:4039990), partial cds.
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VERSION
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SOURCE
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ORGANISM
Homo sapiens
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Eumarkaria; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Straussberg,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Pahay,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Matra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1523)
Direct Submission
Straussberg,R.
Submitted (08-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 9, 2003 this sequence version replaced gi:14349361.
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DP/Gazdar
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
http://www.systemsbio.org
contact: anadan@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettner, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Location/Qualifiers

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 Job time : 3736 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 07:40:00 ; Search time 391 Seconds
(without alignments)
2335.966 Million cell updates/sec

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Perfect score: 1173
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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ALIGNMENTS

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XX PF 30-SEP-1999; 99JP-00279566.
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XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA K.

DR WPI: 2001-360493/38.
 DR P-PSDB; AAG64619.
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
 XX
 XX
 PS Claim 3; Page 9; 12pp; Japanese.
 XX
 CC This invention relates to a cancer cell specific HLA-F antigen. The
 CC invention includes DNA encoding the antigen, and a method for the
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
 CC used in a method to diagnose cancer, in which the protein is used to
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
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 CC of the invention
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 Pred. No.: 1,24e-110 Length: 645
 Score: 1164.00 Matches: 214
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.53% Mismatches: 0
 Query Match: 99.23% Indels: 0
 DB: 4 Gaps: 0
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 QY 161 AspProGlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
 Db 481 GATCTCTCAAAGGCACACGTTGCCACCCACCCCATCTCTGACCATGAGGCCACCTGAGG 540
 QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
 Db 541 TGTGGCGCCCTGGGCTCTACCTGGCGAGATCACGCTGACCTGGCAGCGGATGGGAG 600
 QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 Db 601 GNACAGCCAGGACACAGAGCTTGTGGAGACCCAGGCGCTGCAGG 645

RESULT 2
 AAC78195

ID AAC78195 standard; cDNA; 816 BP.
 AC AAC78195;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 XX Human cancer associated gene sequence SEQ ID NO:589.
 DE
 XX Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnerrary; immunomodulator;
 KW antidiabetic; antisthmatic; antirheumatic; antithyroid; antiviral;
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; organ rejection;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening; ss.
 XX
 XX Homo sapiens.
 OS WO2000055350-A1.
 XX
 PN 21-SEP-2000.
 XX
 PD 08-MAR-2000; 2000WO-US005882.
 XX
 PF 12-MAR-1999; 99US-0124270P.
 XX
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 FA Rosen CA, Ruben SM;
 XX WPI; 2000-587533/55.
 XX P-PSDB; AAB43986.
 DR Novel isolated nucleic acids comprising sequences encoding peptides
 DR useful for treating or diagnosing e.g. cancer.
 XX
 PS Claim 1; Page 1111-1112; 2352pp; English.
 XX
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given in
 CC AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnerrary; immunomodulator;
 CC antidiabetic; antisthmatic; antirheumatic; antithyroid; antiviral;
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 816 BP; 165 A; 258 C; 268 G; 125 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.67e-110 Length: 816
 Score: 1164.00 Matches: 214
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.53% Mismatches: 0
 Query Match: 99.23% Indels: 0
 DB: 3 Gaps: 0

US-09-819-371-6 (1-215) x AAC78195 (1-816)

QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaIle 20
DB 149 ATCGCGTGGAGTACGTAGACACGCAATTCCTGCGGTTCGACGAGCGCGCGATT 208
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 209 CCGAGGATGACCGCGGAGCGGTGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGG 268
QY 41 ThrThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 269 ACCACAGGTACGCCAAGCCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGTC 328
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 329 CCGCGCTACACAGACGAGCGGTGGTCTCACCCCTCCAGGGAATGATGGCTGCCAC 388
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 389 ATGGGCGCCGACGCGCTCTCCGCGGTATCACAGCACGCGTACGACGCAAGGAT 448
QY 101 TyrIleSerLeuAsnGlnAspLeuArgSerTrpThrAlaAspThrValAlaGlnIle 120
DB 449 TACATCTCCCTGAACGAGACCTGGCTCTCGACCGCGCGGACACCGTGGCTCAGATC 508
QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
DB 509 ACCACGCTTCTATGAGCAGAGGAATATGACAGGAGTTCAGGACCTACCTGGAGGCG 568
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 569 GAGTGCCTGGAGTGTCTCGCGATATCTTGGAGAAATGGAGAGACGCTACAGCGCGCA 628
QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
DB 629 GATCTCTCCAAAGCACACGTGGTCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 688
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
DB 689 TGTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGGCAGCGGATGGGAG 748
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
DB 749 GAACACACCCAGGACACAGAGCTTGTGGAGACCGAGCGCTGCAGG 793

RESULT 3

AAH45556

ID AAH45556 standard; DNA; 822 BP.

XX AC AAH45556;

XX DT 12-SEP-2001 (first entry)

XX DE Human cancer cell specific HLA-F antigen encoding DNA SEQ ID 2.

XX DE HLA-F antigen; cancer cell specific; human; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..822

XX FT /*tag= a

XX FT /partial

XX FT /product= "Cancer cell specific HLA-F antigen"

XX PN JP2001095584-A.

XX PD 10-APR-2001.

XX PF 30-SEP-1999; 99JP-00279566.

XX PF 30-SEP-1999; 99JP-00279566.

XX PR

XX (EGAW/) EGAWA K.
PA (MEDI-) MEDINET KK.
PA (KIMU/) KIMURA K.
XX WPI; 2001-360493/38.
DR P-PSDB; AAG64618.
XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.

XX Claim 3; Page 9; 12pp; Japanese.

XX This invention relates to a cancer cell specific HLA-F antigen. The

XX invention includes DNA encoding the antigen, and a method for the

XX preparation of the cancer cell specific HLA-F antigen. The antigen may be

XX used in a method to diagnose cancer, in which the protein is used to

XX detect anti-HLA-F antibodies in bodily fluids of the patient. The present

XX sequence represents DNA encoding the cancer cell-specific HLA-F antigen

XX of the invention

XX SQ Sequence 822 BP; 174 A; 250 C; 273 G; 125 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 1.69e-110 Length: 822

XX Score: 1164.00 Matches: 214

XX Percent Similarity: 100.00% Conservative: 1

XX Best Local Similarity: 99.53% Mismatches: 0

XX Query Match: 99.23% Indels: 0

XX DB: 4 Gaps: 0

XX US-09-819-371-6 (1-215) x AAH45556 (1-822)

QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaIle 20

DB 67 ATCGCGTGGAGTACGTAGACACGCAATTCCTGCGGTTCGACGAGCGCGCGATT 126

QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40

DB 127 CCGAGGATGAGCCCGCGGAGCCCTGGTGGAGCAAGGGGCGCGAGTATGGGAGTGG 186

QY 41 ThrThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60

DB 187 ACCACAGGATACGCCAAGGCCCAACGACAGACTACCGAGTGGCCCTGAGGAACCTGTC 246

QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80

DB 247 CGCGCTACAAACAGAGAGCGCTGGGTCTCACACCTCCAGGGAATGATGGCTGCAC 306

QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100

DB 307 ATGGGCGCCGACGCGCGCTCTCCGCGGTATCACACGACGCGGTACGACGCAAGGAT 366

QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120

DB 367 TACATCTCCCTGAACGAGAGACCTGGCTCTCGGACCGCGCGGACACCGTGGCTCAGATC 426

QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluPheArgThrTyrLeuGluGly 140

DB 427 ACCACAGCGCTTCTATGAGCGAGAGGAATATGACAGGAGTTCAGGACCTACCTGGAGGCG 486

QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160

DB 487 GAGTGCCTGGAGTGTCTCCGAGATACCTGGAGAATGGAAAGGAGACGCTACGCGCGCA 546

QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180

DB 547 GATCTCTCAAGAGCACAGTGTGCCCAACCCCATCTCTGACCATGAGGCCACCTGAGG 606

QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200

DB 607 TGTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGGCAGCGGATGGGAG 666

QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215

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Db      667 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAGGCTGCAGGG 711
RESULT 4
AAH45555
ID      AAH45555 standard; DNA; 1089 BP.
XX
AC      AAH45555;
XX
DT      12-SEP-2001 (first entry)
DE      Human cancer cell specific HLA-F antigen encoding DNA SEQ ID 1.
XX
DE      HLA-F antigen; cancer cell specific; human; ds.
XX
OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
FH      CDS      1..1089
FT      CDS      /*tag= a
FT      CDS      /product= "Cancer cell specific HLA-F antigen"
XX
XX      JP2001095584-A.
XX
PD      10-APR-2001.
XX
XX
PF      30-SEP-1999; 99JP-00279566.
XX
PR      30-SEP-1999; 99JP-00279566.
XX
XX      (EGAW/) EGAWA K.
PA      (MEDI-) MEDINET KK.
PA      (KIMU/) KIMURA K.
XX
DR      WPI: 2001-360493/38.
DR      P-PSDB; AAG64617.
XX
XX      Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
PT
XX
PS      Claim 3; Page 8-9; 12pp; Japanese.
XX
CC      This invention relates to a cancer cell specific HLA-F antigen. The
CC      invention includes DNA encoding the antigen, and a method for the
CC      preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC      used in a method to diagnose cancer, in which the protein is used to
CC      detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC      sequence represents DNA encoding the cancer cell-specific HLA-F antigen
CC      of the invention
XX
SQ      Sequence 1089 BP; 222 A; 327 C; 356 G; 184 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      Length:      1089
Score:          1164.00      Matches:      214
Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 99.53%      Mismatches: 0
Query Match:     99.23%      Indels:      0
DB:              4          Gaps:        0

us-09-819-371-6 (1-215) x AAH45555 (1-1089)
QY      1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
Db      130 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTGCACAGCGACGCGCGATT 189
QY      21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db      190 CCGAGGATGGACCGCGGAGCGCTGGGTGGAGCAAGAGGGCGCCGATATTGGGAGTGG 249
QY      41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db      250 ACCACAGGGTAGCCGAGGCCAAGCCACGACAGACTGACCGAGTGGCCCTGAGGACCTGCTC 309

61  ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
310  CGCCGCTACAAACAGAGCGAGGCTGGGTCTCAACCTCCAGGGGAATGATGGCTGCGAC 369
81  MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
370  ATGGGCGCGGACGAGCGCTCTCCGCGGTATCACCAGCAGCGCGTACGACGCGCAAGGAT 429
101  TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
430  TACATCTCCCTGAAACGAGGACCTGCTCTCTGACCGCGCGGACACCGTGGCTCAGATC 489
121  ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGluPheArgThrTyrLeuGluGly 140
490  ACCCAGCGCTTCTATGAGGCAGAGGAATATGCGAGAGTATGCGAGGAGTTCAGGACCTAC 549
141  GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
550  GAGTGCCTGGAGTTGCTCCGAGATACTTGGAGATGGGAGAGGACGCTACAGCCGCGCA 609
161  AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
610  GATCCTCCAAAGGCACACAGCTTGCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGG 669
181  CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
670  TGCTGGGCGCTGGGCTTCTACCTGCGGAGATACGCTGACCTGGCAGCGGGATGGGGAG 729
201  GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
730  GAACAGACCCAGGACACAGAGCTTGTGGAGACCAGGCTGCAGGG 774

RESULT 5
AAS90913
ID      AAS90913 standard; cDNA; 2034 BP.
XX
AC      AAS90913;
XX
DT      13-FEB-2002 (first entry)
XX
DE      DNA encoding novel human diagnostic protein #26717.
XX
KW      Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW      food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS      Homo sapiens.
XX
PN      WO200175067-A2.
XX
PD      11-OCT-2001.
XX
PF      30-MAR-2001; 2001WO-US008631.
XX
PR      31-MAR-2000; 2000US-00540217.
PR      23-AUG-2000; 2000US-00649167.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Drmanac RT, Liu C, Tang YT;
XX
DR      WPI; 2001-639362/73.
XX
DR      P-PSDB; ABG26726.
XX
PT      New isolated polynucleotide and encoded polypeptides, useful in
PT      diagnostics, forensics, gene mapping, identification of mutations
PT      responsible for genetic disorders or other traits and to assess
PT      biodiversity.
XX
PS      Claim 1; SEQ ID NO 26717; 103pp; English.
XX
CC      The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC      sequences. (I) is useful as hybridisation probes, polymerase chain
CC      reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

```

CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2034 BP; 545 A; 511 C; 628 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,26e-110 Length: 2034
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 5 Gaps: 0

US-09-819-371-6 (1-215) x AAS90913 (1-2034)

QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaIle 20
Db 1057 ATCGCGTGGAGTACGTAGACACACGCAATCTCTCGGTTCGACAGCGCCGCGATT 1116
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 1117 CCGAGATGGAGCGCGGAGCGCTGGTGGAGCAAGAGCGCGCGAGTTTGGAGTGG 1176
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 1177 ACCACAGGGTACGCCAAGCCACACGACACGACGAGCTGACGAGTGCCCTGAGGAACCTGCTC 1236
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 1237 CGCGCGTACAAACAGAGCGAGGCTGGGTCTCACCCCTCAGGGAATGAATGGCTGCGAC 1296
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 1297 ATGGGCGCCGACGAGCGCTCTCTCCGCGGTATCACAGCAGCGTACGACGCGAAGGAT 1356
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 1357 TACATCTCCCTGAACGAGGACCTGCGCTCTCTGGACCGCGCGACACCGTGGCTCAGATC 1416
QY 121 ThrGluArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 1417 ACCCAGCGCTCTATGAGGAGAGGAGATATGAGAGAGTTTACGACCTACCTGGAGGCG 1476
QY 141 GluCysLeuGluLeuLeuArgTyrGlyLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 1477 GAGTGCTCGAGTTGCTCCGACATCTTGAGAAATGGGAAGAGACGCTACAGCGCGCA 1536
QY 161 AspProProlysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Db 1537 GATCCTCCAAAGGCACAGTGGCCACACCCCATCTCTGACCATGAGGCCACCTTGAGG 1596
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 1597 TGCTGGCCCTTGGCTTCTACCTGCGAGATCACGCTGACCTGGCAGCGGGATGGGAG 1656
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215

Db 1657 GAACAGACCCAGACACAGAGCTTGTGGAGACACAGCGCTGCAGGG 1701

RESULT 6
AAS90740
ID AAS90740 standard; cDNA; 2037 BP.
XX
AC AAS90740;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #26544.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR P-PSDB; ABG26553.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
XX biodiversity.
PS Claim 1; SEQ ID NO 26544; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2037 BP; 547 A; 511 C; 629 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,26e-110 Length: 2037
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 5 Gaps: 0

US-09-819-371-6 (1-215) x AAS90740 (1-2037)

QY 67 ----- 67
 Db 1349 ACCCCCATCCGCGACCGACCGCGGTCCTCCCGAGTCTCCGGATCCGAATCTACCC 1408
 QY 67 ----- 67
 Db 1409 CGAGGCGGACCGCGCGCGAGACCTCCACCGCGGAGATCCAGCGCCCTTACCGAGG 1468
 QY 67 ----- 67
 Db 1469 TTCAATTTTTCAGTTTAGCCAAAATCCCGCGGTTGGCGGGGAGCGGCGGTAGCT 1528
 QY 68 ----- Ala-GlySerHisThrLeuGlnGlyMetAsnGlyCY 79
 Db 1529 GGGCGGGGCTACTCGGGGACCGGTAGGTCTCACACCTCCAGGGAATGAATGGCTG 1588
 QY 79 sAepMetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLY 99
 Db 1589 CGACATGGGCGCGACCGCGCGCTCTCCCGGGGTATCACCAGCACGGGTACAGCGCAA 1648
 QY 99 sAepTyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaG 119
 Db 1649 GGATTACATCTCCCTGAACGAGACCTGCGCTCCCTGGACCGCGCGGACACCGTGGCTCA 1708
 QY 119 nileThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuG 139
 Db 1709 GATCACCAGCGCTTCTATGAGCGAGAGAAATATGCAGAGGAGTTTCAGGACCTACCTGGA 1768
 QY 139 uGlyGluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnAR 159
 Db 1769 GGGCGAGTGCCTGGAGTTCTCCGCGAGTACTTGGAGAAATGGGAGGAGACCTACAGCG 1828
 QY 159 sAla----- 160
 Db 1829 CGCAGTACAGGGGCGCATGGGGCGCTTCCCTATCTCTGTAGATCTCTGGGATGGCT 1888
 QY 160 ----- 160
 Db 1889 CGCACAAAGTTGGAGGAAATGGGGCCCAATGCTAGGATATCGCCCTCCCTCTAGTCTGT 1948
 QY 160 ----- 160
 Db 1949 AGTAGGAAGAATCTTCTCGGTTTCGAGATCCGTTACAGAGAGTACTGTGAGAGTCGG 2008
 QY 160 ----- 160
 Db 2009 CCTGTCTCTGGACAAATTAAGGGATGAAATCTCTGAGGAATGAGGGAAGACAGTCC 2068
 QY 160 ----- 160
 Db 2069 CTGGAATACCGATCCCGGTCCTTTGAGCCCTCCAAACAGCCTTGGGCGCCGTGACTTT 2128
 QY 160 ----- 160
 Db 2129 TCTCTCAAGTTTGTCTGTGCTCCTACATCAATGTGTGGGGCTCTGATTCAGTCC 2188
 QY 160 ----- 160
 Db 2189 TGGGCTCCACTAGGTGAGGCGGACAGAGTCCCTGTCTCCCACTCAGAGACTCGAATTT 2248
 QY 160 ----- 160
 Db 2249 CCAAGGAATAGGAGATTTTCCAGGTGTCTGTGTCCAGGCTGGTCTGGGTCTGTGCT 2308
 QY 160 ----- 160
 Db 2309 CCTTCCCGACCCAGGTGTCTGTCTCCATTCAGGTGTGTTCACATGGGTGCTGGGG 2368
 QY 161 ----- AspProProlYSAL 165
 Db 2369 TTTCCCATGAGGAGTCAAAGTGCCTGAATTTTCTGACTTCTTCAGATCTCTCAAAGGC 2428

QY 165 aHisValAlaHisHieProIleSerAspHisGluAlaThrLeuArgCysTrpAlaLeuG 185
 Db 2429 ACAGTTGCCACACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCTGGG 2488
 QY 185 yPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGluGluGlnThrGlnAs 205
 Db 2489 CTTTCACTCCCTGGGAGATCACGCTGACCTGGCAGCGGATGGGGAGAAACAGACCCAGGA 2548
 QY 205 pThrGluLeuValGluThrArgProAlaGly 215
 Db 2549 CACAGAGCTTGTGGAGACCGGCTCGAGGG 2579
 RESULT 8
 ABN97218
 ID ABN97218 standard; DNA; 4316 BP.
 XX ABN97218;
 DT 13-AUG-2002 (first entry)
 DE Gene #3716 used to diagnose liver cancer.
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 OS Homo sapiens.
 XX WO200229103-A2.
 PN 11-APR-2002.
 PD 02-OCT-2001; 2001WO-US030589.
 PF 02-OCT-2000; 2000US-0237054P.
 PR (GENE-) GENE LOGIC INC.
 PA Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 PI WPI; 2002-426119/45.
 DR Diagnosing and detecting the progression of liver cancer, hepatocellular
 PT carcinoma or metastatic liver tumor in a patient, involves detecting the
 PT level of expression of two or more genes in a liver tissue sample.
 PS Claim 1; SEQ ID NO 3716; 298pp; English.
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumour in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 4316 BP; 1000 A; 1090 C; 1292 G; 934 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 5e-92 Length: 4316
 Score: 993.50 Matches: 214
 Percent Similarity: 43.79% Conservative: 1
 Best Local Similarity: 43.58% Mismatches: 0
 Query Match: 84.70% Indels: 276
 DB: 6 Gaps: 2

CC dinucleotides within the target nucleic acid. The molecules of the
 CC invention demonstrate cytosolic activity whilst the method may be useful
 CC for detecting and differentiating between colon cell proliferative
 CC disorders, including cancers such as colon adenoma and colon carcinoma.
 CC The PNA (peptide nucleic acid)-oligos are useful as probes for
 CC determining cytosine methylation state or single nucleotide
 CC polymorphisms. The current sequence is that of the genomic DNA region of
 CC the invention. This sequence is not shown within the specification but is
 CC taken from Wipoweb.

XX SQ Sequence 4316 BP; 1000 A; 1090 C; 1292 G; 934 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5e-92 Length: 4316
 Score: 993.50 Matches: 214
 Percent Similarity: 43.79% Conservative: 1
 Best Local Similarity: 43.58% Mismatches: 0
 Query Match: 84.70% Indels: 276
 DB: Gaps: 2

US-09-819-371-6 (1-215) x ADB53954 (1-4316)

QY 1 IleAlaValGluThrValAspThrGlnPheLeuArgPheAspSerAspAlaIle 20
 DB 1109 ATCCCGTGGAGTACGTAGACGACACGCAATCTCTGGGTTCGACAGCGCGCGGATT 1168
 QY 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTrpGluTrp 40
 DB 1169 CCGAGATGAGCGCGCGGAGCGTGGGTGACAAAGAGCGCGCGCAGTATTGGAGTGG 1228
 QY 41 ThrThrGlyTrpAlaValAlaAsnAlaGlnThrAspArgValAlaLeuArgGlnLeu 60
 DB 1229 ACCACAGGGTACCCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGAACCTGCTC 1288
 QY 61 ArgArgTrpAsnGlnSerGlu----- 67
 DB 1289 CGCGGTACACACAGACGAGGCTGGTGTAGTGAACCCGCGCGGCGCGAGGTACGACC 1348
 QY 67 ----- 67
 DB 1349 ACCCCCCATCCGACGAGACCGCGCGGTCCCGCGAGTCTCCGATCCGAAATCTACCC 1408
 QY 67 ----- 67
 DB 1409 CGAGGACGCGACCGCGCCAGACCTCCACCGGAGAGTCCCGAGGCGCTTTACCGAG 1468
 QY 67 ----- 67
 DB 1469 TTCATTTTCAGTTTAGGCCAAATCCCGCGGTTGGCGCGGAGCGCGGCGGTAGCT 1528
 QY 68 -----Ala-GlySerHisThrLeuGlnGlyMetAsnGlyCY 79
 DB 1529 GGGCGGGGTGACTGCGGGGACCGGTAGGGTCTTCACACCTCCAGGGAATGAATGGCTG 1588
 QY 79 sAspMetGlyProAspGlyArgLeuLeuArgGlyTrpHisGlnHisAlaTrpAspGlyLY 99
 DB 1589 CGCATGGGCGCGACGAGCGCTCTCCCGGGGTATCACACGACGCGTACGACGGCAA 1648
 QY 99 sAspTrpIleSerLeuAsnGlnAspLeuArgSerTrpThrAlaAlaAspThrValAlaGI 119
 DB 1649 GGATATATCTCCCTGAACAGGACCTCGCTCTCGACCGCGCGGACACCGTGGCTCA 1708
 QY 119 nIleThrGlnArgPheTrpGluAlaGluGluTrpAlaGluGluPheArgThrTrpLeuGI 139
 DB 1709 GATCACCAGCGCTTCTATGAGGACAGAGGATATGACAGAGGATTCAGGACCTACCTGGA 1768
 QY 139 uGlyGluCysLeuGluLeuLeuArgArgTrpLeuGluAsnGlyLysGluThrLeuGlnAr 159
 DB 1769 GGGCGAGTGCCTGGAGTGTCTCCGACATATTGGAGATGGGAAGAGACGCTACAGCG 1828
 QY 159 gAla----- 160
 DB 1829 CGCAGGTACAGGGGCGCATGGGCGCTTCCCTATCTCTGTAGATCTCTCTGGATGSCCT 1888

QY 160 ----- 160
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 DB 2009 CCCTGCTCTCTGGGACAAATTAAGGATGAATCTCTGAGGGAATGGAGGAAGACAGTCC 2068
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 QY 161 -----AspProProLysAl 165
 DB 2369 TTTCCATGAGAGTGCAGAGTCCGTAATTTCTGACTCTTCTCAGATCTCTCCAAAGGC 2428
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 DB 2429 ACAGTTGCCACACCCCACTCTGACCATAGGCCACCTGAGTGTCTGGGCTGG 2488
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 ID AAK86871 standard; DNA; 3098 BP.
 XX AC AAK86871;
 XX DT 07-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41683.
 XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX OS Homo sapiens.
 XX PN WO200157182-A2.
 XX XX 09-AUG-2001.
 XX PD 17-JAN-2001; 2001WO-US001354.
 XX PF 31-JAN-2000; 2000US-0179065P.
 XX PR 04-FEB-2000; 2000US-0180628P.
 XX PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-02559678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-483426/52.
 DR
 XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 PS Disclosure; SEQ ID NO 41683; 3071pp + Sequence Listing; English.
 XX
 XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

XX
PN WO200155320-A2

XX Isolated nucleic acid molecule encoding a reproductive system antigen is
 PT used in preventing, treating or ameliorating a medical condition.
 XX
 PS Disclosure; SEQ ID NO 6712; 1297bp + Sequence Listing; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention
 XX
 SQ Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,496-91 Length: 3098
 Score: 982.50 Matches: 213
 Percent Similarity: 43.58% Conservative: 1
 Best Local Similarity: 43.38% Mismatches: 1
 Query Match: 83.76% Indels: 277
 DB: 4 Gaps: 2

US-09-819-371-6 (1-215) x AAL04024 (1-3098)

QY	1	11eAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAlaAlaIle	20
DB	293	ATCGCGTGGAGTACGTAGCACACGCAATTCCTCGGTTTCGACAGCCGCCCGATT	352
QY	21	ProArgMetGluProArgGluProTrpValGluGlnGluGluProGlnTyrTrpGluTrp	40
DB	353	CCGAGGATGAGCGCGGAGCGGTGGTGGAGGAGAGCGCGCGCAGTATTGGAGTGG	412
QY	41	ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu	60
DB	413	ACCACAGGTACGCCAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC	472
QY	61	ArgArgTyrAsnGlnSerGluAla	68
DB	473	CGCCGCTACACGACGAGCGAGGC-TGGTGAGTGAACCCGCGCGGGCGCAGGTACGAC	531
QY	68	-----	68
DB	532	CACCCGCCCATCCGCCACGACCGCGGGTCCCTCAGAGTCTCCGGATCCGAAATCTACC	591
QY	68	-----	68
DB	592	CCGAGGACGGGACCGCGCCACAGCCCTCCGCCGGAGAGTCCCGAGGCGCTTTACCCA	651
QY	68	-----	68
DB	652	GGTTCATTTTCACTTTAGGCCAAATCCCGCGGGTTGGCGGGGAGGGCGGGGCTAG	711
QY	69	-----GlySerHisThrLeuGlnGlyMetAsnGly	78
DB	712	CTGGCGGGGCTGACTCGCGGGACCGGCTAGGGTCTCACACCCCTCCAGGGAATGAATGC	771
QY	79	CysAspMetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGly	98
DB	772	TGGCATATGGGGCCGACGACGCTCTCCCGGGTATCACACGACCGGTACGACGCG	831
QY	99	LysAspTyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAla	118
DB	832	AAGGATTACATCTCCCTGACGAGGACCTCTCCCGGGTATCACACGACCGGTACGACGCG	891
QY	119	GlnIleThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeu	138
DB	892	CAGATACCCAGCGCTTCTATGAGGACAGAGAAATATGACAGAGGTTCAGGACCTACCTG	951
QY	139	GluGlyGlyCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGln	158
DB	952	GAGGGCGAGTGCCTGGAGTTGCTCCGACAGATCTTGAGGAATGGGAGGAGGCTACAG	1011
QY	159	ArgAla-----	160

DB	1012	CGCGCAGGTACACAGGGGCCAATGGCGCCTTCCCTATCTCTCTGTAGATCTCTTGGGATGGC	1071
QY	160	-----	160
DB	1072	CTCCACACAGGTTGGGAGGAAGTGGACCAATGCTAGGATATCGCCCTCCCTCTAGTCC	1131
QY	160	-----	160
DB	1132	TGAGTAGGAAGAATCTTCTTGGCTTCGAGATCCGGTACCGAGAGTGACTGTGAGAGTC	1191
QY	160	-----	160
DB	1192	CGCCCTGCTCTCTGGGACAATTAAGGATGAATTTCTGAGGGAATGGAGGAAGACAGT	1251
QY	160	-----	160
DB	1252	CCCTGGAATACCGATCCGCGTCCCTTTTGAGGCCCTCCAAACAGCCTTGGGCCCGTGA	1311
QY	160	-----	160
DB	1312	TTTCTCTCAAGTTTGTCTCTGCTCCTCAGCTCACTCAATGTGTTGAGGCTCTGATCCAGTC	1371
QY	160	-----	160
DB	1372	CCTCGGCTCCACTTAGGTTCAGGCCCAGAAAGTCCCTGCTCCCTCCCTCAGAGACTCTAACT	1431
QY	160	-----	160
DB	1432	TTCAGGAATPAGGAGATTTTCCAGGTGTCTGTCTCAGGCTGTCTCTGGGTCTGTG	1491
QY	160	-----	160
DB	1492	CTCCCTTCCCAACCCAGGTGCTCTGCTCCATCTCAGTTGGTTCACATGGTGTCTGTG	1551
QY	161	-----AspProProlys	164
DB	1552	GGTTTCCCATGAGGAGTGCAAAGTGCCTGAATTTTCTGACTCTTCTCAGATCTCTCCAAAG	1611
QY	165	AlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArgCysTrpAlaLeu	184
DB	1612	GCACAGTTGGCCACCCCATCTGACCATGAGCCACCTTCTGAGTGTCTGGGCTGTG	1671
QY	185	GlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGluGlnThrGln	204
DB	1672	GGCTTCTACCTGCGGAGTCACTGACCTGGCGGAGTGGGAGGAGGAGGAGGAGGAG	1731
QY	205	AspThrGluLeuValGluThrArgProAlaGly	215
DB	1732	GACACAGAGCTTGTGGAGACCGAGGCTGCAGGG	1764
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XX	23-JAN-2002 (first entry)		
XX	Human nervous system related polynucleotide SEQ ID NO 10456.		
XX	Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;		
XX	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;		
XX	antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;		
XX	antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;		
XX	antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;		
XX	antiparasitic; cardiant; immune disorder; cardiovascular disorder;		
XX	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.		
XX	Homo sapiens.		
XX	OS		
XX	WO200159063-A2.		
XX			

PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001334.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249365P.
PR 17-NOV-2000; 2000US-0249397P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 01-DEC-2000; 2000US-0251160P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251866P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0255967P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
DR

XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 XX Disclosure; SEQ ID NO 10456; 1701pp + Sequence Listing; English.

XX The invention relates to novel genes (AB11004-AB21534) and proteins
 CC (AB114678-AB218001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,49e-91 Length: 3098
 Score: 982.50 Matches: 213
 Percent Similarity: 43.58% Conservative: 1
 Best Local Similarity: 43.38% Mismatches: 1
 Query Match: 83.76% Indels: 277
 DB: 5 Gaps: 2

US-09-819-371-6 (1-215) x AB118125 (1-3098)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaIle 20
 DB 293 ATCCGGTGGAGTACGTAGACACACGCAATCTCTGGGTTCGACAGCCGCCGAT 352
 QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 DB 353 CCGAGATGAGCCCGCGGAGCGTGGTGGAGAGAGAGCGCCAGTATTGGAGTGG 412
 QY 41 ThrThrGlyTyrAlaIysAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
 DB 413 ACCACAGGTACGCCAAGGCCAACGCACAGACTGACCCGAGTCCGCTGAGAACCTGCTC 472
 QY 61 ArgArgTyrAsnGlnSerGluAla 68
 DB 473 CGCCGCTACACACGAGCGAGGC-TGGTGTGTAACCCCGCGGGCGGCAGGTCAACGAC 531
 QY 68 68
 DB 532 CACCCGCCATCCGCCACGAGCCGCCGGTCCCTCAGAGTCTCCGATCCGAAATCTACC 591
 QY 68 68
 DB 592 CCGAGGACAGGGACCCGCCACAGCCCTCCACCCGGGAGAGTCCCGAGGCGCCTTTACCCA 651
 QY 68 68
 DB 652 GGTTCATTTTCAGTTTAGCCAAATCCCGCGGGTTGGCGGGAGGGCGGGCGGTAG 711
 QY 69 69
 DB 712 CTGGCGGGGCTGACTCGGGGACCGGCTAGGGTCTCACACCCCTCCAGGGAATGATGCG 771
 QY 79 CysAspMetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGly 98
 DB 772 TGGGACATGGGCGCCACGAGCGCTCTCTCCGGGTATCACACGACACCGCTACGAGCGC 831

QY 99 LysAspTyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAla 118
 DB 832 AAGGATTACATCTCCCTGAACGAGGACCTCGCTCTCGACCGCGCGGACACCGTGGCT 891
 QY 119 GluIleThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgTrpTyrLeu 138
 DB 892 CAGATACCCAGCGCTTCTATGAGGAGAGGATATGAGAGGAGTTCAGAGCTACCTG 951
 QY 139 GluGlyGluCysLeuGluLeuLeuArgTyrGlyLeuGluAsnGlyLysGluThrLeuGln 158
 DB 952 GAGGGGAGTGCCTGGAGTTGCTCCGAGATACTTGGAGAATGGGAAGGAGACGCTACAG 1011
 QY 159 ArgAla 160
 DB 1012 CGCGCAGGTACCGAGGGGCCCATGGGCGCTTCCCTATCTCTGTAGATCTCTTGGGATGGC 1071
 QY 160 160
 DB 1072 CTCGCACAGGTTGGGAGGAAAGTGGACCAATGCTAGGATATCGCCCTCCTCTAGTCC 1131
 QY 160 160
 DB 1132 TGAGTAGGAAGAATCTTCTCGCTTTCGAGATCCGGTACCAGAGAGTGACTGTGAGATC 1191
 QY 160 160
 DB 1192 CGCCCTCTCTCGGACAAATTAAGGATGAATTTCTGAGGGAATGGAGGAGACAGCT 1251
 QY 160 160
 DB 1252 CCCTGGAATACCGATCCGCGTCCCTTTTGAGCCCTCCAAACAGCTTGGGCGCGTGACT 1311
 QY 160 160
 DB 1312 TTTCTCTCAAGTTTGTGTCTCTGCTCCACTCAATGTGTGTAGGCTCTGATTTCCAGTC 1371
 QY 160 160
 DB 1372 CCTCGGCTCCACTTAGGTGAGGCGCAGAGTCCCTGCTCCCGCTCAGAGACTTAAC 1431
 QY 160 160
 DB 1432 TTCCAAGGAATAGGAGATTTTCCAGGTGTCTGTCTCCAGGCTGGTGTCTGGTCTGTG 1491
 QY 160 160
 DB 1492 CTCCTTCCCGACCCCGAGGTGCTCTGTCTCAGTTGGTTCACATGGTGTCTGTG 1551
 QY 161 161
 DB 1552 GGTTCCTCATGAGGAGTGCAAGTGCCCTGAATTTCTGACTCTCTCAGATCTCTCCAAAG 1611
 QY 165 AlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArgCysTrpAlaLeu 184
 DB 1612 GCACACGTTGCCACCCCATCTCTGACCATGAGGCCACCTTGAGGTGTCTGGGCCCTG 1671
 QY 185 GlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGluGluInThrGln 204
 DB 1672 GCCTTCTACCTCGCGAGATCACGCTGACCTGGCAGCGGATGGGAGGAGAACAGACCCAG 1731
 QY 205 AspThrGluLeuValGluThrArgProAlaGly 215
 DB 1732 CACACAGAGCTTGTGGAGACGAGGCTGCAGG 1764

RESULT 13
 AAS40421
 ID AAS40421 standard; DNA; 3098 BP.
 XX
 AC AAS40421;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE DNA encoding human prostate cancer antigen, Seq ID No 573.

XX Human; prostate cancer antigen, cytostatic; uropathic; diagnostic;
KW reproductive system; chromosomal marker; forensic; urinary disorder;
KW chronic nephritis; blood-related disorder; thrombosis; ds.
XX

OS Homo sapiens.

XX WO20015316-A2.

XX PD 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001328.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 11-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 14-JUL-2000; 2000US-0217496P.

XX 26-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244517P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249277P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.

PR	08-DEC-2000; 2000US-0251990P.
PR	11-DEC-2000; 2000US-0254097P.
FR	05-JAN-2001; 2001US-0259678P.
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	
XX	Rosen CA, Barash SC, Ruben SW;
PI	WPI; 2001-451929/48.
XX	
DR	Isolated polypeptide for treating, preventing and/or prognosing
PT	disorders related to the reproductive system including prostate cancer
PT	and also for testing and detection e.g. diagnosis.
XX	
PS	Disclosure; SEQ ID NO 573; 546pp; English.
XX	
CC	The invention relates to novel isolated human prostate cancer antigen
CC	polynucleotides (I) and polypeptides (II). (I) and (II) are useful for
CC	preventing, treating or ameliorating a medical condition when
CC	administered (I), (II) and the antibody to (II) are useful for treating,
CC	preventing and/or prognosing disorders related to the reproductive
CC	system including prostate cancers; urinary disorders e.g. chronic
CC	nephritis; and blood-related disorders e.g. thrombosis. (II) can be used
CC	for testing and detection e.g. as a chromosomal marker and in forensics.
CC	(I) and the anti-(II) antibody can be used in testing and detection in
CC	immunoassays. AAS4061-AAS4075 represent the human prostate cancer
CC	antigen coding sequences, and related PCR primers and sequences of the
CC	invention. Note: The sequence data for this patent did not form part of
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at: ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	4,49e-91 Length: 3098
Score:	982.50 Matches: 213
Percent Similarity:	43.58% Conservative: 1
Best Local Similarity:	43.38% Mismatches: 1
Query Match:	83.76% Indels: 277
DB:	Gaps: 2
US-09-819-371-6 (1-215) x AAS40421 (1-3098)	
Qy	1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaLalle 20
Db	293 ATCCCGTGAGTAGCTAGACGACACCAATTCCTGGCGTTCCAGCAGCGCGCGCAT 352
Qy	21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db	353 CCAGAGTATGAGCGCGGAGCGCGGTGGTGGAGCAAGAGGGCGCGCATTTGGAGTGG 412
Qy	41 Thr-ThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db	413 ACCACAGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTTGAGAACTGTC 472
Qy	61 ArgArgTyrAsnGlnSerGluAla----- 68
Db	473 CGCGCGTACAACACAGACGCGAGGC-TGGTGTAGTGAACCGCGCGGGCGCGAGTCCAGC 531
Qy	68 ----- 68
Db	532 CACCCCCCATCCGCCACGACGCGCCGGGTCCCTCAGAGTCCCGATCCGAAATCCACC 591
Qy	68 ----- 68
Db	592 CCGAGGCAGCGGACCGCGCCAGACCCCTCCACCGCGGAGAGTCCCGAGCGCCTTTACCCA 651
Qy	68 ----- 68
Db	652 GGTTCAATTTCAGTTTAGCGCAAAAATCCCGCGGGTTGGCGGGAGCGGGCGGGGCTAG 711
Qy	69 -----GlySerHisThrLeuGlnGlyMetAsnGly 78

XX
SQ Sequence 148834 BP; 38942 A; 33672 C; 34501 G; 41719 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.79e-89 Length: 148834
Score: 982.50 Matches: 213
Percent Similarity: 43.58% Conservative: 1
Best Local Similarity: 43.38% Mismatches: 1
Query Match: 83.76% Indels: 277
DB: 6 Gaps: 2

US-09-819-371-6 (1-215) x ABK83570 (1-148834)

QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAila 20
DB 116857 ATCGCGGTGGAGTAGACGACACGCAATCTCGGGTTCGACAGCGCGCGATT 116798

QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr 40
DB 116797 CCGAGGATGGAGCCCGCGGAGCCGCTGGGTGGAGCAAGAGGGCGCGCGAGTATTGGAGTGG 116738

QY 41 ThrThrGlyTyrAlaAlaValAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 116737 ACACAGGGTACGCCACAGGCCACACGACAGACTGACCGAGTGGCCCTGAGGACCTGCTC 116678

QY 61 ArgArgTyrAsnGlnSerGluAla 68
DB 116677 CGCGGCTACACACAGAGCGAGGC-TGGTGTAGTGAACCGCGCGCGCGCGAGTTCACGAC 116619

QY 68 68
DB 116618 CACCCCGCATCGCCACGACCGCCCGGGTCCCTCAGAGTCTCCGGATCCGGAATCTACC 116559

QY 68 68
DB 116558 CCGAGGACGGGAGCCCGCGCCAGACCCCTCCACCCGGGAGAGTCCCGAGCGCGCTTTACCCA 116499

QY 68 68
DB 116498 GGTTCATTTTCAGTTTGGCCAAATATCCCGCGGGTGGCGGGGAGGGCGGGCGGTAG 116439

QY 69 69
DB 116438 CTGGCGGGGGTGTACTCGCGGACCGCGGTAGGGTCTCACACCTCCAGGGAATGATGCG 116379

QY 79 CysAspMetGlyProAspGlyArgLeuArgGlyTyrHisGlnHisAlaTrpAspGly 98
DB 116378 TGGCATATGGGCGCGACGACGCGCTCTCCCGGGTATCACACACCGCTACCGACGCG 116319

QY 99 LysAspTyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAla 118
DB 116318 AAGATTTACATCTCTCCCTGACAGGAGCTGCGCTCTCGACCGCGCGGACACCGTGGCT 116259

QY 119 GlnIleThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeu 138
DB 116258 CAGATCACCCAGCGCTCTATGAGGAGAGGAATATGACAGAGAGTTACGAGACCTACCTG 116199

QY 139 GluGlyGluCysLeuGluLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGln 158
DB 116198 GAGGCGAGTGGCTGGAGTGTCTCCGACATACTTGGGAAATGGGAGGAGAGCTACAG 116139

QY 159 ArgAla 160
DB 116138 CGCGCAGGTACCAGGCGCCATGGGCGCTTCCCTATCTCTGTAGATCTCTTGGGATGCG 116079

QY 160 160
DB 116078 CTCGCACAGGTTGGGAGGAAAGTGGACCCCAATGTAGGATATCGCCCTCCCTTAGTCC 116019

QY 160 160
DB 116018 TGAGTAGGAAGATCTTCTCTGGCTTTTCGAGATCCGCTACGAGAGTGAAGTGTGAGAGTC 115959

ABK83570;
14-AUG-2002 (first entry)
Human cDNA differentially expressed in granulocytic cells #141.
Human; ss; granulocytic cell; DNA chip; bacterial infection;
viral infection; parasitic infection; protozoal infection;
fungal infection; sterile inflammatory disease; peoriasis;
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
cardiac reperfusion injury; renal reperfusion injury; ARDS;
adult respiratory distress syndrome; inflammatory bowel disease;
Crohn's disease; ulcerative colitis; periodontal disease;
granulocyte activation; chronic inflammation; allergy.
Homo sapiens.
WO200228999-A2.
11-APR-2002.
03-OCT-2001; 2001WO-US030821.
03-OCT-2000; 2000US-0237189P.
(GENE-) GENE LOGIC INC.
Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
WPI; 2002-435328/46.
Detecting granulocyte activation by detecting differential expression of
genes associated with granulocyte activation, which serves as diagnostic
markers that is useful for monitoring disease states and drug toxicity.
Claim 1; SEQ ID NO 141; 114pp; English.
The invention relates to detecting (M1) granulocyte (GC) activation
(GCA), by detecting the level of expression of gene(s) (Gs) identified by
DNA chip analysis as given in the specification, and comparing the
expression level to an expression level in an unactivated GC, where
differential expression of Gs is indicative of GCA. Also included are
modulating (M2) GA by contacting GC with an agent that alters the
expression of at least one gene in Gs; (2) screening (M3) for an agent
capable of modulating GCA or an inflammation (especially chronic) in a
tissue, an allergic response in a subject, exposure of a subject to a
pathogen or sterile inflammatory disease using the gene expression
profile; (3) detecting (M4) an inflammation (especially chronic) in a
tissue, an allergic response in a subject, exposure of a subject to a
pathogen or sterile inflammatory disease, by detecting the level of
expression in a sample of the tissue of gene(s) from Gs, where the level
of expression of the gene is indicative of inflammation; (4) treating
(M5) an inflammation (especially chronic) or in a tissue, an allergic
response in a subject, exposure of a subject to a pathogen or sterile
inflammatory disease, by contacting a tissue having inflammation with an
agent that modulates the expression of gene(s) from Gs in the tissue. M1
is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
for screening an agent capable of modulating GCA preferably in an
inflammation in a tissue; M4 is useful for detecting an inflammation
(especially chronic) in a tissue, an allergic response in a subject,
exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
peoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
respiratory distress syndrome, inflammatory bowel disease, Crohn's
disease, ulcerative colitis, periodontal disease; also bacterial
infection, viral infection, parasitic infection, protozoal infection,
fungal infection and M5 is useful for treating one of the above
conditions. The present sequence represents a gene differentially
expressed in granulocytes. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

QY 160 ----- 160
Db 115958 CGCCCTGCTCTCGGACAAATTAGGGATGAAATTTCTGAGGAATGAGGAGACAGT 115899
QY 160 ----- 160
Db 115898 CCTGGAATACGATCCGCGGTCCCTTTGAGCCCTCCACAGCCCTGGGCCCCGTGACT 115839
QY 160 ----- 160
Db 115838 TTTCTCTCAAGTTTGTCTCTGCTGCCTCACACTCAATGTGTTTGAGGCTCTGATTCACGTC 115779
QY 160 ----- 160
Db 115778 COTCGGCTTCCACTTAGGTACGGGCGAGAGTCCCTGCTGCCCTCCAGACTTAAC 115719
QY 160 ----- 160
Db 115718 TTCCAGGATAGGAGATTTTCCAGGTCTCTGTGTCCAGGCTGTGTCTGGGTCTGTG 115659
QY 160 ----- 160
Db 115658 CTCCCTTCCCCAGCCAGGTGCTCTGCTCCATTTCTCAGGTGTGTCCATGCTGCTGG 115599
QY 161 -----AspProProlys 164
Db 115598 GGTTCCTCCATGAGGAGTGCAAGTGCTGAATTTCTGACTCTTCTCAGATCTCTCCAAAG 115539
QY 165 AlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArgCysTrpAlaLeu 184
Db 115538 GCACAGTTGCCCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTG 115479
QY 185 GlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGluGluGlnThrGln 204
Db 115478 GGCCTTCTACCTCGCGAGATCACGCTGACCTGGCAGCGGATGGGAGAGAACAGACCCAG 115419
QY 205 AspThrGluLeuValGluThrArgProAlaGly 215
Db 115418 GACACAGACTGTGGAGACCGAGGCTGCAGGG 115386

RESULT 15
AAN70935
ID AAN70935 standard; DNA; 1026 BP.
XX
AC AAN70935;
XX
DT 10-APR-1991 (first entry)
DE
DE Sequence encoding the human histocompatibility antigen HLA B27.
XX
XX Rheumatic disorder; genetic screening; diagnosis; ankylosing spondylitis;
XX SS.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 1. .1026
FT
PN DE3542024-A.
XX
XX 04-JUN-1987.
XX
XX 28-NOV-1985; 85DE-03542024.
XX
XX 21-DEC-1985; 85DE-03545576.
XX
XX (BEHW) BEHRINGWERKE AG.
XX
XX Riethmulle G, Meo T, Weiss E, Szots H;
XX
XX WPI; 1987-157893/23.
XX P-PSDB; AAP70590.
XX

PT DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA,
PT antigen or antibody.
XX
PS Claim 2; Page 4; Spp; German.
XX
CC The DNA may be used as a hybridisation probe for detecting the HLA B27
CC gene, e.g. for assessing susceptibility to rheumatic disorders such as
CC ankylosis spondylitis, or may be used to transform cells for prodn. of
CC HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human
CC serum, or to produce mono- or polyclonal HLA B27 antibodies for use in
CC immunoassay
XX
SQ Sequence 1026 BP; 213 A; 307 C; 344 G; 162 T; 0 U; 0 Other;

Alignment Scores: 8.79e-87 Length: 1026
Pred. No.: 935.00 Matches: 173
Percent Similarity: 85.58% Conservative: 11
Best Local Similarity: 80.47% Mismatches: 31
Query Match: 79.71% Indels: 0
DB: 1 Gaps: 0

US-09-819-371-6 (1-215) x AAN70935 (1-1026)
QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
Db 67 ATCACCGTGGCTACGTGGACGACACGCTGTTCTGTGAGGTTCCACAGCGACGCGGAGT 126
QY 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 127 CCGAGAGAGAGCGCGCGCGCGTGTGATAGACAGAGGCGCGCGAGTATTGGGACCGG 186
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 187 GAGACACAGATCTGCAAGGCCAGGACACAGCTGACCCAGAGGACCTGGGACCCCTGCTC 246
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 247 CGCTACTACACACAGAGCGAGCGCGGCTCTCACACCTCCAGATATGTATGGCTGGAC 306
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 307 GTGGGCGCGACCGGGCGCTCTCTCCGCGGTACCCACAGGACCGCTACGACGCGCAGGAT 366
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 367 TACATCGCCTGAACGAGGACCTGAGCTCTGGACCGCGCGGACACGCGGCTCAGATC 426
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 427 ACCCAGCGCAAGTGGAGCGCGCGCGCTGTGTGCGGAGCAGCTGAGAGCTACCTGGAGGGC 486
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 487 GAGTGGGTGGAGTGGCTCCGCGATACCTGTGAGAACCGGAGAGAGAGCTGCACGCGGTG 546
QY 161 AspProProlysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Db 547 GACCCCCCAAAGACACACAGCTGACCCACCCATCTCTGACCATGAGGCCACCCCTGAGG 606
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAsnGlyGlu 200
Db 607 TGTGGGCGCTGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAG 666
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 667 GACCAACTCAGGACACTGAGCTTGTGGAGACACAGACCCAGCAGGA 711

Search completed: June 18, 2004, 08:01:35
Job time : 427 secs

RESULT 3
PCT-US94-06069-2/c
; Sequence 2, Application PC/TUS9406069
; GENERAL INFORMATION:
; APPLICANT: Vical Incorporated
; APPLICANT: Regents of the University of Michigan
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06069
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033VPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN: HLA-B7
PCT-US94-06069-2

Alignment Scores:
Pred. No.: 1.61e-99 Length: 4059
Score: 921.00 Matches: 170
Percent Similarity: 86.98% Conservative: 17
Best Local Similarity: 79.07% Mismatches: 28
Query Match: 78.52% Indels: 0
DB: 5 Gaps: 0

US-09-819-371-6 (1-215) x PCT-US94-06069-2 (1-4059)

Qy 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
Db 2745 ATCTCAGTGGGCTAGTGGACACACCCAGTTCGTGAGTTCGACGCGCGCGAGT 2686

Qy 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 2685 CCGAGAGAGGAGCG 2626

Qy 41 ThrThrGlyTyrAlaAlaLeuAsnAlaGlnThrAspArgValAlaLeuAsnLeuLeu 60

Db 2625 AACACACAGATCTACAGGCCCCAGGCACAGACTACCGAGAGAGCGCTGCGC 2566
Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCyAsp 80
Db 2565 GCGTACTACAAACAGAGCGAGCGCGGCTCTCACACCTCTCCAGAGCATGTACGGCTGGAC 2506
Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLeuAsp 100
Db 2505 GTGGGCGCGAGCGCGCGCTCTCTCGCGGCGATGACCCAGTACGCTAGCAGCGCAAGAT 2446
Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 2445 TACATCGCCCTGAACGAGGAGCTCGCTCTCTGAGCGGAGCGGAGAGCCCTACCTGGAGGCG 2386
Qy 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 2385 ACCCAGCGCAAGTGGAGCGCGCGCTGAGCGGAGCGGAGCGGAGCCCTACCTGGAGGCG 2326
Qy 141 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 2325 GAGTGGCTGGAGTGGCTCCGCGAGATACCTGGAGACGCGGAGGACAAGCTGGAGCGCT 2266
Qy 161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Db 2265 GACCCCGCAAAAGACACACGTCGACCCACCCCATCTCTGACCATGAGGCCACCCCTGAG 2206
Qy 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 2205 TGCTGGCGCTGGGTTTCTACCTCGCGAGATCACACTGACCTGGCAGCGGATGCGCGAG 2146
Qy 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 2145 GACCAAACTCAGGACACTGAGCTTGTGGAGACCGACCGAGGAGCA 2101

RESULT 4
US-08-564-313-1
; Sequence 1, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:

; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4965 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; IMMEDIATE SOURCE:
 ; CLONE: HLA-B7 and Beta-2

US-08-564-313-1

Alignment Scores:
 Pred. No.: 2,16e-99 Length: 4965
 Score: 921.00 Matches: 170
 Percent Similarity: 86.98% Conservative: 17
 Best Local Similarity: 79.07% Mismatches: 28
 Query Match: 78.52% Indels: 0
 DB: 2 Gaps: 0

US-09-819-371-6 (1-215) x US-08-564-313-1 (1-4965)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
 DB 673 ATCTCAGTGGCTACGTGGACGACACCCAGTTCGTGAGGTTCACAGCGACGCCGCGAGT 732
 QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 DB 733 CCGAGAGAGGAGCGCGCGCGCGTGTGATAGACAGAGGCGCGGAGTATTGGACCGG 792
 QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60
 DB 793 AACACACAGATCTACAGGCGCCAGGACAGACTGACCGAGAGCGCTGGACCTGGCGC 852
 QY 61 ArgArgTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 DB 853 GGCTACTACACAGAGCGAGCGCGGCTCTCACACCTCCAGAGCATGTACGGCTCGAC 912
 QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
 DB 913 GTGGGCGCGACGCGCGCTCTCCGCGGCGCATGACCCAGTACCGCTACGACGCGAGGAT 972
 QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
 DB 973 TACATGCCCTGAACGAGGACCTGCGCTCTGACCGCGCGGACACGCGGCTCGATC 1032
 QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluLupPheArgThrTyrLeuGluGly 140
 DB 1033 ACCCAGCGCAAGTGGGAGGCGCGCGTGGAGCGGAGCAGCGGAGCGCTACCTGGAGGCG 1092
 QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 DB 1093 GAGTGGCTGGAGTGGCTCCCGACATACCTGGAGAACGGGAAGACAAAGCTGGAGCGCGCT 1152
 QY 161 AspProProlysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
 DB 1153 GACCCCCAAGACACACAGTGAACCCACCCATCTGACCATGAGCCACCTGAGG 1212
 QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
 DB 1213 TGTGGCCCTGGGTTTCTACCTGGGAGATCACATGACCTGGCAGCGGATGCGCAG 1272
 QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 DB 1273 GACCAACTCAGGACACTGAGCTGTGGAGACACAGACACGACGAGA 1317

RESULT 5

PCT-US94-06069-1

; Sequence 1, Application PC/TUS9406069

; GENERAL INFORMATION:

; APPLICANT: Vical Incorporated

; APPLICANT: Regents of the University of Michigan
 ; APPLICANT: Nabel, Elizabeth
 ; APPLICANT: Nabel, Gary
 ; APPLICANT: Lew, Denise
 ; APPLICANT: Marquet, Megda
 ; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/06069
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/074,344
 ; FILING DATE: 07-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israel, Ned
 ; REGISTRATION NUMBER: 29,655
 ; REFERENCE/DOCKET NUMBER: VICAL.033VPC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8650
 ; TELEFAX: 619-235-0176
 ; TELEX:

; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4965 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; STRAIN: HLA-B7 and Beta-2
 ; PCT-US94-06069-1

Alignment Scores:
 Pred. No.: 2,16e-99 Length: 4965
 Score: 921.00 Matches: 170
 Percent Similarity: 86.98% Conservative: 17
 Best Local Similarity: 79.07% Mismatches: 28
 Query Match: 78.52% Indels: 0
 DB: 5 Gaps: 0

US-09-819-371-6 (1-215) x PCT-US94-06069-1 (1-4965)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
 DB 673 ATCTCAGTGGCTACGTGGACGACACCCAGTTCGTGAGGTTCACAGCGACGCCGCGAGT 732
 QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 DB 733 CCGAGAGAGGAGCGCGCGCGCGTGTGATAGACAGAGGCGCGGAGTATTGGACCGG 792
 QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60
 DB 793 AACACACAGATCTACAGGCGCCAGGACAGACTGACCGAGAGCGCTGGACCTGGCGC 852
 QY 61 ArgArgTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 DB 853 GGCTACTACACAGAGCGAGCGCGGCTCTCACACCTCCAGAGCATGTACGGCTCGAC 912

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QY      81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db      913 GTGGGGCCGGAGCGGGCGCTCTCCGGCGGCATGCCAGTACGCTACGACGGCAAGGAT 972
QY      101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db      973 TACATCGCCCTGACGAGGACCTCGCTCTCGACCGCGCGGACACGGCGGCTCAGATC 1032
QY      121 ThrGlnArgPheTyrGluAlaGluGlnTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db      1033 ACCCAGCGCAAGTGGGAGCGCGCCCGTGGAGCGGACGAGCGGACCTACCTGGAGGGC 1092
QY      141 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db      1093 GAGTGGCTGGAGTGGCTCCGCGAGATACCTGGAGACGGGAGGACCAAGCTGGAGCGGCT 1152
QY      161 AspProProlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Db      1153 GACCCGCCAAGACACACCTGACCCACCAACCCCATCTCTGACCATGAGCCACCCCTGAGG 1212
QY      181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db      1213 TGTGGGCCCTGGGTTTCTACCTCGGAGATCACACTGACCTGGAGCGGATGGCGAG 1272
QY      201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db      1273 GACCAAACTCAGACACTGAGCTTGTGGAGACGACGACGACGAGGA 1317

RESULT 6
US-08-914-372C-2
; Sequence 2, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1083)
US-08-914-372C-2

Alignment Scores:
Pred. No.: 4, 86e-86 Length: 1086
Score: 801.00 Matches: 147
Percent Similarity: 80.93% Conservative: 27
Best Local Similarity: 68.37% Mismatches: 41
Query Match: 68.29% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-6 (1-215) x US-08-914-372C-2 (1-1086)
QY      1 IleAlaValGlnTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
Db      130 ATCTCGTGGCTACGTGGACGACACCGAGTTCGTGGCGTTGACAGCGACGCCCCCAAT 189
QY      21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db      190 CCGCGATGGAGCGCGCGCGCGCTGGATACAGCAGGAGGGGAGAGATTGGGATGAG 249
QY      41 ThrThrGlyTyrAlaLysAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db      250 GAGACGAGAAACCCATGGGCGACGACAGACTTCCGAGTGAACCTGAAGAACCTGGCG 309

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QY      61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db      310 GGCTACTACAAACAGAGCGAGCGGGCTTCACACCTCCAGAGCATGTACGGCTGGGAC 369
QY      81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db      370 GTGGGACACAGCGGCTCTTCCTCCGCGGTTACCATCAGGACGCTACGACGGCGCGAT 429
QY      101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db      430 TACATCGCCCTGACGAGGACCTCGCTCTCGACCGCGCGGACACGGCGGCTCAGATC 489
QY      121 ThrGlnArgPheTyrGluAlaGluGlnTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db      490 GCCAAGCGCAAGTGGGAGCGCGCGTGTGGCTGAGCAGTGGAGGAGCTACTTGGAGGGC 549
QY      141 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db      550 GCGTGTGTGGAGTGGCTCCAGAAATACCTGGAGATGGGAAATACACGCTGCAGCGCGCA 609
QY      161 AspProProlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Db      610 GAGCTTCAAGACACATGTGACCCGCCACCCAGCTTGACCTGGGGGTCACTTGGAG 669
QY      181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db      670 TGCTGGGCCCTGGGCTTCTACCTAAGAGATCTCCCTGACCTGGCAGCGGAGGGGCGAG 729
QY      201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db      730 GACCAGAGCCAGGACATGGAGCTGGTGAGACGACGACGCGCCCTCAGGG 774

RESULT 7
US-08-914-372C-36
; Sequence 36, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: consensus sequence
; NAME/KEY: misc feature
; LOCATION: (271)...(271)
; OTHER INFORMATION: n = A,C or G
; NAME/KEY: misc feature
; LOCATION: (272)...(272)
; OTHER INFORMATION: n = G,A or C
; NAME/KEY: misc feature
; LOCATION: (275)...(275)
; OTHER INFORMATION: n = A,G or T
; NAME/KEY: misc feature
; LOCATION: (527)...(527)
; OTHER INFORMATION: n = T,C or A
; NAME/KEY: misc feature
; LOCATION: (560)...(560)
; OTHER INFORMATION: n = T,G or C
US-08-914-372C-36

Alignment Scores:
Pred. No.: 1, 01e-84 Length: 1095
Score: 790.00 Matches: 147
Percent Similarity: 79.53% Conservative: 24
Best Local Similarity: 68.37% Mismatches: 44

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Query Match: 67.35% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-6 (1-215) x US-08-914-372C-36 (1-1095)

QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
DB 139 ATCGCGCTGGCTACGTGACACACGAGCTCGTGAGGTTCCGACGACGCCCGCAAT 198
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 199 CCGCGGATGGAGCGCGCGCGCGGTGATACAGCAGGAGGCGCAGGAGTATTGGATCGG 258
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 259 GAGACACAGATCNCNANGGACACCGCACAGACTTACCAGGTGGACCTGAACACCCCTGGC 318
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 319 GGCTACTACACAGCAGCGCGCGGTCTCACACCTCCAGAGCATGTACGGCTGGCAG 378
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 379 GTGGACCAACAGCGGCTCTCTCCGCGGTACAGTCAGTTCCGCTACGACGCGCGCAT 438
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
DB 439 TACCTCGCCTGACACAGACCTGGCTCTCGACCGCGCGGACACCGCGGCTCAGATC 498
QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
DB 499 TCCAAAGCGCAATGGGAGCGCGCAATGNGCGGAGCAGGAGGAGGAGTACCTGCGGCG 558
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 559 CNGTGTGGAGTGGCTCCGCGAGTACCTGGAGATGGGAGAGACACCGCTGACGCGCGCA 618
QY 161 AspProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
DB 619 GAGCTCCAAAGACACATGTGACCCGCCACCCAGCTCTGACCTGGGGTCACTTGAGG 678
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
DB 679 TCGTGGCGCTGGCTTCTACCTTAAGGAGATCTCCCTGACCTGGCAGCGGAGGCGCAG 738
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
DB 739 GACCAGCGCAGGACATGGAGCTGGTGAGACCGCCCTCAGG 783

RESULT 8
US-08-914-372C-6
; Sequence 6, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1092)
US-08-914-372C-6

Alignment Scores: 2.07e-83 Length: 1095
Pred. No.:

Score: 779.00 Matches: 145
Percent Similarity: 79.53% Conservative: 26
Best Local Similarity: 67.44% Mismatches: 44
Query Match: 66.41% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-6 (1-215) x US-08-914-372C-6 (1-1095)

QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
DB 139 ATCGAAATCGGCTACGTGACGACACGAGCTTCGTGGTTCGACAGCGCCCGCAAT 198
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 199 CCGCGGATGGAGCTGGGCGCGGTGATACAGCAGGAGGCGCAGGAGTATTGGATAGG 258
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 259 AACACGCGGAACCCATGGCAACGACAGATTACCGAGGAGAAACCTGGCGCACAGCTCTC 318
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 319 GGCTACTACACAGCAGCGCGGTCTCACACCTCCAGAGCATGTACGGCTGGCAG 378
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 379 GTGGACCAACAGCGGCTCTCTCCGCGGTACAGTCAGTTCCGCTACGACGCGCGCAT 438
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
DB 439 TACATCGCCTGAACAGGAGCCTGGCTCTCGACCGCGCGGACACCGCGGCTCAGATC 498
QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
DB 499 ACCAAGCGCAATGGGAGCGCGCGATGAGCGGAGGAGGAGTACCTGCGGCG 558
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 559 ACGTGTGGAGTGGCTCCAGAAATACCTGCAGATGGGAGAGACACCGCTGACGCGCGCA 618
QY 161 AspProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
DB 619 GAGCTCCAAAGACACATGTGACCCGCCACCCAGCTCTGACCTGGGGTCACTTGAGG 678
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
DB 679 TCGTGGCGCTGGCTTCTACCTTAAGGAGATCTCCCTGACCTGGCAGCGGAGGCGCAG 738
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
DB 739 GACCAGCGCAGGACATGGAGCTGGTGAGACCGCCCTCAGG 783

RESULT 9
US-08-914-372C-5
; Sequence 5, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1092)
US-08-914-372C-5

Alignment Scores: 3.58e-83 Length: 1095
Pred. No.: 777.00 Matches: 144
Score: 777.00
Percent Similarity: 79.53% Conservative: 27
Best Local Similarity: 66.98% Mismatches: 44
Query Match: 66.24% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-6 (1-215) x US-08-914-372C-5 (1-1095)

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QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
DB 139 ATCCGCTGGTACTGTGACGACGACGAGTTCGTGGTTCGACAGCGACCCCGAAT 198
QY 21 ProArgMetGluProArgGluProTyrValGluGluGluGluProGlnTyrTrpGluTrp 40
DB 199 CCGCGATGAGCGCGCGCGCGCGTGTGATAGAGAGAGGCGGCGAGGATTTGGGATCGG 258
QY 41 ThrThrGlyTyrAlaLysAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 259 GAGACACAGATACAAAGGACACCTCACAGACTTACCGAGTGGACCTGAGACCTTGGCG 318
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 319 GGCTACTACACACGAGCGGCGGCTCTCACACCTCCAGAGCATGTACGGCTGTCTAC 378
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 379 TTGGGACACAGCGGCTCTCTCCGCGGTACAGACAGTTCGCCCTACGACGCGCCGAT 438
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
DB 439 TACTTGCCTTGAACGAGACCTTCGCTCTGACCGCGGCGGACATGGCGGCTCAGATC 498
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
DB 499 TCCAAAGCGCAAGTGGGAGGCGGCAATCGCGCGAGCAGGAGGAGTACCTGCAGGCG 558
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 559 CGGTGTGTGGAGTGGCTTCCGACATACCTCGAGATGGGAGGACACGCTGACGCGCA 618
QY 161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
DB 619 GAGCTTCAAAGACACATGTGACCGCCACCCAGCTCTGACCTGGGGGTACCTTGAGG 678
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
DB 679 TGCTGGGCGCTGGGCTTCTACCTAAGGAGATCTCCCTGACCTGGGCGAGCGGCGCAG 738
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
DB 739 GACCAGACCGAGACATGGAGCTGTGTGGAGACCGAGCCCTCAGGG 783
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RESULT 10

US-08-914-372C-1
; Sequence 1, Application US/08914372C

; Patent No. 6521448

; GENERAL INFORMATION:

; APPLICANT: Edge, Albert S.B.

; APPLICANT: Oettinger, Henry F.

; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF

; FILE REFERENCE: 05742/009001

; CURRENT APPLICATION NUMBER: US/08/914.372C

; CURRENT FILING DATE: 1997-08-19

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1086

; TYPE: DNA

; ORGANISM: Sus scrofa

; FEATURE:

; NAME/KEY: CDS
; LOCATION: (1)...(1083)
US-08-914-372C-1

Alignment Scores:

Pred. No.: 1.4e-82 Length: 1086
Score: 772.00 Matches: 145
Percent Similarity: 78.14% Conservative: 23
Best Local Similarity: 67.44% Mismatches: 47
Query Match: 65.81% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-6 (1-215) x US-08-914-372C-1 (1-1086)

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QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
DB 130 ATCCGCTGGTACTGTGACGACGACGAGTTCGTGGTTCGACACTACGCCCGCAAT 189
QY 21 ProArgMetGluProArgGluProTyrValGluGluGluGluProGlnTyrTrpGluTrp 40
DB 190 CCGCGATGAGCGCTCGGTGCGGTATACAGCAGAGGCGGCGAGGACTATTGGGATGAG 249
QY 41 ThrThrGlyTyrAlaLysAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 250 GAGACGCGGAAAGTCAAGGACACGACAGACTCTCCGAGTGGGCTGAAACACCTTGGC 309
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 310 GGCTACTACACACGAGCGGCGGCTCTCACACCTCCAGAGCATGTGTGGTGTCTAC 369
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 370 TTGGGACACAGCGGCTCTCTCCGCGGTACAGACAGGACGCGCTACGACGCGCGCAT 429
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
DB 430 TACTTGCCTTGAACGAGACCTTCGCTCTGACCGCGGCGGACATGGCGGCTCAGATC 489
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
DB 490 TCCAAAGCGCAAGTGGGAGGCGGCAATCGCGCGAGCAGGAGTACCTGCAGGCG 549
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 550 CGGTGTGTGGAGTGGCTTCCGACATACCTCGAGATGGGAGGACACGCTGACGCGCA 609
QY 161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
DB 610 GAGCTTCAAAGACACATGTGACCGCCACCCAGCTCTGACCTGGGGGTACCTTGAGG 669
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
DB 670 TGCTGGGCGCTGGGCTTCTACCTAAGGAGATCTCCCTGACCTGGGCGAGCGGCGCAG 729
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
DB 730 GACCAGACCGAGACATGGAGCTGTGTGGAGACCGAGCCCTCAGGG 774
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RESULT 11

US-08-914-372C-4

; Sequence 4, Application US/08914372C

; Patent No. 6521448

; GENERAL INFORMATION:

; APPLICANT: Edge, Albert S.B.

; APPLICANT: Oettinger, Henry F.

; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF

; FILE REFERENCE: 05742/009001

; CURRENT APPLICATION NUMBER: US/08/914.372C

; CURRENT FILING DATE: 1997-08-19

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 1095

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; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1092)
US-08-914-372C-4

Alignment Scores:
Pred. No.: 2,45e-82 Length: 1095
Score: 770.00 Matches: 142
Percent Similarity: 78.14% Conservativeness: 26
Best Local Similarity: 66.05% Mismatches: 47
Query Match: 65.64% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-6 (1-215) x US-08-914-372C-4 (1-1095)
QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
DB 139 CTCACCGTGGTACGTGGACACACGAGTTCGTGGAGTTCGACGAGCGCCCGGAT 198
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 199 CCGAGGGAGGACCGGGGGCGGTGGATACAGCAGGAGGGGCGAGGACTATTGGGATCGG 258
QY 41 ThrThrGlyTyrAlaAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 259 GAGACACACATCAGCAAGGAAACCCGACAGACTTACCGAGTGGACCTGAACACCCCTGGC 318
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 319 AGCTACTACACAGACGAGCGCGGTCTCACCCCTCCAGAGCATGTACGGCTGGCAG 378
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 379 GTGGGGCCAGACGGGCTCTTCCTCCGGGTACAGTTCAGTTTGGCTACGAGCGGCCGAT 438
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
DB 439 TACCTGCTCCCTGAACAGAGACTTGGCTCTCGAGCCGCGGAGACCGCGGCTCAGATC 498
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
DB 499 TCCAGCGCAAGTTTGATGTCAGCAATGTGGCGGAGCAGAGAGGAGTACCTGCGAGGCG 558
QY 141 GluCysLeuLeuLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 559 CTGTGTGTGGAGGGGCTCCGCGAGATACCTGGAGATGGGGAAGGACACGCTGCGAGCGCA 618
QY 161 AspProGlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
DB 619 GAGCTCCAAAGACACATGTGACCCGCCACCCAGCTCTGACCTGGGGGTCACTTGAGG 678
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
DB 679 TGCTGGGCGCTGGGCTTCTACCTAAGAGATCTCCCTGACCTGGCGAGGGGCGGCGCAG 738
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
DB 739 GACCAGCGCAGGACATGTGAGCTGTGGAGACACAGGCCCTTCAGGG 783

RESULT 12
US-08-914-372C-35
; Sequence 35, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: consensus sequence
; NAME/KEY: misc feature
; LOCATION: (126)...(126)
; OTHER INFORMATION: n = G,T or C
; NAME/KEY: misc feature
; LOCATION: (261)...(261)
; OTHER INFORMATION: n = A,C or T
; NAME/KEY: misc feature
; LOCATION: (272)...(272)
; OTHER INFORMATION: n = A,G or C
; NAME/KEY: misc feature
; LOCATION: (490)...(490)
; OTHER INFORMATION: n = T,G or A
; NAME/KEY: misc feature
; LOCATION: (551)...(551)
; OTHER INFORMATION: n = G,C or T
; NAME/KEY: misc feature
; LOCATION: (939)...(939)
; OTHER INFORMATION: n = T,C or G
US-08-914-372C-35

Alignment Scores:
Pred. No.: 1,26e-81 Length: 1086
Score: 764.00 Matches: 144
Percent Similarity: 77.21% Conservativeness: 22
Best Local Similarity: 66.98% Mismatches: 49
Query Match: 65.13% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-6 (1-215) x US-08-914-372C-35 (1-1086)
QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
DB 130 ATCCGCGTGGCTACGTGGACACACGAGTTCGTGGTTCGACAACTACGCCCGGAT 189
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
DB 190 CCGCGGATGAGGCTCGGGTGGTGGATACAGCAGGAGGGGCGAGGACTATTGGGATGAG 249
QY 41 ThrThrGlyTyrAlaAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
DB 250 GAGACGGGAAGTCAAGGACACGACAGCTTCCGAGTGGGCTGAACACCCCTGGC 309
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
DB 310 GGCTACTACAACACGAGCGGCGGTCTCACACCTCCAGAGCATGTACGGCTGCTAC 369
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
DB 370 TTGGGACACAGCGGCTCTCTCCAGGATACAGCAGGACGCTTACGACGCGCGGAT 429
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
DB 430 TACATCGCCTGAACAGGAGCCTCGGCTCTGGACCGCGGAGACATGGCGGCTCAGATC 489
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
DB 490 NCCAGCGCAAGTGGGAGCGCGCGATGAGCGGAGCGGAGGAGGAGGAGTACCTTGCAGGGC 549
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
DB 550 CNGTGTGTGGAGTGGCTCCGCGAGATACCTGGAGATGGGGAAGGACACGCTGCGAGCGCA 609
QY 161 AspProGlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
DB 610 GAGCCTCCAAAGACACATGTGACCCGCCACCCAGCTCTGACCTGGGGGTCACTTGAGG 669
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QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 200
 DB 670 TGCTGGGCGCTGGGCTTCTACCTTAAGGAGATCTCCCTGACCTGGCAGCGGAGGCGCAG 729
 QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 DB 730 GACCAGAGCCAGGATCGAGCTGGTGAGACCAAGCCCTCAGGG 774

RESULT 13
 US-08-914-372C-3
 ; Sequence 3, Application US/08914372C
 ; Patent No. 6521448
 ; GENERAL INFORMATION:
 ; APPLICANT: Edge, Albert S.B.
 ; APPLICANT: Oettinger, Henry F.
 ; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
 ; FILE REFERENCE: 05742/009001
 ; CURRENT APPLICATION NUMBER: US/08/914,372C
 ; CURRENT FILING DATE: 1997-08-19
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1086
 ; TYPE: DNA
 ; ORGANISM: Sus scrofa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1083)
 US-08-914-372C-3

Alignment Scores:
 Pred. No.: 1,65e-81 Length: 1086
 Score: 763.00 Matches: 144
 Percent Similarity: 77.67% Conservative: 23
 Best Local Similarity: 66.98% Mismatches: 48
 Query Match: 65.05% Indels: 0
 DB: 4 Gaps: 0

US-09-819-371-6 (1-215) x US-08-914-372C-3 (1-1086)

QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
 DB 130 ATCGCGCTGGGCTAGTGTGACGACGCGAGTTCGTGGCTTCGACACTACGCCCGCAAT 189
 QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 DB 190 CCGCGGATGAGCTCGGCTGGTGGTATACAGACGAGGAGGCGGAGGATTTGGGATCGG 249
 QY 41 ThrThrGlyTyrAlaLysAlaGlnThrArgValAlaLeuArgAsnLeuLeu 60
 DB 250 GAGACGCGGATGTCAAGGAAACCGACAGACTTACGGAGTGGCGCTGAACACCTCGCGC 309
 QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 DB 310 GGCTACTACACAGAGAGCGCGGCTCTCACCTCCAGAGCATGTACGGCTGTCTAC 369
 QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
 DB 370 TTGGGACACAGACGGGCTCTCTCCACGGGTACAGACGAGCGCTACACGCGCGCCGAT 429
 QY 101 TyrIleSerLeuAsnGlnAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
 DB 430 TACATCGCTTGAACAGGACCTTCGCTCTCTGACCGCGGAGCATGCGGCTCAGATC 489
 QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
 DB 490 ACCAAGCGCAAGTGGGAGCGCGCGATGAGCGGAGCGGTAGGAGGAGTACCTGCGAGGA 549
 QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 DB 550 CTGTGTGTGAGTGTGCTCGCAGATACCTCGGATCGGAGTGGGAGGACACGCTGCGAGCGCA 609
 QY 161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180

DB 610 GAGCTTCAAGACACATGTGACCCGCCACCTCTGACCTCGGGTCACTTGAGG 669
 QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 200
 DB 670 TGCTGGGCGCTGGGCTTCTACCTTAAGGAGATCTCCCTGACCTGGCAGCGGAGGCGCAG 729
 QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 DB 730 GACCAGAGCCAGGATCGAGCTGGTGAGACCAAGCCCTCAGGG 774

RESULT 14
 US-08-522-942-1
 ; Sequence 1, Application US/08522942
 ; Patent No. 5753442
 ; GENERAL INFORMATION:
 ; APPLICANT: Tynd, Dolly B.
 ; TITLE OF INVENTION: METHOD FOR DETERMINING GENETIC
 ; PREPOSITION FOR SERONEGATIVE SPONDYLOARTHROPATHIES AND
 ; TITLE OF INVENTION: PRODUCTS THEREFOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 4365 Executive Drive, Suite 1500
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/522,942
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ramos, Robert T.
 ; REGISTRATION NUMBER: 37,915
 ; REFERENCE/DOCKET NUMBER: P07 33624
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-1995
 ; TELEFAX: 619-546-9392
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6553 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: DNA (genomic)
 US-08-522-942-1

Alignment Scores:
 Pred. No.: 5,91e-80 Length: 6553
 Score: 759.50 Matches: 173
 Percent Similarity: 37.63% Conservative: 11
 Best Local Similarity: 35.38% Mismatches: 31
 Query Match: 64.75% Indels: 275
 DB: 1 Gaps: 2

US-09-819-371-6 (1-215) x US-08-522-942-1 (1-6553)
 QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
 DB 946 ATCACCCTGGGCTACGTGGACGACACCTGTCTGAGGTTCGACGCGCGCGAGT 1005
 QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 DB 1006 CCGAGAGGAGGAGCGCGCGCGCTGTGTATAGACAGAGGCGGCGGAGTATTGGGACCG 1065
 QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrArgValAlaLeuArgAsnLeuLeu 60

Db 1066 GAGACACAGATCTGCAAGGCCAAGGCACAGACTGACCGAGAGACCTGCGGACCTGCTC 1125
Qy 61 ArgArgTyrAsnGlnSerGluAla----- 68
Db 1126 CGCTACTACACAGAGAGAGCGCGGTGAGTGACCCCGGCGCGCGGCGCAGGTACAGACT 1185
Qy 68 ----- 68
Db 1186 CCCCATCCCCCAGCTAAGCGCGCGGTGCGCGGAGTCTCGGGTCCGAGATCCGCCCGCG 1245
Qy 68 ----- 68
Db 1246 AGCGCGCGGACCCCGCCAGACCTCGACCGCGGAGACCCCGCGCGGCTTTTACCCGGTT 1305
Qy 68 ----- 68
Db 1306 TCATTTTCAGTTGAGGCCCAAAATCCCCCGGGTTGGTGGCGGCGCGGGGCTCGGGGG 1365
Qy 69 -----GlySerHisThrLeuGlnGlyMetAsnGly 78
Db 1366 GACGGGGGTGACCGCGGGGGGACCGGGGCTCACCCCTCCAGAAATATGTATGGC 1425
Qy 79 CysAspMetGlyProAspGlyValArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGly 98
Db 1426 TCGGACGTGGGCGCGGACCGGGCGCTCTCGCGGGGTACCCAGGAGCGCTACGACGGC 1485
Qy 99 LysAspTyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAla 118
Db 1486 AAGGATTACATCGCCCTGAACGAGACCTGAGCTCTCGGACCGCGCGGACACGCGCGCT 1545
Qy 119 GlnIleThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeu 138
Db 1546 CAGATCACCGCAAGTGGGAGCGCGCGCGGTGGCGGAGCAGCTGAGAGCGCTTACCTG 1605
Qy 139 GluGlyGluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGln 158
Db 1606 GAGGCGAGTGGTGGAGTGGCTCCGAGATACCTGGAGACGCGGAGAGAGCGTGGAG 1665
Qy 159 ArgAla----- 160
Db 1666 CGCGC-GGGTACCAGGGGCGAGTGGGAGCGCTTCCCATCTCTATAGTGCAGCGGGAGT 1724
Qy 160 ----- 160
Db 1725 GCCTCCACGAGAGAGGAGAAATGGATGAGCGCTAGATGTCGGCCCTCCCTTGAAT 1784
Qy 160 ----- 160
Db 1785 GGAGATGGCATGAGTTTCTGAGTTTCTCTGAGGCGCCCTCTCTCTCTAGGACAA 1844
Qy 160 ----- 160
Db 1845 TTAAGGATGACGTCTCTGAGAAATGGAGGGAAGACAGTCCCTAGATGATGATCAGG 1904
Qy 160 ----- 160
Db 1905 GGTCCCTTTGACCCCTGACGAGCGCTTGGGAACCGTGACTTTTCTCTCAGGCGCTTGT 1964
Qy 160 ----- 160
Db 1965 CTCGTGCTCACACTGAGTGTGTTGGGGCTCTGATTCAGACACTTCTGAGTCACTTTACC 2024
Qy 160 ----- 160
Db 2025 TCCACTCAGATCAGGAGCAGAGTCCCTGTTCGCCGCTCAGAGACTCGAACTTTCCAAATG 2084
Qy 160 ----- 160
Db 2085 AATAGGAGATTATCCAGGTGCGTCCAGGCTGGTGTCTGGGTTCGTGGCCCTTCC 2144
Qy 160 ----- 160
Db 2145 CCACCCAGGTGTCTGTCCATCTCAGGCTGGTCAATGGTGGTGGTCTAGGGTGTCCCA 2204

Qy 161 -----AspProProlLysAlaHis 166
Db 2205 TGAGAGATCAAGCGCCTGAATTTTCTGACTTCTCCCATCAGACCCCAAGACACAC 2264
Qy 167 ValAlaHisHisProIleSerAspHisGluAlaThrLeuArgCysTyrAlaLeuGlyPhe 186
Db 2265 GTGACCCAGCACCCCATCTCTGACCATGAGGCGACCCCTGAGGTGTGGCCCTGGGCTTC 2324
Qy 187 TyrProAlaGluIleThrLeuThrTyrGlnArgAspGlyGluGluGlnThrGlnAspThr 206
Db 2325 TACCTCGGAGATCACTGACCTGGCAGCGGGATGGCGAGGACCAAACTCAGGACACT 2384
Qy 207 GluLeuValGluThrArgProAlaGly 215
Db 2385 GAGCTTGTGAGACCAAGACAGCAGCAGGA 2411

RESULT 15
US-09-029-045-11
; Sequence 11, Application US/09029045
; Patent No. 6056952
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Amy Sonva
; TITLE OF INVENTION: Selective Elimination of T Cells That
; TITLE OF INVENTION: Recognize Specific Preselected Targets
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,045
; FILING DATE: 02-JUN-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,964
; FILING DATE: 30-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/13873
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-236100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..1107
; OTHER INFORMATION: /product= "d-d MHC"
; OTHER INFORMATION: /note= "nucleic acid encoding d-d MHC"
US-09-029-045-11

Alignment Scores: 8,76e-80 Length: 1183
Pred. No.: 749.00 Matches: 143
Score: 76.53% Conservative: 20
Percent Similarity:

Best Local Similarity: 67.14% Mismatches: 50
 Query Match: 63.85% Indels: 0
 DB: 3 Gaps: 0

US-09-819-371-6 (1-215) x US-09-029-045-11 (1-1183)

Qy	3	ValGluTyrValAspAspThrGlnPheLeuAsgPheAspSerAspAlaAlaIleProArg	22
Db	154	GTGGCTAGCTGGACAAACGCGAGTTCGGCGCTTCGACAGCGACCGGAGATCCGAGA	213
Qy	23	MetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrpThrThr	42
Db	214	TATGAGCGCGCGCGCTGGATAGACAGAGGCGCGGAGTATTGGGAGCGGAGACA	273
Qy	43	GlyTyrAlaIleAlaSerAlaGlnThrAspArgValAlaLeuArgAsnLeuLeuArgArg	62
Db	274	CGAGAGCCCAAGGCAATGAGCAGAGTTCCGAGTGGACCTGAGGACCGCGCTGGGCTAC	333
Qy	63	TyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAspMetGly	82
Db	334	TACACACAGACCGCGCGGCTCTCACACACTCCAGTGGATGGCTGGCTGTGACGTGGAG	393
Qy	83	ProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAspTyrIle	102
Db	394	TCGACCGCGCGCTCTCCCGGCTACTGGCAGTTCGCTTACGACGCGCTGCGATTACATC	453
Qy	103	SerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIleThrGln	122
Db	454	GCCTTGAAACGAACCTGAAACAGTGGACGCGCGGACATGGCGCGCAGATCACCCGA	513
Qy	123	ArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGlyGluCys	142
Db	514	CGCAAGTGGGAGCAGGCTGGTGTGCAGAGAGAGACCGGGCTTACCTGGAGGGCGAGTGC	573
Qy	143	LeuGluLeuLeuArgArgTyrLeuGluAsnGlyLeuThrLeuGlnArgAlaAspPro	162
Db	574	GTGGAGTGGTCCGCAGATACCTGAAGACCGGAATGCTACGCTGCTGGCGCACAGATCCC	633
Qy	163	ProlysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArgCysTrp	182
Db	634	CCAAAGGCCCATGTGACCCATCACCGCAGACCTGAGGTGATGTCACCCCTGAGGTGCTGG	693
Qy	183	AlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGluGln	202
Db	694	GCCCTGGGCTTCTACCCCTGCTGACATCACCCCTGACCTGGCAGTTGAATGGGAGAGCTG	753
Qy	203	ThrGlnAspThrGluLeuValGluThrArgProAlaGly	215
Db	754	ACCGGAATGGAGCTTGTGGACCCAGGCCTGACGGG	792

Search completed: June 18, 2004, 09:53:48
 Job time : 88 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 07:46:25 ; Search time 419 Seconds

(without alignments)

2350.678 Million cell updates/sec

Title: US-09-819-371-6

Perfect score: 1173

Sequence: 1 IAVEYDDTQFLRFDSDAI.....QRDGEQQTDLVETRPAG 215

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Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delpop 6.0	Delpext 7.0	

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUFFI=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:
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- 9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:
- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq2:
- 14: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:
- 15: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:
- 16: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:
- 17: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:
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- 19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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RESULT 1

US-09-925-301-589
; Sequence 589, Application US/0925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925.301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 589
; TYPE: DNA
; LENGTH: 816
; ORGANISM: Homo sapiens
US-09-925-301-589

Alignment Scores:

ALIGNMENTS

1	1164	99.2	816	9	US-09-925-301-589	Sequence 589, App
2	1164	99.2	1089	13	US-09-819-371-1	Sequence 1, Appli
3	1164	99.2	1188	13	US-10-342-887-1806	Sequence 1806, Ap
4	1164	99.2	1188	13	US-10-172-118-1806	Sequence 2, Appli
5	1160	98.9	822	13	US-09-819-371-2	Sequence 3, Appli
6	1151	98.1	645	13	US-09-819-371-3	Sequence 3713, Ap
7	993.5	84.7	4316	9	US-09-880-107-3713	Sequence 81, Appl
8	993.5	84.7	4316	13	US-10-257-021-81	Sequence 6712, Ap
9	982.5	83.8	3098	10	US-09-764-891-6712	Sequence 573, App
10	982.5	83.8	3098	15	US-10-091-572-573	Sequence 1160, Ap
11	921	78.5	1089	13	US-10-342-887-1160	Sequence 1160, Ap
12	921	78.5	1089	13	US-10-172-118-1160	Sequence 576, App
13	919	78.3	1571	14	US-10-044-090-576	Sequence 322, App
14	915	77.0	1221	13	US-10-302-172-322	Sequence 235, App
15	911	77.7	1271	9	US-09-989-708-235	Sequence 11, Appl
16	900	76.7	1533	10	US-09-971-429B-11	Sequence 563, App
17	897	76.5	1377	14	US-10-044-090-563	Sequence 317, App
18	896	76.4	1559	13	US-10-302-172-317	Sequence 318, App
19	895	76.3	2225	13	US-10-302-172-318	Sequence 318, App
20	886	75.5	2225	13	US-10-302-172-318	Sequence 375, App
21	869	74.1	1840	13	US-10-388-360-375	Sequence 218, App
22	863	73.6	1082	9	US-09-989-347-218	Sequence 159, App
23	859.5	73.3	1210	13	US-10-210-172-159	Sequence 77, Appl
24	859.5	73.3	1210	16	US-10-093-463-77	Sequence 323, App
25	858	73.1	1546	13	US-10-302-172-323	Sequence 711, App
26	852	72.6	1080	10	US-09-960-706-711	Sequence 449, App
27	852	72.6	1080	10	US-09-873-319-449	Sequence 79, Appl
28	852	72.6	1175	16	US-10-093-463-79	Sequence 316, App
29	852	72.6	1495	13	US-10-302-172-316	Sequence 324, App
30	850	72.5	1491	13	US-10-302-172-324	Sequence 46, Appl
31	848	72.3	1098	15	US-10-173-138A-46	Sequence 1, Appli
32	848	72.3	1170	13	US-10-108-511-1	Sequence 564, App
33	848	72.3	1466	14	US-10-044-090-564	Sequence 561, App
34	848	72.3	1526	14	US-10-044-090-561	Sequence 4, Appli
35	848	72.3	1530	13	US-10-108-511-4	Sequence 6, Appli
36	842	71.8	1083	13	US-10-398-308-6	Sequence 1, Appli
37	838	71.4	1092	13	US-10-398-308-16	Sequence 16, Appl
38	836	71.3	1069	13	US-10-398-308-16	Sequence 321, App
39	835	71.2	1113	13	US-10-302-172-321	Sequence 155, App
40	832	70.9	1159	13	US-10-210-172-155	Sequence 71, Appl
41	832	70.9	1159	16	US-10-085-198-71	Sequence 19, Appl
42	828	70.6	1077	13	US-10-398-308-19	Sequence 22, Appl
43	826	70.4	1086	13	US-10-398-308-22	Sequence 25, Appl
44	825	70.3	1014	13	US-10-398-308-25	Sequence 12, Appl
45	825	70.3	1077	13	US-10-398-308-12	

Pred. No.: 2,06e-138 Length: 816
 Score: 1164.00 Matches: 214
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.53% Mismatches: 0
 Query Match: 99.23% Indels: 0
 DB: 9 Gaps: 0

US-09-819-371-6 (1-215) x US-09-925-301-589 (1-816)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
 DB 149 ATCGCGTGGAGTACGTAGACACGCAATTCCTCGGTTCCGACGACGCGCGGATT 208
 QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 DB 209 CCGAGATGGAGCGCGGAGCGCGTGGTGGAGCAAGAGGGCGCGAGTATGGAGTGG 268
 QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
 DB 269 ACCACAGGTACGCGCAAGCCACGACAGCTGACCGAGTGGCGCTGAGGAACTGCTC 328
 QY 61 ArgArgTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 DB 329 CGCGCGTACAAACAGAGCGAGCGTGGTCTCACCCCTCCAGGGAATGAATGGCTGGC 388
 QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
 DB 389 ATGGGCGCCGACGAGCGCTCTCCCGCGGTATCACCCAGCGGTACGACGCGCAAGGAT 448
 QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
 DB 449 TACATCTCCCTGAACAGAGACCTGCGCTCTCGACCGCGCGGACACCCCTGCTCAGATC 508
 QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluPheArgThrTyrLeuGluGly 140
 DB 509 ACCACAGCGCTTATAGGCGAGGGAATATGAGAGAGTTTACGACCTTACCTGGAGGCG 568
 QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 DB 569 GAGTGCCTGGAGTTGCTCCGAGATCTTGGAGATGGAGAGGAGTACGACGCGGTACAGCGCGCA 628
 QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
 DB 629 GATCTCTCAAGGACACGCTGCGCCACCCCATCTCTGACCATGAGGCCACCTTGAGG 688
 QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
 DB 689 TGCTGGCGCTTCTACCTGCGGAGATCACGCTGACCTGGCGGAGTGGGAG 748
 QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 DB 749 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGCGCTGCGAGG 793

RESULT 2

US-09-819-371-1
 ; Sequence 1, Application US/09819371
 ; Publication No. US2004005334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Egawa, Kohji
 ; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
 ; TITLE OF INVENTION: Using Thereof
 ; FILE REFERENCE: 30815
 ; CURRENT APPLICATION NUMBER: US/09/819,371
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1089
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-819-371-1
 Alignment Scores:

Pred. No.: 3,02e-138 Length: 1089
 Score: 1164.00 Matches: 214
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.53% Mismatches: 0
 Query Match: 99.23% Indels: 0
 DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x US-09-819-371-1 (1-1089)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
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 QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 DB 190 CCGAGATGGAGCGCGGAGCGCGTGGTGGAGCAAGAGGGCGCGAGTATGGAGTGG 249
 QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
 DB 250 ACCACAGGTACGCGCAAGCCACGACAGCTGACCGAGTGGCGCTGAGGAACTGCTC 309
 QY 61 ArgArgTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 DB 310 CGCGCGTACAAACAGAGCGAGCGTGGTCTCACCCCTCCAGGGAATGAATGGCTGGC 369
 QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
 DB 370 ATGGGCGCCGACGAGCGCTCTCCCGCGGTATCACCCAGCGGTACGACGCGCAAGGAT 429
 QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
 DB 430 TACATCTCCCTGAACAGAGACCTGCGCTCTCGACCGCGCGGACACCCCTGCTCAGATC 489
 QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluPheArgThrTyrLeuGluGly 140
 DB 490 ACCACAGCGCTTATAGGCGAGGGAATATGAGAGAGTTTACGACCTTACCTGGAGGCG 549
 QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 DB 550 GAGTGCCTGGAGTTGCTCCGAGATCTTGGAGATGGAGAGGAGTACGACGCGGTACAGCGCGCA 609
 QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
 DB 610 GATCTCTCAAGGACACGCTGCGCCACCCCATCTCTGACCATGAGGCCACCTTGAGG 669
 QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
 DB 670 TGCTGGCGCTTCTACCTGCGGAGATCACGCTGACCTGGCGGAGTGGGAG 729
 QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 DB 730 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGCGCTGCGAGG 774

RESULT 3

US-10-342-887-1806
 ; Sequence 1806, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710

;; PRIOR FILING DATE: 2002-05-14
;; PRIOR APPLICATION NUMBER: 10/172,118
;; PRIOR FILING DATE: 2002-06-14
;; NUMBER OF SEQ ID NOS: 2699
;; SEQ ID NO 1806
;; LENGTH: 1188
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-342-887-1806

Alignment Scores:
Pred. No.: 3,38e-138 Length: 1188
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x US-10-342-887-1806 (1-1188)

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Db 130 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGGTTCGACGAGCGCGCGATT 189
QY 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 190 CCGAGGATGGAGCCGCGGAGCGCTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 249
QY 41 ThrThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 250 ACCACAGGATACGCCAAGCCCAACGACAGCTGACCGAGTGGCGCTCGAGACCTGCTC 309
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 310 CGCCGCTACACACAGAGCGAGCTGGTCTCACACCTCCAGGGAATGAATGGCTGCGAC 369
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 370 ATGGGCGCCGAGCGAGCGCTCTCCGCGGGTATCACCAGCAGCGGTACGACGCAAGAT 429
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 430 TACATCTCCCTGAAACGAGGACCTGCGCTCTGGACCGCGCGGACACCGTGGCTCAGATC 489
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 490 ACCACGCGCTTCTATGAGCGAGAGGAATATGACAGGAGGAGTTCCAGGACCTACCTGAGG 549
QY 141 GluCysLeuLeuLeuLeuLeuArgTyrLeuGluAsnGlyLysGlnThrLeuGlnArgAla 160
Db 550 GAGTGCTTGAGTTGCTCCGAGATCTTGGAGATCTGGAGATGGAGAGCGCTACAGCGCGCA 609
QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 610 GATCCTCCAAAGGCACACGCTTGCCACCCACCTCTGACCCATCTGACATGAGGCCACCTGAGG 669
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 670 TGCTGGGCGCTTCTACCTGCGGAGATCACGCTACCTCCGCGGAGATGGAGATGGAGGAG 729
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 730 GAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCGCTGCAGGG 774

RESULT 4
US-10-172-118-1806
;; Sequence 1806, Application US/10172118
;; Publication No. US20030224374A1
;; GENERAL INFORMATION:
;; APPLICANT: Dai, Hongyue
;; APPLICANT: He, Yudong
;; APPLICANT: Linsley, Peter
;; APPLICANT: Mao, Hao

;; APPLICANT: Roberts, Chris
;; APPLICANT: Van 't Veer, Laura
;; APPLICANT: Van de Vijver, Marc
;; APPLICANT: Bernards, Rene
;; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;; FILE REFERENCE: 9301-175-999
;; CURRENT APPLICATION NUMBER: US/10/172,118
;; CURRENT FILING DATE: 2002-06-14
;; PRIOR APPLICATION NUMBER: 60/380,770
;; PRIOR FILING DATE: 2002-05-14
;; NUMBER OF SEQ ID NOS: 2699
;; SEQ ID NO 1806
;; LENGTH: 1188
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: NM 018950
;; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1806

Alignment Scores:
Pred. No.: 3,38e-138 Length: 1188
Score: 1164.00 Matches: 214
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x US-10-172-118-1806 (1-1188)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
Db 130 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGGTTCGACGAGCGCGCGATT 189
QY 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 190 CCGAGGATGGAGCCGCGGAGCGCTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 249
QY 41 ThrThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 250 ACCACAGGATACGCCAAGCCCAACGACAGCTGACCGAGTGGCGCTCGAGACCTGCTC 309
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 310 CGCCGCTACACACAGAGCGAGGCTGGTCTCACACCTCCAGGGAATGAATGGCTGCGAC 369
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 370 ATGGGCGCCGAGCGAGCGCTCTCCGCGGGTATCACCAGCAGCGGTACGACGCAAGAT 429
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 430 TACATCTCCCTGAAACGAGGACCTGCGCTCTGGACCGCGCGGACACCGTGGCTCAGATC 489
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 490 ACCACGCGCTTCTATGAGCGAGAGGAATATGACAGGAGGAGTTCCAGGACCTACCTGAGG 549
QY 141 GluCysLeuLeuLeuLeuLeuArgTyrLeuGluAsnGlyLysGlnThrLeuGlnArgAla 160
Db 550 GAGTGCTTGAGTTGCTCCGAGATCTTGGAGATCTGGAGATGGAGAGCGCTACAGCGCGCA 609
QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 610 GATCCTCCAAAGGCACACGCTTGCCACCCACCTCTGACCCATCTGACATGAGGCCACCTGAGG 669
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 670 TGCTGGGCGCTTCTACCTGCGGAGATCACGCTACCTCCGCGGAGATGGAGATGGAGGAG 729
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 730 GAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCGCTGCAGGG 774

RESULT 5

US-09-819-371-2
; Sequence 2, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-819-371-2

Alignment Scores:
Pred. No.: 6,73e-138 Length: 822
Score: 1160.00 Matches: 213
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.07% Mismatches: 0
Query Match: 98.89% Indels: 0
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x US-09-819-371-2 (1-822)

Qy 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAlaAlaIle 20
Db 67 ATCCGCGTGGAGTACGTAGACGACCAATTCCTGCGGTTCCGACAGCGCGCGATT 126
Qy 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 127 CCGAGGATGGACCGCGGAGCGGTGGTGGAGGAGGCGCGCGCGATTATGGGAGTGG 186
Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 187 ACCACAGGAGTACGCCAGGCGCACACGACGACGAGTGGCGCTCCGAGGACCTGCTC 246
Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 247 CGCCGCTCAACACAGAGCGAGGCTGGTCTCACCCCTCCAGGGAATGAATGGCTGGCAC 306
Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 307 ATGGGCGCCGACCGAGCGCTCTCCCGCGGTATCACACGACGCGTACGACGCGCAGGAT 366
Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 367 TACATCTCCCTGAACGAGGACCTGCGCTCTCGACCGCGCGACACCGCTGCTCAGATC 426
Qy 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluPheArgThrTyrLeuGluGly 140
Db 427 ACCACGCGTCTTATGAGGAGAGGAATATGACAGAGATTGAGGACCTACCTGGAGGCG 486
Qy 141 GluCysLeuGluLeuLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 487 GAGTGCTGGAGTTGCTCCGACATATCTGGAGATGGGAGAGAGAGAGCTACAGCGCGCA 546
Qy 161 AspProProlLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 547 GATCTCTCCAAAGGACACGCTGGCCACCCATCTCTGACCATGAGGCCACCTGGAG 606
Qy 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 607 TGTGGGCGCTGGGCTTCTACCTGGGAGATCACCTGACCTGACCTGGCGGCGGATGGGAG 666
Qy 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 667 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGGCGCTGCAGGG 711

RESULT 6

US-09-819-371-3
; Sequence 3, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-819-371-3

Alignment Scores:
Pred. No.: 6,85e-137 Length: 645
Score: 1151.00 Matches: 212
Percent Similarity: 99.07% Conservative: 1
Best Local Similarity: 98.60% Mismatches: 2
Query Match: 98.12% Indels: 0
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x US-09-819-371-3 (1-645)

Qy 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAlaAlaIle 20
Db 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCCGACAGCGCGCGGATT 60
Qy 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 61 CCGAGGATGGACCGCGGAGCGGTGGTGGAGGAGGCGCGCGCGATTATGGGAGTGG 120
Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 121 ACCACGCGTACGCCAAGGCGCACACGACGACGAGTGGCGCTCCGAGGACCTGCTC 180
Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 181 CGCCGCTTACACACAGAGCGAGGCTGGTCTCACCCCTCCAGGGAATGAATGGCTGGCAC 240
Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 241 ATGGGCGCCGACCGAGCGCTCTCCCGCGGTATCACACGACGCGTACGACGCGCAGGAT 300
Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 301 TACATCTCCCTGAACGAGGACCTGCGCTCTCGACCGCGCGGACACCGCTGCTCAGATC 360
Qy 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluPheArgThrTyrLeuGluGly 140
Db 361 ACCACGCGTCTTATGAGGAGAGGAATATGACAGAGATTGAGGACCTACCTGGAGGCG 420
Qy 141 GluCysLeuGluLeuLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 421 GAGTGCTGGAGTTGCTCCGACATATCTGGAGATGGGAGAGAGAGCTACAGCGCGCA 480
Qy 161 AspProProlLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 481 GATCTCTCCAAAGGACACGTTGGCCACCCATCTCTGACCATGAGGCCACCTGGAGG 540
Qy 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 541 TGTGGGCGCTGGGCTTCTACCTGGGAGATCACCTGACCTGACCTGGCGGCGGATGGGAG 600
Qy 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGGCGCTGCAGGG 645

RESULT 7
US-09-880-107-3713
; Sequence 3713, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherff, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3713
; LENGTH: 4316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X17093
US-09-880-107-3713

Alignment Scores:
Pred. No.: 9,76e-116 Length: 4316
Score: 993.50 Matches: 214
Percent Similarity: 43.79% Conservative: 1
Best Local Similarity: 43.58% Mismatches: 0
Query Match: 84.70% Indels: 276
DB: 9 Gaps: 2

US-09-819-371-6 (1-215) x US-09-880-107-3713 (1-4316)

Qy 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
Db 1109 ATCGCGTGGAGTACGACGACGCAATTCCTGCGGTTCCGACAGCGAGCGCGGATT 1168
Qy 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 1169 CCGAGGATGAGCGCGGAGCGCGTGGTGGAGCAAGAGGGCGCGGCGGCGGATTGGGAGTGG 1228
Qy 41 ThrThrGlyTyrAlaLysAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 1229 ACCACAGGTTACGCCAGGCCACACGACAGACTGACCGAGTGGCCCTGAGGAACTGCTC 1288
Qy 61 ArgArgTyrAsnGlnSerGlu 67
Db 1289 CGCCGCTACAACACAGAGCGAGGTGGTGTAGTGAAACCCCGCGGGGCGCGAGTCCAGACC 1348
Qy 67 67
Db 1349 ACCCCCATCCGCCACGAGACCGCCCGGGTCCCGCCGAGTCTCCGATCCGAAATCTACCC 1408
Qy 67 67
Db 1409 CGAGGCGAGCGGACCCCGCCAGACCCCTCCACCGGGAGAGTCCCGCGGCGCTTTTACCGAGG 1468
Qy 67 67
Db 1469 TTCATTTTCAGTTTAGTCCCAAAATCCCGCGGTGGCGGGAGGGGCGGGGTAGCT 1528
Qy 68 -----Ala-GlySerHisThrLeuGlnGlyMetAsnGlyCy 79
Db 1529 GGGCGGGGTGACTGCGGGGACCGGCTAGGGTCTCACACCTCCAGGGAATGAATGGCTG 1588
Qy 79 sAspMetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyIy 99
Db 1589 CGACATGGGGCCCGACGAGCGGCTCTCTCGCGGGTATCCAGCAGCGCGCTACGCGCAA 1648

Qy 99 sAspTyrIleSerIleuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlu 119
Db 1649 GGAATTACATCTCCCTGAACGAGACCTGGCTCTGGACCGCGCGGACACCTGGGTCTCA 1708
Qy 119 nileThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGlu 139
Db 1709 GATCACCACCGGCTTCTATGAGGACAGAGGATATGAGAGGAGTTTCAAGACCTACCTGGA 1768
Qy 139 uGlyGluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyIysGluThrLeuGlnAr 159
Db 1769 GGGCGAGTGGCTGGAGTTGCTCCGCGATACTTGGAGAAATGGGAAGAGAGCGCTACAGCG 1828
Qy 159 gAla----- 160
Db 1829 CGAGGTACCAAGGGGCCATGGGGCCCTTCCCTATCTCCTGTAGATCTCTTGGGATGSCCT 1888
Qy 160 ----- 160
Db 1889 CGCACAAGTTGGGAGGAGAAAGTGGGCCCAATGCTAGGATATCGCCCTCCCTCTAGTCTG 1948
Qy 160 ----- 160
Db 1949 AGTAGGAAGAATCTTCTGGCTTTCGAGATCCCGTACCAGAGAGTGAAGTGAAGTCCG 2008
Qy 160 ----- 160
Db 2009 CCCTGCTCTCTGGGACAAATTAGGGATGAAATCTCTGAGGGAATGGAGGGAAGACACTCC 2068
Qy 160 ----- 160
Db 2069 CTGGAATACCGATCCGCGGTCCCTTTTGAGCCCTCCAAACAGCCCTTGGGCCCCCGTACTTT 2128
Qy 160 ----- 160
Db 2129 TCTCTCAAGTTTGTCTCTGCTGCCTCACACTCAATGTGTTTGGGGCTCTGATTCAGTCCC 2188
Qy 160 ----- 160
Db 2189 TCGGCTCTCCTAGGTGAGGCGCAGAAAGTCCCTGTCTCCCACTCAGAGACTCGAAGCTTT 2248
Qy 160 ----- 160
Db 2249 CCAAGGAATAGGAGATTTTCCAGGTGTGTGTCCAGGCTGTGTGTGGTCTGTGTCTGTGCT 2308
Qy 160 ----- 160
Db 2309 CCCTTCCCGCCAGGTGTCTGTCCATTCTCAGGTTGGTTCATCGGGTGTGTGTGGGG 2368
Qy 161 -----AspProProlysAl 165
Db 2369 TTTCCCATGAGGAGTGCAAGTGCTGAATTTTCTGACTCTTCTCAGATCTCTCAAGGC 2428
Qy 165 aHisValAlaHisProIleSerAspHisGluAlaThrLeuArgCysTrpAlaLeuGlu 185
Db 2429 ACAGTTGCCACACACCCCATCTCTGACCATGAGGCCACCTGAGGTGTGGGGCTGGG 2488
Qy 185 yPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGluGluGlnThrGlnAs 205
Db 2489 CTTTACCTGCGGAGATCACGCTGACCTGCGCGGATGGGAGGAGAACAGACCCAGGA 2548
Qy 205 pThrGluLeuValGluThrArgProAlaGly 215
Db 2549 CACAGAGCTTGTGGAGACCAAGGCTTCGAGG 2579

RESULT 8
US-10-257-021-81
; Sequence 81, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pfizer, Ellen S.

; APPLICANT: Hough, Colleen D.
 ; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
 ; FILE REFERENCE: 14014.036902
 ; CURRENT APPLICATION NUMBER: US/10/257,021
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: PCT/US01/10947
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/194,336
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 81
 ; LENGTH: 4316
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-257-021-81

Alignment Scores:
 Pred. No.: 9,76e-116 Length: 4316
 Score: 993.50 Matches: 214
 Percent Similarity: 43.79% Conservatives: 1
 Best Local Similarity: 43.58% Mismatches: 0
 Query Match: 84.70% Indels: 276
 DB: 13 Gaps: 2

US-09-819-371-6 (1-215) x US-10-257-021-81 (1-4316)

Qy	1	IleAlaValGluTyrValAspSerThrGlnPheLeuArgPheAspSerAspAlaLalle	20
Db	1109	ATCGCGTGGAGTACGTAGACACGCAATTCCTGCGGTTCGACAGCGACCCCGGAT	1169
Qy	21	ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr	40
Db	1169	CCGAGGATGGACCGCGGAGCGCGTGGGTGGAGCAGAGCGGCGCGAGTATTGGAGTGG	1228
Qy	41	ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu	60
Db	1229	ACCACAGGGTACGCCAAGCCCAACGACACAGACTGACCGAGTGGCGCTGAGGAACCTGTC	1289
Qy	61	ArgArgTyrAsnGlnSerGlu	67
Db	1289	CGCCGCTACACAGAGCGAGCGCTGGTGTAGTGAAACCCGCGCGGGCGGAGGTACGACC	1348
Qy	67	-----	67
Db	1349	ACCCGCCATCCGACAGCGACCGCGGTCCTCCCGGAGTCTCCGATCCGAAATCTACCC	1408
Qy	67	-----	67
Db	1409	CGAGCGAGCGACCCGCCACAGACCCCTCCACCCGCGGAGAGTCCCGAGGCGCTTTACCGAGG	1469
Qy	67	-----	67
Db	1469	TTCAATTTTACGTTAGGCCCAATCCCGCGGGTTGGCGGGGAGGGCGGGGTAGCT	1528
Qy	68	-----Ala-GlySerHisThrLeuGlnGlyMetAsnGlyCy	79
Db	1529	GGCGCGGGTGTACTGCGGGGACCGGCTAGGTCTCACACCTCCAGGGAATGAATGGGTG	1589
Qy	79	sAspMetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLy	99
Db	1589	CGACATGGGGCCGACGAGCGCTCTCCCGGGGTATCACACGACGCGGTACACCGGCA	1648
Qy	99	sAspTyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaG	119
Db	1649	GGATTACATCTCCCTGAACGAGGACCTGGCTCTCTGGACCGCGGGCGGACACCGTGGCTCA	1708
Qy	119	nIleThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuG	139
Db	1709	GATCACCCAGCGCTCTATGAGCAGAGGAATATGACAGAGGAGTTCAGGACCTACTCGA	1769
Qy	139	uGlyGluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnAr	159

Db	1769	GGCGAGTGCCTGGAGTTGCTCCGAGATACCTTGGAGAAATGGGAAGAGACGCTCAGCG	1828
Qy	159	gala-----	160
Db	1829	CGCAGGTACCAGGGCCATGGGCGCTTCCCTATCTCTCTAGATCTCTTGGGATGGCCT	1888
Qy	160	-----	160
Db	1889	CGCACAAGTTGGGAGGAAAGTGGGCCAATGCTAGGATATCGCCCTCCTTAGTCTG	1948
Qy	160	-----	160
Db	1949	ASTAGGAAGAATCTTCTGCTTCGAGATCCGGTACCAGAGAGTGACTGTGAGAGTCCG	2008
Qy	160	-----	160
Db	2009	CCCTGCTCTCTGGACAATTAAGGATGAATCTCTGAGGGAATGGAGGAAGACAGATCC	2068
Qy	160	-----	160
Db	2069	CTGGAATACCGATCCGCGGTCCTCTTGGAGCCCTCCACAGCCCTTGGGCCCTGACTTT	2128
Qy	160	-----	160
Db	2129	TCTCTCAAGTTTGTCTCTGCTCACCCTCACTCACTCACTCACTCACTCACTCACTCACT	2188
Qy	160	-----	160
Db	2189	TCGGCTCTCACTTAGTGCAGGGCCAGAGTCCCTGCTCCCACTCAGAGACTCGAATTT	2248
Qy	160	-----	160
Db	2249	CCAGGAATAGGAGATTTTCCAGGTGTCTGTCTCCAGGTGTCTGTCTGTCTGTCTGTCT	2308
Qy	160	-----	160
Db	2309	CCCTTCCCAACCCAGGTGTCTGTCTCCATCTCAGGTGTCTCAGTGTCTGTCTGTCTGT	2368
Qy	161	-----AspProGlySA1	165
Db	2369	TTTCCCATGAGAGTGCAGAGTGCCTGAATTTCTGACTCTCTCTCAGATCTCTCAAGGC	2428
Qy	165	aHisValAlaHisHisProIleSerHisGlnAlaThrLeuArgCysTrpAlaLeuG	185
Db	2429	ACAGTTGGCCACCCACCCATCTCTGACATGAGGCCACCTGAGGTGTCTGGGCCCTGGG	2488
Qy	185	yPheTyrProAlaGluThrLeuThrTrpGlnArgAspGlyGluGluGlnThrGlnAs	205
Db	2489	CTTCTACCTTGGGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2548
Qy	205	pThrGluLeuValGluThrArgProAlaGly	215
Db	2549	CACAGAGCTTGTGGAGACCGAGGCTGCAGGG	2579

RESULT 9
 US-09-764-891-6712
 ; Sequence 6712, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6712
 ; LENGTH: 3098
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-891-6712

Alignment Scores:
 Pred. No.: 1.59e-114 Length: 3098
 Score: 982.50 Matches: 213
 Percent Similarity: 43.58% Conservative: 1
 Best Local Similarity: 43.38% Mismatches: 1
 Query Match: 83.76% Indels: 277
 DB: 10 Gaps: 2

US-09-819-371-6 (1-215) x US-09-764-891-6712 (1-3098)

Qy	1	IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAlaAlaIle	20
Db	293	ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTGCACAGCGACCCCGGATT	352
Qy	21	ProArgMetGluProArgGluProThrValGluGlnGluGlyProGlnTyrTrpGluTrp	40
Db	353	CCGAGGATGGAGCGCGGAGCGCTGGGTGGAGCAAGAGCGCGCAGTATTGGAGTGG	412
Qy	41	ThrThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu	60
Db	413	ACACAGGTACGCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGTCT	472
Qy	61	ArgArgTyrAsnGlnSerGluAla	68
Db	473	CGCCGCTACAAACAGAGCGAGGC-TGGTGTAGTGAACCCGCGCGGGCGCGAGGTCAACGAC	531
Qy	68	-----	68
Db	532	CACCCGCCATCCGCCACGACCGCCGCGGTCCCTCAGACTCTCCGATCCGAAATCTACC	591
Qy	68	-----	68
Db	592	CCGAGCGAGCGGACCGCGCCAGACCCCTCCACCCGGGAGAGTCCCAAGCGCCCTTTACCCA	651
Qy	68	-----	68
Db	652	GGTTCAATTTTACGTTTAGGCCAAATCCCGCGGGTTGGCGGGAGGGCGGGCGGTAG	711
Qy	69	-----GlySerHisThrLeuGlnGlyMetAsnGly	78
Db	712	CTGGCGGGGCTGACTGTCGGGGACCGGGTAGGGTCTCACACCTCCAGGGATGATGGC	771
Qy	79	CysAspMetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGly	98
Db	772	TGCGACATGGGCGCCGACGAGCGCTCTCCCGGGGTATCACAGCACGCGTACGACGCG	831
Qy	99	LysAspTyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAla	118
Db	832	AAGGATTACATCTCCCTGAACGAGSACCTCGCTCTGGACCGCGCGGACACCGTGGCT	891
Qy	119	GlnIleThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeu	138
Db	892	CAGATCACCGAGCGCTTCTATGAGGAGAGGATATGCAGAGAGTTTCAGGACCTACCTG	951
Qy	139	GluGlyGluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGln	158
Db	952	GAGGGCGAGTGGCTGGAGTTGCTCCGACAGATCTTGAGAAATGGGAGGAGCGCTACAG	1011
Qy	159	ArgAla	160
Db	1012	CGCGAGGTACAGGGGCCATGGCGGCTTCCCTATCTCCTGTAGATCTCTTGGGATGGC	1071
Qy	160	-----	160
Db	1072	CTCGCAAGGTTGGGAGAAAGTGGACCAATGCTAGGATATCGCCCTCCCTCTAGTCC	1131
Qy	160	-----	160
Db	1132	TGAGTAGAAGAATCTTCCTGGCTTTTCGAGATCCGGTACAGAGAGTGACTGTGAGAGTC	1191
Qy	160	-----	160
Db	1192	CGCCTGCTCTCTGGACAAATTAAGGATGAATTTCTGAGGAATGAGGAGAGACGT	1251

Qy	160	-----	160
Db	1252	CCCTGGAATACCGATCGCGGTCCCTTTGAGGCCCTCAAACAGCCTTGGGCCCGTGAAT	1311
Qy	160	-----	160
Db	1312	TTTCTCTCAAGTTTTGTCTCTCGCTCACACTCAATGTGTGTAGGCTCTGATTCAGATC	1371
Qy	160	-----	160
Db	1372	CCTCGGCTCCACTTAGGTAGGTCAGGCGCAGAAAGTCCCTGCTCCCTCCCTCAGAGACTCTAACT	1431
Qy	160	-----	160
Db	1432	TTCAAGAAATAGAGATTTTCCAGGTGTCTGTGTCCAGGCTGTCTCTGGGTCTGTGTG	1491
Qy	160	-----	160
Db	1492	CTCCCTTCCCAACCCAGGTGTCTGTGTCCATCTCAGTTGGTCCATGCGTGTGCTGG	1551
Qy	161	-----AspProProlys	164
Db	1552	GGTTTCCCATGAGGAGTGCAAAGTGCCTGAATTTTCTGACTCTTCTCAGATCTCTCCAAAG	1611
Qy	165	AlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArgCysTrpAlaLeu	184
Db	1612	GCACAGTTGGCCACCCCACTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTG	1671
Qy	185	GlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGluGlnThrGln	204
Db	1672	GGCTTACCTCGGAGATCACGCTGACCTGGCAGCGGATGGGAGGAGAACAGACCCAG	1731
Qy	205	AspThrGluLeuValGluThrArgProAlaGly	215
Db	1732	GACACAGAGCTTGTGGAGACAGGCGCTGCAGGG	1764

RESULT 10

US-10-091-572-573
 ; Sequence 573 Application US/10091572
 ; Publication No. US20030054373A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P118C1
 ; CURRENT APPLICATION NUMBER: US/10/091,572
 ; CURRENT FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: 09/764,850
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 60/179,065
 ; PRIOR FILING DATE: 2000-01-31
 ; PRIOR APPLICATION NUMBER: 60/180,628
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: 60/214,886
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/217,487
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,758
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,963
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/217,496
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,447
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/218,290
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/225,757
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/226,868
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/216,647
 ; PRIOR FILING DATE: 2000-07-07

, PRIOR APPLICATION NUMBER: 60/225,267
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/216,880
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,270
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/251,869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/234,274
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234,223
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/228,924
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/224,518
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,369
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/224,519
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,964
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241,809
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249,299
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/236,327
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225,268
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,368
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/251,856
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251,868
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/229,344
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 60/229,343
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,287
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,513
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/231,413
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/229,509
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/236,367
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/237,039
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,038
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/236,370
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,802
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,037
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/240,960
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/239,935
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/239,937
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,787
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,532
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,216
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,210
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226,681
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,759
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,213
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227,182
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,218
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,208
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,212
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,207
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,245
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,244
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,217
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,211
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,215
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,264
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,297
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/232,400
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/231,242
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,081
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,080
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,244
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,064
PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Alignment Scores:
Pred. No.: 1,59e-114 Length: 3098
Score: 982.50 Matches: 213
Percent Similarity: 43.58% Conservative: 1
Best Local Similarity: 43.38% Mismatches: 1
Query Match: 83.76% Indels: 277
DB: 15 Gaps: 2

US-09-819-371-6 (1-215) x US-10-091-572-573 (1-3098)

Qy 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAlaAlaIle 20
Db 293 ATGCGCGTGGAGTACGTAGACGACACGCAATTCCTGGGTTCACAGCGCGCGGATT 352
Qy 21 ProArgMetGluProArgGluProTyrValGlnGluGlyProGlnTyrTrpGluTyr 40
Db 353 CCGAGGATGGAGCCGCGGAGCCGCTGGGTGGAGCAAGAGGGCGCGAGTATTGGAGTGG 412
Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 413 ACCACAGGTACGCCAAGGCCACACGACACTACCGAGTGGCGCTTGAGGAACCTGCTC 472
Qy 61 ArgArgTyrAsnGlnSerGluAla----- 68
Db 473 CGCGCGTACACACGAGCGAGGC-TGGTGTAGTGAACCGCGCGGGGGCGGAGGTACAGCAG 531
Qy 68 ----- 68
Db 532 CACCCCCATCCGCCACGCGCCGCGGTCCCTCAGAGTCTCCGGATCCGAAATCTACC 591
Qy 68 ----- 68
Db 592 CCGAGGACGCGGACCCGCCAGACCTCCACCCGGAGAGTCCCGCGGCTTTACCCA 651
Qy 68 ----- 68
Db 652 GGTTCATTTTCAGTTAGTCCAAATATCCCGCGGTTGGCGGGGAGGGCGCGGGCTAG 711
Qy 69 -----GlySerHisThrLeuGlnGlyWetAsnGly 78
Db 712 CTGGCGGGGCTGACTGCGGGGACCGGCTAGGCTCTCACCCCTCCAGGGAATGAATGC 771
Qy 79 CysAspMetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGly 98
Db 772 TCGCAGATGGGCGCGAGCGCTCTCCCGGGGTATCACAGCAGCGGTACAGCGGC 831
Qy 99 LysAspTyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAla 118
Db 832 AAGGATTACATCTCCCTACAGGACCTCGCTCTGGACCGCGGCGGACACCGTGCT 891
Qy 119 GlnIleThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeu 138

Db 892 CAGATCACCCAGCGCTTCTATAGGAGAGGAATATGACAGGAGTTTCAGGACCTTACCTG 951
Qy 139 GluGlyGluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGln 158
Db 952 GAGGCGAGTGCCTGGAGTTGCTCCGAGATACCTTGAGAAATGGAGGAGACGCTACAG 1011
Qy 159 ArgAla----- 160
Db 1012 CGCGCAGGTACACAGGGGCCATGCGCGCTTCCTATATCTCTGTAGATCTCTTGGGATGGC 1071
Qy 160 ----- 160
Db 1072 CTCGCACAAGTGGGAGGAAGTGGACCCCAATGCTAGGATATCGCCCTCCTCTAGTCC 1131
Qy 160 ----- 160
Db 1132 TGAGTAGGAAGAATCTTCTGGCTTTTGAGATCCGATCCGATACAGAGTACTGTGAGATC 1191
Qy 160 ----- 160
Db 1192 CGCCCTGCTCTCTGGGACAATTAAGGGATGAATTTCTGAGGGAATGGAGGAGACAGT 1251
Qy 160 ----- 160
Db 1252 CCTCGAATACGATCCGCGGTCCCTTTGAGCCCTCCACAGCCTTGGGCCCCGTGACT 1311
Qy 160 ----- 160
Db 1312 TTCTCTCAAGTTTGTCTCTGCTCCTCACATCAATGTGTTGAGGCTCTGATTCAGTC 1371
Qy 160 ----- 160
Db 1372 CCTCGGCTCCACTTAGTTCAGGGCCAGAGTCCCTGCTCCCTCCCTCAGAGACTCTAAT 1431
Qy 160 ----- 160
Db 1432 TTCCAAGGAATAGAGATTTTCCAGGTCTCTGTCTCCAGGTGGTGTCTGGTCTGTG 1491
Qy 160 ----- 160
Db 1492 CTCCTTCCACCCAGGTGCTCTGTCCATCTCAGGTGGTGCATCGGTGCTGTG 1551
Qy 161 -----AspProProlys 164
Db 1552 GGTTCCTCATGAGGATGCANAAGTGCCTGAATTTTCTGACTCTTCTCAGATCTCCAAAG 1611
Qy 165 AlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArgCysTrpAlaLeu 184
Db 1612 GCACAGTGTGCCACCCACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTG 1671
Qy 185 GlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGluGlnThrGln 204
Db 1672 GGTTCCTACCTCGGAGATCAGCTGACTGCGAGCGGATGGGAGGGAACAGACCCAG 1731
Qy 205 AspThrGluLeuValGluThrArgProAlaGly 215
Db 1732 GACACAGAGCTTGTGGAGACCAAGGCTGAGGG 1764

RESULT 11

US-10-342-887-1160
; Sequence 1160, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999

; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1160
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1160

Alignment Scores:
Pred. No.: 2,74e-107 Length: 1089
Score: 921.00 Matches: 170
Percent Similarity: 86.05% Conservative: 15
Best Local Similarity: 79.07% Mismatches: 30
Query Match: 78.52% Indels: 0
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x US-10-342-887-1160 (1-1089)

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QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
Db 139 ATCTCAGTGGGTACGTGACGACACGCGAGTTCGTGAGGTTCCGACGCGCGGAGT 198
QY 21 ProArgMetGluProArgGluProTTPValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 199 CCGAGAGAGGAGCGCGCGCGCGCGTGGATAGACGAGGCGCGCGGATATTGGGACCGG 258
QY 41 ThrThrGlyTyrAlaLysAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 259 AACACACAGATCTGCAGACCAACACACAGACTGACCGAGAGCGCTCGGGAACCTGGCG 318
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 319 GGCTACTACAAACAGAGCGCGCGGCTCTCACACCTCCAGTGGATGATGGCTGCGGAC 378
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 100
Db 379 GTGGGCGCGGACCGGGCGCTCTCCGCGGGTATAACCACTTCGCTACGCGCGCAAGGAT 438
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
Db 439 TACATCGCCCTGAACGAGGACCTGAGCTCTCGGAGCGCGCGGACACCGCGGCTCAGATC 498
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 499 ACCGAGCGCAAGTGGGAGCGCGCGCGTGGAGCGGAGCAGCTGAGACCTACCTGGAGGCG 558
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 559 ACCTGGCTGGAGTGGCTTCCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAG 618
QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 619 GACCCCGGCAAGACACATGATGACCCACCCCATCTCTGACCATGAGCGCCACCTCGAGG 678
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTyrGlnArgAspGlyGlu 200
Db 679 TGTGGGCGCTGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAG 738
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 739 GACCAACTCAGGACACCGAGCTTGTGGAGACCAACGACGAGCA 783
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RESULT 12

US-10-172-118-1160
; Sequence 1160, Application US/10172118
; Publication No. US20030224374A1

; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1160
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005514
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1160

Alignment Scores:
Pred. No.: 2,74e-107 Length: 1089
Score: 921.00 Matches: 170
Percent Similarity: 86.05% Conservative: 15
Best Local Similarity: 79.07% Mismatches: 30
Query Match: 78.52% Indels: 0
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x US-10-172-118-1160 (1-1089)

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QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
Db 139 ATCTCAGTGGGTACGTGACGACACGCGAGTTCGTGAGGTTCCGACGCGCGGAGT 198
QY 21 ProArgMetGluProArgGluProTTPValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 199 CCGAGAGAGGAGCGCGCGCGCGTGGATAGACGAGGCGCGCGGATATTGGGACCGG 258
QY 41 ThrThrGlyTyrAlaLysAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 259 AACACACAGATCTGCAGACCAACACACAGACTGACCGAGAGCGCTCGGGAACCTGGCG 318
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 319 GGCTACTACAAACAGAGCGCGCGGCTCTCACACCTCCAGTGGATGATGGCTGCGGAC 378
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 100
Db 379 GTGGGCGCGGACCGGGCGCTCTCCGCGGGTATAACCACTTCGCTACGCGCGCAAGGAT 438
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
Db 439 TACATCGCCCTGAACGAGGACCTGAGCTCTCGGAGCGCGCGGACACCGCGGCTCAGATC 498
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 499 ACCGAGCGCAAGTGGGAGCGCGCGCGTGGAGCGGAGCAGCTGAGACCTACCTGGAGGCG 558
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 559 ACCTGGCTGGAGTGGCTTCCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAG 618
QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 619 GACCCCGGCAAGACACATGATGACCCACCCCATCTCTGACCATGAGCGCCACCTCGAGG 678
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTyrGlnArgAspGlyGlu 200
```



```
Db 679 TCGTGGGCGCTTCTACCTGGGAGATCACACTGACCTGGGAGCGGATGGCGAG 738
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 739 GACCAAACTCAGACACCGAGCTGTGGAGACACAGACGACGAGGA 783

RESULT 13
US-10-044-090-576
; Sequence 576, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 576
; LENGTH: 1571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1382902.13
; LOCATION: 1568
; NAME/KEY: unsure
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-576

Alignment Scores:
Pred. No.: 7,98e-107 Length: 1571
Score: 919.00 Matches: 170
Percent Similarity: 85.12% Conservative: 13
Best Local Similarity: 79.07% Mismatches: 32
Query Match: 18.35% Indels: 0
DB: 14 Gaps: 0

US-09-819-371-6 (1-215) x US-10-044-090-576 (1-1571)
QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAlaAlaIle 20
Db 178 ATACCGTGGGCTACGTGGGACGACACGCTCTCGTAGGTTCGACGCGCACGAGT 237
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 238 CCGAGGAAGGACCGCGCGCCATGATAGACGAGGCGCGGATTCGGACCGG 297
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60
Db 298 GAGACACAGATCTCCAAGACCAACACACAGACTTACCGAGAGCGCTGCGGAACCTGGCG 357
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 358 GGCTACTACCAACAGACGAGCGCGGTCTCACACCTCCAGAGGATGTTTGGCTGGAC 417
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 418 GTGGGGCCGACGCGCGCTCTCTCCGCGGCTACCAACGAGACGCTACGACGCGCAAGGAT 477
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 478 TACATCCCTTGAACAGGAGACCTGAGCTCTCTGACCGCCGCGGACGACGCGGCTCAGATC 537
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 538 ACCCAGCGCAAGTGGGAGCGCGCGGTGGCGGAGCAGCTGAGAGCTACCTGGAGGCG 597
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGlnThrLeuGlnArgAla 160
Db 598 GAGTGCCTGGAGTGGCTCCGCGATACCTGAGAACCGGAGGAGACGCTGCGACGCGCG 657
QY 161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
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Db 658 GACCCCAAGACACACGTCAGCCACCCACCATCTCTGACCATGAGGCCACCTGAGG 717
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 718 TGTCTGGGCGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGATGGCGAG 777
QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
Db 778 GACCAAACTCAGGACACTGAGCTTGTGGAGACCAACGACGACGAGGA 822

RESULT 14
US-10-302-172-322
; Sequence 322, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids an
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803 ICNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 322
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(213)
US-10-302-172-322

Alignment Scores:
Pred. No.: 1,85e-106 Length: 1221
Score: 915.00 Matches: 169
Percent Similarity: 86.05% Conservative: 16
Best Local Similarity: 78.60% Mismatches: 30
Query Match: 78.01% Indels: 0
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x US-10-302-172-322 (1-1221)
QY 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAlaAlaIle 20
Db 267 ATCTCAGTGGGCTACGTGGACGGCACCCAGTTCGTAGGTTCGACAGCGACGCCCGAGT 326
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db 327 CCGAGGACGAGCGCGCGCGCGCGGTGATAGCAGAGGCGCGGATTTGGGACCGG 386
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60
Db 387 AACACACAGATCTCCAGACCAACACACAGACTTACCGAGAGGACCTGCGGACCTGCTC 446
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 447 CGCTACTACCAACGAGGAGCGCGGTCTCACACCATCCAGAGGATGTCTGGCTGGCAG 506
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 507 GTGGGGCGGAGCGCGCGCTCTCTCCGCGGTATACACAGTTCGCTACGACGCGCAGGAT 566
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
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Db 567 TACATCGCCCTGACGAGACCTGAGCTCTCGGACCGCGGACACCGCGCTCAGATC 626
 Qy 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
 Db 627 ACCCAGCGCAAGTGGGAGCGCCCGTGTGGCGGACGAGCAGAGCCCTACTCTGAGGGC 686
 Qy 141 GluCysLeuGluLeuLeuArgTyrTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 Db 687 ACGTGGCTGGAGTGGCTCCGCGAGATCTCTGGAGAACGGGAGGAGACGCTGCAGCGCG 746
 Qy 161 AspProProLysAlaHisValAlaHisHisProLysSerAspHisGluAlaThrLeuArg 180
 Db 747 GACCCCGCCAAAGACACATGTGACCCACCAACCCCATCTCTGACCATGAGGCCACCTGAGG 806
 Qy 181 CysTTPAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTyrGlnArgAspGlyGlu 200
 Db 807 TGTGGGCGCTGGGCTTCTACCTGGCGAGATCACTACCTGGCAGCGGATGGCGAG 866
 Qy 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 Db 867 GACCAAACTCAGGACACCGAGCTTGTGGAGACGAGACGAGGAGGA 911

RESULT 15

US-09-969-708-235
 ; Sequence 235, Application US/09969708
 ; Patent No. US20020102532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Augustus, Meena
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
 ; FILE REFERENCE: 869290-70
 ; CURRENT APPLICATION NUMBER: US/09/969, 708
 ; CURRENT FILING DATE: 2001-10-03
 ; PRIOR APPLICATION NUMBER: US/60/237, 606
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: US/60/237, 608
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: US/60/237, 425
 ; PRIOR FILING DATE: 2000-10-03
 ; NUMBER OF SEQ ID NOS: 658
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 235
 ; LENGTH: 1271
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-969-708-235

Alignment Scores:
 Pred. No.: 6.31e-106 Length: 1271
 Score: 911.00 Matches: 170
 Percent Similarity: 86.05% Conservative: 15
 Best Local Similarity: 79.07% Mismatches: 30
 Query Match: 77.66% Indels: 0
 DB: Gaps: 0

US-09-819-371-6 (1-215) x US-09-969-708-235 (1-1271)

Qy 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaIle 20
 Db 139 ATCGCAGTGGCTACCTGGACGACACCCAGTTCGTGAGTTGACAGCGACCGCGAGT 198
 Qy 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 Db 199 CCAGAGATGGCGCCCGCGCGCCATGGATAGACAGAGGGCGCGAGTATTGGGACCGG 258
 Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 50
 Db 259 GAGACACAGATCTCCAAAGACCAACACACAGACTTACCGAGAGAGCCCTGGGAACTGGCGC 318
 Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 Db 319 GGCTACTAACCAACGAGCGAGCGGGGTCTCACACCTCCAGAGAGATGTAAAGGCTCGGAC 378

Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
 Db 379 GTGGGCGCGACGCGCGCTCTCTCGCGGCGATGACAGTCCGCTACGACGSCAAGGAT 438
 Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
 Db 439 TACATCGCCCTGACGAGGACCTGAGCTCTGACCGCGCGGACACCGCGGCTCAGATC 498
 Qy 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
 Db 499 ACCCAGCGCAAGTGGGAGCGCGCCCTGAGCGGAGCAGCTGGAGAGCCTACCTGGAGGGC 558
 Qy 141 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 Db 559 CTGTGCGTGGAGTGGCTCCGCGAGATACCTGGAGAACGGGAGGAGACGCTGCAGCGCGG 618
 Qy 161 AspProProLysAlaHisValAlaHisHisProLysSerAspHisGluAlaThrLeuArg 180
 Db 619 GACCCCGCCAAAGACACATGTGACCCACCAACCCCATCTCTGACCATGAGGCCACCTGAGG 678
 Qy 181 CysTTPAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTyrGlnArgAspGlyGlu 200
 Db 679 TGTGGGCGCTGGGCTTCTACCTGGCGAGATCACACTGACCTGGCAGCGGATGGCGAG 738
 Qy 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 Db 739 GACCAAACTCAGGACACCGAGCTTGTGGAGACGAGACGAGCAGGAGGA 783

Search completed: June 18, 2004, 08:50:05

Job time : 429 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 09:57:17 ; Search time 26 Seconds
(without alignments)
795.430 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 1173
Sequence: 1 TAVEYVDDTQFLRFDSDAAI.....QRDGEQTDTELVTETPAG 215
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1164	99.2	362	2 A60384	MHC class I histoc
2	1149	98.0	345	2 S07114	MHC class I histoc
3	1100	93.8	348	2 S29990	histocompatibility
4	960	81.8	340	2 S11143	class I histocompa
5	939	80.1	362	1 HLHUB2	MHC class I histoc
6	936	79.8	338	2 I56116	MHC HLA-B*27-HS - h
7	935	79.7	354	2 I80170	class I histocompa
8	932	79.5	363	1 S42102	MHC class I histoc
9	931	79.4	362	2 I37515	MHC class I histoc
10	927	79.0	362	2 I54505	lymphocyte antigen
11	927	79.0	362	2 I59845	HLA-B*6701 - human
12	927	79.0	362	2 I54314	MHC HLA-B*39N - hum
13	927	79.0	362	2 I68850	MHC class I histoc
14	924	78.8	362	2 I61865	MHC HLA-B*42, HLA-
15	923	78.7	362	2 I68724	MHC class I histoc
16	923	78.7	362	2 I59651	lymphocyte antigen
17	922	78.6	350	2 I68747	MHC class I lympho
18	922	78.6	354	2 S24440	class I histocompa
19	922	78.6	362	2 I84431	MHC HLA-B*8 chain -
20	922	78.6	362	2 I72755	HLA-B*5602 - human
21	922	78.6	362	2 I62045	gene HLA B-1517 pr
22	922	78.6	363	2 S07113	class I histocompa
23	921	78.5	361	2 I54418	MHC class I histoc
24	921	78.5	362	1 HLHUB7	MHC class I histoc
25	921	78.5	362	2 C25397	MHC class I histoc
26	921	78.5	362	2 I61863	MHC class I histoc
27	921	78.5	362	2 I61859	MHC HLA-B*46 hum
28	920	78.4	274	2 S24439	class I histocompa
29	920	78.4	355	2 I80169	class I histocompa

30	919	78.3	362	2 S60601	HLA-B*POT (class I)
31	918	78.3	354	2 I59308	class I histocompa
32	918	78.3	355	2 I80171	class I histocompa
33	918	78.3	362	2 JH0341	class I histocompa
34	918	78.3	362	2 I84488	lymphocyte antigen
35	918	78.3	362	2 I72753	HLA-B*5502 - human
36	918	78.3	362	2 I56130	HLA-B*5401 - human
37	918	78.3	363	2 S03537	class I histocompa
38	917	78.2	362	2 I72752	HLA-B*5501 - human
39	917	78.2	362	2 I59655	lymphocyte antigen
40	916	78.1	362	2 I72754	HLA-B*5401 - human
41	915	78.0	359	2 S03538	class I histocompa
42	915	78.0	366	2 I72113	MHC histocompatibl
43	915	78.0	366	2 I38507	MHC class I histoc
44	914	77.9	342	1 HLHUC4	MHC class I histoc
45	914	77.9	357	2 S11133	class I histocompa

ALIGNMENTS

RESULT 1

A60384
MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Jul-1999
C:Accession: A60384; J0147
R:Lury, D.; Epstein, H.; Holmes, N.
Int. Immunol. 2, 531-537, 1990
A:Title: The human class I MHC gene HLA-F is expressed in lymphocytes.
A:Reference number: A60384; UID:91197889; PMID:1707659
A:Accession: A60384
A:Molecule type: DNA
R:Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.
J. Exp. Med. 171, 1-18, 1990
A:Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I
A:Reference number: J0147; UID:90111605; PMID:1588605
A:Accession: J0147
A:Molecule type: DNA
A:Residues: 1-362 <GER>
A:Cross-references: GB:X17093; NID:G32223; PIDN:CAA34947.1; PID:G312407
A:Experimental source: lymphoblastoid cell line
C:Genetics:
A:Gene: GDB:HLA-F
A:Cross-references: GDB:125714
A:Map position: 6p21.3-6p21.3
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 362/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-111/Domain: alpha-1 <Al1>
F:78-104/Region: hypervariable
F:112-203/Domain: alpha-2 <Al2>
F:164-192/Region: hypervariable
F:204-295/Domain: alpha-3 <Al3>
F:217-282/Domain: immunoglobulin homology <IMM>
F:107/Binding site: carbohydrate (Asn) #status predicted

Query Match 99.2%; Score 1164; DB 2; Length 362;
Best Local Similarity 99.5%; Pred. NO. 1.9e-90;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	TAVEYVDDTQFLRFDSDAAI	PRMEPREPWVQEGPQYWEWTTGYAKANAQTDRAVRLNL	60
DB	44	TAVEYVDDTQFLRFDSDAAI	PRMEPREPWVQEGPQYWEWTTGYAKANAQTDRAVRLNL	103
QY	61	RRYNSQAGSHTLQGMNCGDMPG	DRLLRGYHQHAWDGKDYISLNEDLSRWTAADTVAQI	120
DB	104	RRYNSQAGSHTLQGMNCGDMPG	DRLLRGYHQHAWDGKDYISLNEDLSRWTAADTVAQI	163
QY	121	TORFYEAEYAEFFTYLEGCELL	RRYLENGKETLORADPPKAYHAHHPISDEATLR	180

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Db      164  TORFYAEAEYAEFRYYLSECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 223
QY      181  CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db      224  CWALGFYPAEITLTWQDGEQTDTELVTETPAG 258

RESULT 2
S07114
MHC class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S07114
R:Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A:Reference number: S06424; MUID:88319000; PMID:3412487
A:Accession: S07114
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-345 <LAW>
A:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; membrane protein
F:217-282/Domain: immunoglobulin homology <IMM>

Query Match      98.0%; Score 1149; DB 2; Length 345;
Best Local Similarity 94.4%; Pred. No. 3.3e-89;
Matches 212; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYEWTTGYAKANAQTDRAVALRNL 60
Db      44  IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYEWTTGYAKANAQTDRAVALRNL 103
QY      61  RRYNQSEAGSHTLQGNMGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAAATVAQI 120
Db      104  RRYNQSEAGSHTLQGNMGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAAATVAQI 163
QY      121  TORFYAEAEYAEFRYYLSECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
Db      164  TORFYAEAEYAEFRYYLSECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 223
QY      181  CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db      224  CWALGFYPAEITLTWQDGEQTDTELVTETPAG 258

RESULT 3
S29990
histocompatibility antigen, HLA-F-like - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S29990
R:Bontrop, R.R.
submitted to the EMBL Data Library, February 1993
A:Reference number: S29990
A:Accession: S29990
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-348 <BON>
A:Cross-references: EMBL:Z21819; NID:G38569; PIDN:CAA79885.1; PID:G38569
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:219-284/Domain: immunoglobulin homology <IMM>

Query Match      93.8%; Score 1100; DB 2; Length 348;
Best Local Similarity 94.4%; Pred. No. 4.5e-85;
Matches 203; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1  IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYEWTTGYAKANAQTDRAVALRNL 60
Db      46  IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYEWTTGYAKANAQTDRAVALRNL 105
QY      61  RRYNQSEAGSHTLQGNMGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAAATVAQI 120

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Db      106  LRYNQSEAGSHTLQGNMGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAAATVAQI 165
QY      121  TORFYAEAEYAEFRYYLSECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
Db      166  TORFYAEAEYAEFRYYLSECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 225
QY      181  CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db      226  CWALGFYPAEITLTWQDGEQTDTELVTETPAG 260

RESULT 4
S11143
class I histocompatibility antigen alpha chain - cotton-top tamarin
C:Species: Saginus oedipus (cotton-top tamarin)
C>Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 23-May-1997
C:Accession: S11143
R:Watkins, D.I.; Chen, Z.W.; Hughes, A.L.; Evans, M.G.; Tedder, T.F.; Letvin, N.L.
Nature 346, 60-63, 1990
A:Title: Evolution of the MHC class I genes of a New World primate from ancestral homology.
A:Reference number: S10934; MUID:90309971; PMID:2114550
A:Accession: S11143
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-340 <WAT>
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:212-277/Domain: immunoglobulin homology <IMM>

Query Match      81.8%; Score 960; DB 2; Length 340;
Best Local Similarity 82.8%; Pred. No. 2.6e-73;
Matches 178; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY      1  IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYEWTTGYAKANAQTDRAVALRNL 60
Db      39  IGVGVDDTLFVRDSDDDPSRMEPRAPWPVEQGPQYEWTTGYAKANAQTDRAVALRNL 98
QY      61  RRYNQSEAGSHTLQGNMGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAAATVAQI 120
Db      99  RRYNQSEAGSHTLQGNMGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAAATVAQI 158
QY      121  TORFYAEAEYAEFRYYLSECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 180
Db      159  TORFYAEAEYAEFRYYLSECELELLRRYLENGKETLQADPPKAAHVAHPISDHEATLR 218
QY      181  CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db      219  CWALGFYPAEITLTWQDGEQTDTELVTETPAG 253

RESULT 5
HLHUB2
MHC class I histocompatibility antigen HLA-B27 alpha chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 13-Aug-1986 #sequence_revision 28-Apr-1995 #text_change 01-Dec-2000
C:Accession: S07441; A25092; B25092; A94087; S34180; S44942; A90493; B24741; I55965; S52;
R:Weisse, E.H.; Kuon, W.; Doerner, C.; Lang, M.; Rietmuller, G.
Immunobiology 170, 367-380, 1985
A:Title: Organization, sequence and expression of the HLA-B27 gene: a molecular approach
A:Reference number: S07441; MUID:86138405; PMID:3912316
A:Accession: S07441
A:Molecule type: DNA
A:Residues: 1-362 <WEI>
A:Cross-references: EMBL:X03945
A:Note: the authors translated the codon GAC for residue 61 as Ala and the codon CAG for
A:Note: this allele is designated B*27052 (formerly 27W)
R:Seemann, G.H.A.; Rein, R.S.; Brown, C.S.; Floegh, H.L.
EMBO J. 5, 547-552, 1986
A:Title: Gene conversion-like mechanisms may generate polymorphism in human class I gene:
A:Reference number: A91061; MUID:86220133; PMID:3011411
A:Accession: A25052
A:Molecule type: DNA
A:Residues: 1-362 <SEE>

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C;Cross-references: GB:X03665; NID:932250; PIDN:CAA27302.1; PID:g871297
A;Note: this allele is designated B*27051 (formerly 27W)
A;Accession: B25092
A;Molecule type: DNA
A;Residues: 1-100,'N',102-103,'IA',106-362 <SE2>
A;Cross-references: GB:X03664; NID:932236; PIDN:CAA27301.1; PID:g871296
A;Note: this allele is designated B*2702 (formerly 27K)
R;Szoets, H.; Rietmueller, G.; Weiss, E.; Meo, T.
Proc. Natl. Acad. Sci. U.S.A. 83: 1428-1432, 1986
A;Title: Complete sequence of HLA-B*27 cDNA identified through the characterization of submitted to the EMBL Data Library, June 1993
A;Reference number: A94087; MUID:86149317; PMID:3485286
A;Accession: A94087
A;Molecule type: mRNA
A;Residues: 25-205,'V',207-362 <SZO>
A;Cross-references: GB:M12678
A;Note: this allele is designated B*27052 (formerly 27W)
R;Vilches, C.
submitted to the EMBL Data Library, June 1993
A;Reference number: S34180
A;Accession: S34180
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100,'S',102-137,'D',139,'Y',141-175,'E',177-362 <VIL>
A;Cross-references: EMBL:X73578
A;Note: this allele is designated B*2706
R;D'Amato, M.; Sorrentino, R.
submitted to the EMBL Data Library, May 1994
A;Description: Identification of a novel HLA-B*27 subtype by restriction analysis of a c submitted to the EMBL Data Library, June 1993
A;Reference number: S44942
A;Accession: S44942
A;Molecule type: protein
A;Residues: 1-139,'H',141-362 <DAV>
A;Cross-references: EMBL:Z33453; NID:9486652; PIDN:CAA83976.1; PID:g486653
R;Ezquerria, A.; Bragado, R.; Vega, M.A.; Strominger, J.L.; Woody, J.; Lopez de Castro, J Biochemistry 24, 1733-1741, 1985
A;Title: Primary structure of papain-solubilized human histocompatibility antigen HLA-B*27
A;Reference number: A90493; MUID:85226361; PMID:2408663
A;Accession: A90493
A;Molecule type: protein
A;Residues: 25-265,'E',267-295 <EQZ>
R;Vega, M.A.; Ezquerria, A.; Rojo, S.; Aparicio, P.; Bragado, R.; Lopez de Castro, J.A. Proc. Natl. Acad. Sci. U.S.A. 82, 7394-7398, 1985
A;Title: Structural analysis of an HLA-B*27 functional variant: identification of residue
A;Reference number: A94070; MUID:86042671; PMID:2414775
A;Accession: B24741
A;Molecule type: protein
A;Residues: 86-100,'N',102-103,'IA',106-107,171-181 <VEG>
R;Coppin, H.L.; McDevitt, H.O.
J. Immunol. 137, 2168-2172, 1986
A;Title: Absence of polymorphism between HLA-B*27 genomic exon sequences isolated from nd
A;Reference number: 155965; MUID:87009855; PMID:3489755
A;Accession: 155965
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 25-298 <RES>
R;Blasczyk, R.; Weber, M.; Salama, A.
submitted to the EMBL Data Library, January 1995
A;Reference number: S52291
A;Accession: S52291
A;Molecule type: DNA
A;Residues: 116-192 <BLA>
R;Del Porto, P.; D'Amato, M.; Fiorillo, M.T.; Tuosto, L.; Piccolella, E.; Sorrentino, R. J. Immunol. 153, 3093-3100, 1994
A;Title: Identification of a novel HLA-B*27 subtype by restriction analysis of a cytotoxi
A;Reference number: 137485; MUID:94375672; PMID:8089488
A;Accession: 137485
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-139,'H',141-362 <RE3>
A;Cross-references: EMBL:Z33453; NID:9486652; PIDN:CAA83876.1; PID:g486653
C;Comment: This allele for HLA-B correlates with the development of ankylosing spondylit

C;Genetics:
A;Gene: GDB:HLA-B
A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
A;Introns: 25/1, 114/1, 207/1, 299/1, 338/1, 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: ankylosing spondylitis; duplication; glycoprotein; heterodimer; transmembran
F:1-24/DNA: signal sequence #status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen HLA-B*27 alpha chain #status predict
F:25-307/DNA: extracellular #status predicted <EXT>
F:25-114/DNA: alpha-1 <EX1>
F:115-206/DNA: alpha-2 <EX2>
F:115-206/DNA: immunoglobulin homology <IMV>
F:220-285/DNA: transmembrane #status predicted <TMV>
F:308-331/DNA: intracellular #status predicted <INT>
F:110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:125-198,227-283/Disulfide bonds: #status experimental

Query Match 80.1%; Score 939; DB 1; Length 362;
Best Local Similarity 80.9%; Pred. No. 1.6e-71;
Matches 174; Conservative 11; Mismatches 30; Indels 0; Gaps 0;

QY	1	IAVEYDDTQFLRFDSDAAIPRMEPRPVEQPGQVWETGYAKANAQTDRLVALNLL	60
DB	47	ITVGVDLTLFVRFDSDAASPRPAPRPIEQEGPEYWDRETQICKAKAQTDREDLRTL	106
QY	61	RRYQSEAGSHTLQMGNGCDMPDGRLLRGVHQHAWGDKYISLNEDLSRWTAADTVAQI	120
DB	107	RYNQSEAGSHTLQMGVCDVPGDRLRGVHQYADGKDYIALNEDLSRWTAADTAAQI	166
QY	121	TQRFYEAEBYAEFRFYLEGECLELLRRYLENGKETLQRPDPKAVHAPHSIDEATLR	180
DB	167	TQKWEAAKVAEQLRAYLEGCVEWLRYLENGKETLQRPDPKTHVTHHPISIDEATLR	226
QY	181	CWALGFYPAETLTWQRGEGEQTQDTLVEPRAG	215
DB	227	CWALGFYPAETLTWQRDGEDTQDTLVEPRAG	261

RESULT 6
I56116
MHC HLA-B*27-HS - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I56116
R;Choo, S.Y.; Fan, L.A.; Hansen, J.A.
J. Immunol. 147, 174-180, 1991
A;Title: A novel HLA-B*27 allele maps B*27 allotype specificity to the region around position 7
A;Reference number: I56116; MUID:91268545; PMID:1711072
A;Accession: I56116
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-338 <RES>
A;Cross-references: GB:M62852; NID:g187760; PIDN:AAA59647.1; PID:g187761
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:196-261/DNA: immunoglobulin homology <IMV>

Query Match 79.8%; Score 936; DB 2; Length 338;
Best Local Similarity 80.5%; Pred. No. 2.7e-71;
Matches 173; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

QY	1	IAVEYDDTQFLRFDSDAAIPRMEPRPVEQPGQVWETGYAKANAQTDRLVALNLL	60
DB	23	ITVGVDLTLFVRFDSDAASPRPAPRPIEQEGPEYWDRETQICKAKAQTDREDLRTL	82
QY	61	RRYQSEAGSHTLQMGNGCDMPDGRLLRGVHQHAWGDKYISLNEDLSRWTAADTVAQI	120
DB	83	RYNQSEAGSHTLQMGVCDVPGDRLRGVHQYADGKDYIALNEDLSRWTAADTAAQI	142
QY	121	TQRFYEAEBYAEFRFYLEGECLELLRRYLENGKETLQRPDPKAVHAPHSIDEATLR	180
DB	143	TQKWEAAKVAEQLRAYLEGCVEWLRYLENGKETLQRPDPKTHVTHHPISIDEATLR	202

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology	
C:Keywords: glycoprotein; transmembrane protein	
F:1-24/Domain: signal sequence #status predicted <IG>	
F:25-363/Product: MHC class I histocompatibility antigen HLA-B*73 alpha chain #status pre	
F:125-114/Domain: alpha-1 <EX1>	
F:115-206/Domain: alpha-2 <EX2>	
F:220-285/Domain: immunoglobulin homology <IMM>	
F:307-331/Domain: transmembrane #status predicted <TM>	
F:332-362/Domain: intracellular #status predicted <INT>	
F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted	
F:125-188,227-283/Disulfide bonds: #status predicted	
Query Match	79.5%; Score 932; DB 1; Length 363;
Best Local Similarity	80.5%; Pred. NO. 6.4e-71;
Matches 173; Conservative	12; Mismatches 30; Indels 0; Gaps 0;
QY	1 IAVEYVDDTQFLRFSDAAIPRMEPRPWPVEQGPQYEWTTGYAKANAQTRVALRNLL 60
DB	47 ITVGYYDDTQFVRFDSDAASPREEPRAPWIEQEGPEYWDRTQICKAKAQTRVGLRNLR 106
QY	61 RRYNQSEAGSHTLQMGNGCDMPDGLRLRGYHQHAWDGKDYISLNEDLRSWTAADTAAQI 120
DB	107 GYNNQSEGSHTWQMYGCDMPDGLRLRGYNQAYDQGDYIALNEDLRSWTAADTAAQI 166
QY	121 TORFYEAEEYAEFFTYLEGECELLRRYLLENGKETLQADPPPKAHVAHPISDHEATLR 180
DB	167 TQKWEAARAEQLRAYLSEGCVEWLRRLHLENGKETLQADPPKTHVTHHPISDHEATLR 226
QY	181 CWALGYPAEITLTWQDGESEOTQDELIVETRPAG 215
DB	227 CWALGYPAEITLTWQDGEDQDELIVETRPAG 261
RESULT 9	
I37515	
MHC class I histocompatibility antigen HLA-B*2706 alpha chain precursor - human	
C:Species: Homo sapiens (man)	
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000	
R:Vilches, C.; de Pablo, R.; Kreisler, M.	
C:Accession: I37515	
Immunogenetics 39, 219, 1994	
A:Title: Nucleotide sequence of HLA-B*2706.	
A:Reference number: I37515; MUID:94102824; PMID:8276469	
A:Accession: I37515	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-362 xRES>	
A:Cross-references: EMBL:X73578; NID:g975658; PIDN:CAA51980.1; PID:g975659	
C:Genetics:	
A:Gene: GDB:HLA-B	
A:Cross-references: GDB:120048; OMIM:142830	
A:Map position: 6p21.3-6p21.3	
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology	
F:220-285/Domain: immunoglobulin homology <IMM>	
Query Match	79.4%; Score 931; DB 2; Length 362;
Best Local Similarity	80.0%; Pred. NO. 7.8e-71;
Matches 172; Conservative	13; Mismatches 30; Indels 0; Gaps 0;
QY	1 IAVEYVDDTQFLRFSDAAIPRMEPRPWPVEQGPQYEWTTGYAKANAQTRVALRNLL 60
DB	47 ITVGYYDDTFLVRFDSDAASPREEPRAPWIEQEGPEYWDRETQICKAKAQTRDRLTL 106
QY	61 RRYNQSEAGSHTLQMGNGCDMPDGLRLRGYHQHAWDGKDYISLNEDLRSWTAADTAAQI 120
DB	107 RYNNQSEGSHTLQNNYMGCDVPDGLRLRGYQAYDQGDYIALNEDLRSWTAADTAAQI 166
QY	121 TORFYEAEEYAEFFTYLEGECELLRRYLLENGKETLQADPPPKAHVAHPISDHEATLR 180
DB	167 TQKWEAARAEQLRAYLSEGCVEWLRRLHLENGKETLQADPPKTHVTHHPISDHEATLR 226
QY	181 CWALGYPAEITLTWQDGESEOTQDELIVETRPAG 215

Db 227 CWALGFYPAEITLTWQDGEQDTQDTVELVETRPAG 261

RESULT 10

I54505 lymphocyte antigen - human

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000

C:Accession: I54505

R:Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.; Juji, T.; Kano, K.; Takiguchi, T.

Immunogenetics 37, 212-216, 1993

A:Title: Molecular analysis of HLA-B*39 subtypes.

A:Reference number: I54505; MUID:93131294; PMID:8420828

A:Accession: I54505

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-362 <RES>

A:Cross-references: GB:M94052; NID:G184163; PIDN:AAAS2658.1; PID:G184164

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 927; DB 2; Length 362;

Best Local Similarity 79.5%; Pred. No. 1.7e-70;

Matches 171; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYWEWTTGYAKANAQTDRAVALNLL 60

Db 47 ISVGYYDDTQFVRFDSDAASPREPAPWIEQEGPEYWDRTQICKTNTQTDRESLNLR 106

QY 61 RRYNQSAGSHTLQGMNGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAATVAQI 120

Db 107 GYINQSEAGSHTLQRMYGCDVGFDPGLRGHNFAYDKDYIALNEDLSSTWADTAQI 166

QY 121 TORFYAEYAEFFRTYLEGECLELRLRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 180

Db 167 TQKWEAARVAEQRLTYLGTCVWELRRYLENGKETLQRAADPPKTHVTHHPISDHEATLR 226

QY 181 CWALGFYPAEITLTWQDGEQDTQDTVELVETRPAG 215

Db 227 CWALGFYPAEITLTWQDGEQDTQDTVELVETRPAG 261

RESULT 11

I59645 HLA-B-6701 - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C:Accession: I59645

R:Little, A.M.; Domona, J.D.; Hildebrand, W.H.; Shen, S.Y.; Barber, L.D.; Marsh, S.G.; E.

Tissue Antigens 43, 38-43, 1994

A:Title: HLA-B*67: a member of the HLA-B*16 family that expresses the ME1 epitope.

A:Reference number: I59645; MUID:94294961; PMID:7517584

A:Accession: I59645

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-362 <RES>

A:Cross-references: GB:L17005; NID:G292147; PIDN:AAAG37548.1; PID:G488426

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 927; DB 2; Length 362;

Best Local Similarity 80.0%; Pred. No. 1.7e-70;

Matches 172; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYWEWTTGYAKANAQTDRAVALNLL 60

Db 47 ISVGYYDDTQFVRFDSDAASPREPAPWIEQEGPEYWDRTQICKTNTQTDRESLNLR 106

QY 61 RRYNQSAGSHTLQGMNGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAATVAQI 120

Db 107 GYINQSEAGSHTLQRMYGCDVGFDPGLRGHNFAYDKDYIALNEDLSSTWADTAQI 166

QY 121 TORFYAEYAEFFRTYLEGECLELRLRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 180

Db 167 TQKWEAARVAEQRLTYLGTCVWELRRYLENGKETLQRAADPPKTHVTHHPISDHEATLR 226

QY 181 CWALGFYPAEITLTWQDGEQDTQDTVELVETRPAG 215

Db 227 CWALGFYPAEITLTWQDGEQDTQDTVELVETRPAG 261

RESULT 12

I54314 HLA-B*39N - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C:Accession: I54314

R:Ogawa, A.; Tokunaga, K.; Nakajima, F.; Kikuchi, A.; Karaki, S.; Kashiwase, K.; Ge, J.; Hum. Immunol. 41, 241-247, 1994

A:Title: Identification of the gene encoding a novel HLA-B*39 subtype. Two amino acid substitutions in the gene encoding a novel HLA-B*39 subtype. Two amino acid substitutions in the gene encoding a novel HLA-B*39 subtype.

A:Reference number: I54314; MUID:95189597; PMID:7533753

A:Accession: I54314

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-362 <RES>

A:Cross-references: GB:L22649; NID:G437369; PIDN:AAA69861.1; PID:G437370

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:120048; OMIM:142830

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 927; DB 2; Length 362;

Best Local Similarity 79.5%; Pred. No. 1.7e-70;

Matches 171; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYWEWTTGYAKANAQTDRAVALNLL 60

Db 47 ISVGYYDDTQFVRFDSDAASPREPAPWIEQEGPEYWDRTQICKTNTQTDRESLNLR 106

QY 61 RRYNQSAGSHTLQGMNGCDMGPDGRLRGYHQHAWDGKDYISLNEDLSRWSAATVAQI 120

Db 107 GYINQSEAGSHTLQRMYGCDVGFDPGLRGHNFAYDKDYIALNEDLSSTWADTAQI 166

QY 121 TORFYAEYAEFFRTYLEGECLELRLRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 180

Db 167 TQKWEAARVAEQRLTYLGTCVWELRRYLENGKETLQRAADPPKTHVTHHPISDHEATLR 226

QY 181 CWALGFYPAEITLTWQDGEQDTQDTVELVETRPAG 215

Db 227 CWALGFYPAEITLTWQDGEQDTQDTVELVETRPAG 261

RESULT 13

I68850 MHC class I histocompatibility antigen precursor - human

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000

C:Accession: I68850; I38464

R:Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.; Juji, T.; Kano, K.; Takiguchi, T.

Immunogenetics 37, 212-216, 1993

A:Title: Molecular analysis of HLA-B*39 subtypes.

A:Reference number: I54505; MUID:93131294; PMID:8420828

A:Accession: I68850

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-362 <RES>

A:Cross-references: GB:M94053; NID:G184165; PIDN:AAAS2659.1; PID:G184166

R:Adams, E.J.; Martinez-Naves, E.; Arnett, K.L.; Little, A.M.; Tyan, D.B.; Parham, P.

Tissue Antigens 45, 18-26, 1995

A:Title: HLA-B*16 antigens: sequence of the ST-16 antigen, further definition of two B*16 antigens.

A:Reference number: I38464; MUID:95242308; PMID:7725307

A:Accession: I38464

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A;Residues: 1-362 <RES2>
A;/Cross-references: EMBL:U04243; NID:g458659; PIDN:AAA87396.1; PID:g458660
C;Genetics:
A;/Gene: GDB:HLA-B
A;/Cross-references: GDB:120048; OMIM:142830
A;/Map position: 6p21.3-6p21.3
C;/Superfamily: class I histocompatibility antigen; immunoglobulin homology
P:/220-285/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 927; DB 2; Length 362;
Best Local Similarity 79.5%; Pred.No. 1.7e-70;
Matches 171; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

QY 1 IAEVYDDTQFLRFDSDAAIPMEPEPPWVEQGPOYWETTGAYAKANAQTDRVALRNLL 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
47 ISVGYYDDDTQFVRFDSDAASPREPRAPPIEQGPGFYNDRETQISKINTQTDRSLNR 106
QY 61 RRYNQSEAGSHITLQGMNGCDMGDGLRLRGYHQAWDGDKDIISLNEDLSRWTAADTVAQI 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
107 GYINQSEAGSHITLQRMVGCVDGPDGLLRGRNFAYDGKDVIALNEDLSRWTAADTAAQI 166
QY 121 TORFYBAEVAEFRRYLECELELLRRYLENKETLQRADPKAHVAHHPTSDHEATLR 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 TORKWEARVAEQIRLYLETCTVEWLRRYLENKETLQRADPPKTHVTHHPISDHEATLR 226
QY 181 CWALGVYPABITLTWORGDGEOTQDELVELVETRPAG 215
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
227 CWALGVYPABITLTWQRGDGEDQTDQLVELVETRPAG 261

RESULT 14
I61865
MHC HLA-Bw42, HLA-Bw65 chain - human
C;Species: Homo sapiens (man)
C;/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;/Accession: I61865; I61862; I79639
R;/Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;/Title: Diversity and diversification of HLA-A,B,C alleles.
A;/Reference number: I36956; MUID:89235215; PMID:2715640
A;/Accession: I61865
A;/Status: preliminary; translated from GB/EMBL/DDBB
A;/Molecule type: DNA
A;/Residues: 1-362 <RES>
A;/Cross-references: GB:M2034; NID:g187822; PIDN:AAA95667.1; PID:g386904
A;/Accession: I61862
A;/Status: preliminary; translated from GB/EMBL/DDBB
A;/Molecule type: DNA
A;/Residues: 1-34, 'A', '36-90, 'C', '92, 'TNT', '96-120, 'W', '122-136, 'Y', '138-139, 'F', '141-154, 'S', '1'
A;/Cross-references: GB:M24032; NID:g187816; PIDN:AAA95664.1; PID:g386902
R;/Bronson, S.K.; Pei, J.; Tailon-Miller, P.; Chorney, M.J.; Geraghty, D.E.; Chaplin, D.
Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
A;/Title: Isolation and characterization of yeast artificial chromosome clones linking th
A;/Reference number: I59188; MUID:91156671; PMID:2000377
A;/Accession: I79639
A;/Status: preliminary; translated from GB/EMBL/DDBB
A;/Molecule type: DNA
A;/Residues: 26-34, 'A', '36-90, 'C', '92, 'TNT', '96-120, 'W', '122-136, 'Y', '138-139, 'F', '141-154, 'S', '1'
A;/Cross-references: GB:M59840; NID:g187758; PIDN:AAA95646.1; PID:g187759
C;Genetics:
A;/Gene: GDB:HLA-B
A;/Cross-references: GDB:120048; OMIM:142830
A;/Map position: 6p21.3-6p21.3
A;/Introns: 115/1
C;/Superfamily: Class I histocompatibility antigen; immunoglobulin homology
C;/Keywords: glycoprotein; transmembrane protein
P:/220-285/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 924; DB 2; Length 362;
Best Local Similarity 79.4%; Pred.No. 3e-70;
Matches 170; Conservative 18; Mismatches 27; Indels 0; Gaps 0;

QY 1 IAEVYDDTQFLRFDSDAAIPMEPEPPWVEQGPOYWETTGAYAKANAQTDRVALRNLL 60

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OM protein - protein search, using sw model

Run on: June 18, 2004, 09:52:27 ; Search time 18 Seconds
(without alignments)

621.949 Million cell updates/sec

Title: US-09-819-371-6

Perfect score: 1173

Sequence: 1 IAVEYVDTRFLRFSDAAI.....QRDGEQTDTELVEPRPAG 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1164	99.2	362	1	HLAF_HUMAN
2	1149	98.0	346	1	1C28_HUMAN
3	1100	93.8	348	1	HLAF_MACMU
4	939	80.1	362	1	1B27_HUMAN
5	932	79.5	363	1	1B73_HUMAN
6	927	79.0	362	1	1B39_HUMAN
7	927	79.0	362	1	1B67_HUMAN
8	924	78.8	362	1	1B42_HUMAN
9	923	78.7	362	1	1B47_HUMAN
10	922	78.6	362	1	1B08_HUMAN
11	921	78.5	362	1	1B07_HUMAN
12	921	78.5	362	1	1B14_HUMAN
13	921	78.5	362	1	1B37_HUMAN
14	921	78.5	362	1	1B46_HUMAN
15	920	78.4	362	1	1B81_HUMAN
16	919	78.3	362	1	1B40_HUMAN
17	918	78.3	359	1	1B01_PANTR
18	918	78.3	362	1	1B03_GORGO
19	918	78.3	362	1	1B54_HUMAN
20	917	78.2	362	1	1B55_HUMAN
21	916	78.1	362	1	1B56_HUMAN
22	915	78.0	362	1	1B02_PANTR
23	915	78.0	366	1	1C12_HUMAN
24	914	77.9	362	1	1B38_HUMAN
25	913	77.8	362	1	1B01_GORGO
26	913	77.8	362	1	1B15_HUMAN
27	913	77.8	366	1	1C08_HUMAN
28	912	77.7	362	1	1A02_PANTR
29	912	77.7	362	1	1B78_HUMAN
30	911	77.7	362	1	1B02_GORGO
31	911	77.7	362	1	1B48_HUMAN
32	910	77.6	366	1	1C07_HUMAN
33	909	77.5	365	1	1A23_HUMAN

ALIGNMENTS

RESULT 1

ID	HLAF_HUMAN	STANDARD	PRT	362 AA
AC	P30511;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CDAL2).			
GN	HLA-F OR HLAF OR HLA-5.4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_SEQUENCE FROM N.A.			
RP	MEDLINE=90111605; PubMed=1688605;			
RX	Geraghty D.E., Wei X., Orr H.T., Koller B.H.;			
RA	"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of			
RT	a class I coding sequence linked to a novel transcribed repetitive			
RT	element."			
RL	J. Exp. Med. 171:1-18(1990).			
RN	[2]_SEQUENCE FROM N.A.			
RP	MEDLINE=91197889; PubMed=1707659;			
RX	Lury D., Epstein H., Holmes N.;			
RA	"The human class I MHC gene HLA-F is expressed in lymphocytes."			
RL	Int. Immunol. 2:531-537(1990).			
RN	[3]_SEQUENCE FROM N.A.			
RP	Shiina S., Tamiya G., Oka A., Inoko H.;			
RA	"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."			
RT	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RL	-!- FUNCTION: Involved in the presentation of foreign antigens to the			
CC	immune system.			
CC	-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-			
CC	microglobulin).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	EMBL; X17093; CAA34947.1; -.			
DR	EMBL; AF000521; BAB6337.1; -.			
DR	PIR; A60384; A60384.			
DR	HSSP; Q30201; 1A6Z.			
DR	Genew; HGNC:4963; HLA-F.			
DR	MIM; 143110; -.			
DR	GO; GO:0030106; F:MHC class I receptor activity; TAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR003006; Ig_MHC.			

34 908 77.4 362 1 1B82_HUMAN Q29718 homo sapien
35 907 77.3 366 1 1C14_HUMAN P30510 homo sapien
36 906 77.2 366 1 1C02_GORGO P30385 gorilla gor
37 906 77.2 366 1 1C04_GORGO P30387 gorilla gor
38 905 77.2 365 1 1A01_SAGO P30515 saginus oe
39 903 77.0 362 1 1B35_HUMAN P30685 homo sapien
40 903 77.0 362 1 1B59_HUMAN Q29940 homo sapien
41 903 77.0 366 1 1C03_GORGO P30386 gorilla gor
42 902 76.9 362 1 1B58_HUMAN P30319 homo sapien
43 902 76.9 365 1 1A24_HUMAN P05534 homo sapien
44 901 76.8 362 1 1B18_HUMAN P30466 homo sapien
45 901 76.8 362 1 1B52_HUMAN P30490 homo sapien

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DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR00129; MHC_I.
DR PRODOM; PD000050; MHC_I.
DR SMART; SM00407; IGC1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR MHC_I; Transmembrane; Glycoprotein; Signal.
FW SIGNAL 1 21
FW CHAIN 22 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN F.
FT DOMAIN 22 111
FT DOMAIN 112 203
FT DOMAIN 204 295
FT DOMAIN 296 305
FT TRANSMEM 306 329
FT DOMAIN 330 362
FT DISULFID 122 185
FT DISULFID 224 280
FT CARBOHYD 107 107
SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 99.2%; Score 1164; DB 1; Length 362;
Best Local Similarity 99.5%; Pred. No. 2.2e-91;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVEYDDTQFLRFDSDAAIPRMEPRFPWVEQEGQYWEWTTGYAKANAQTDRAVALRNL 60
DB 44 IAVEYDDTQFLRFDSDAAIPRMEPRFPWVEQEGQYWEWTTGYAKANAQTDRAVALRNL 103
QY 61 RRYNQSEAGSHTLQNGMGCDMPGDRLLRGYHQHAWDGKDYISLNEDLSRWTAADTVAQI 120
DB 104 RRYNQSEAGSHTLQNGMGCDMPGDRLLRGYHQHAWDGKDYISLNEDLSRWTAADTVAQI 163
QY 121 TORFYAEAEYAEFRYLSGECLELLRRLRYLNGKETLQADPPKHAHVAHPISDHEATLR 180
DB 164 TORFYAEAEYAEFRYLSGECLELLRRLRYLNGKETLQADPPKHAHVAHPISDHEATLR 223
QY 181 CVALGFYPAEITLTWQDGEQTDTELVEPTRAG 215
DB 224 CVALGFYPAEITLTWQDGEQTDTELVEPTRAG 258

RESULT 2
1C28 PANTR STANDARD; PRT; 346 AA.
AC P16215;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CHLA class I histocompatibility antigen, CH28 alpha chain precursor.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201944; PubMed=1690682;
RA Lawlor D.A., Warren E., Ward F.E., Parham P.;
RT "Comparison of class I MHC alleles in humans and apes.";
RL Immunol. Rev. 113:147-185 (1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88319000; PubMed=3412487;
RA Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.;
RT "HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.";
RL Nature 335:268-271 (1988).
CC -1- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M30685; AAA87973.1; -.
CC HSP; Q30201; 1A6Z.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig cl.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00129; MHC_I.
CC PRINTS; PR01638; MHCCLASSI.
CC PRODOM; PD000050; MHC_I.
CC SMART; SM00407; IGC1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC MHC_I; Transmembrane; Glycoprotein; Signal.
FW SIGNAL 1 21
FW CHAIN 22 346
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT CH28 ALPHA CHAIN.
FT DOMAIN 22 111
FT DOMAIN 112 203
FT DOMAIN 204 295
FT DOMAIN 296 305
FT TRANSMEM 306 329
FT DOMAIN 330 346
FT DISULFID 122 185
FT DISULFID 224 280
FT CARBOHYD 107 107
SQ SEQUENCE 346 AA; 39064 MW; F83E882D5C2E0971 CRC64;

Query Match 98.0%; Score 1149; DB 1; Length 346;
Best Local Similarity 98.6%; Pred. No. 3.9e-90;
Matches 212; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IAVEYDDTQFLRFDSDAAIPRMEPRFPWVEQEGQYWEWTTGYAKANAQTDRAVALRNL 60
DB 44 IAVEYDDTQFLRFDSDAAIPRMEPRFPWVEQEGQYWEWTTGYAKANAQTDRAVALRNL 103
QY 61 RRYNQSEAGSHTLQNGMGCDMPGDRLLRGYHQHAWDGKDYISLNEDLSRWTAADTVAQI 120
DB 104 RRYNQSEAGSHTLQNGMGCDMPGDRLLRGYHQHAWDGKDYISLNEDLSRWTAADTVAQI 163
QY 121 TORFYAEAEYAEFRYLSGECLELLRRLRYLNGKETLQADPPKHAHVAHPISDHEATLR 180
DB 164 TORFYAEAEYAEFRYLSGECLELLRRLRYLNGKETLQADPPKHAHVAHPISDHEATLR 223
QY 181 CVALGFYPAEITLTWQDGEQTDTELVEPTRAG 215
DB 224 CVALGFYPAEITLTWQDGEQTDTELVEPTRAG 258

RESULT 3
HLAF MACMU STANDARD; PRT; 348 AA.
AC P33617;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (leukocyte antigen F).
GN HLA-F OR HLAF.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;

```

[1] SEQUENCE FROM N.A. (B*2701).
RP MEDLINE=93246295; PubMed=8482576;
RA Otting N., Bontrup E.,
RT "Characterization of the rhesus macaque (Macaca mulatta) equivalent
of HLA-B*27";
RL Immunogenetics 38:141-145(1993).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
CC -----
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CC -----
CC EMBL; Z21819; CAA79885.1; -.
CC PIR; S29990; S29990.
CC DR HSP; Q30201; 1A6Z.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003597; Ig_c1.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR001039; MHC_I.
CC DR Pfam; PF00047; Ig; 1.
CC DR Pfam; PF00129; MHC_I; 1.
CC DR PRINTS; PR01638; MHCCLASS1.
CC DR PRODOM; PD000050; MHC_I; 1.
CC DR SMART; SM00407; Igcl; 1.
CC DR PROSITE; PSS0835; IG_LIKE; 1.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC DR MHC I; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 21
CC FT CHAIN 22 348
CC FT DOMAIN 22 113
CC FT DOMAIN 114 205
CC FT DOMAIN 206 297
CC FT DOMAIN 298 307
CC FT TRANSMEM 308 331
CC FT DOMAIN 332 348
CC FT DISULFID 124 187
CC FT DISULFID 226 282
CC FT CARBOHYD 109 109
CC FT SEQUENCE 348 AA; 39300 MW; 77BD7E3B9B11E0F7 CRC64;
Query Match 93.8%; Score 1100; DB 1; Length 348;
Best Local Similarity 94.4%; Pred. No. 5.5e-86;
Matches 203; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 IAVYVDDTQFLRPSDAAPRMEPRFPWVEQEGPQYWEWTTGYAKANACTDRVALNLL 60
Db 46 IAVSYVDDTQFLRPSDAAPRMEPRFPWVEQEGPQYWEWTTGYAKANACTDRVALKLL 105
QY 61 RYVQSEAGSHLQMGKCDMPGRLRLRGVHAWDGKDYISLNEDLRSWTAADTVAQI 120
Db 106 LRYVQSEAGSHLQMGKCDMPGRLRLRGVHAWDGKDYISLNEDLRSWTAADTVAQI 165
QY 121 TORVEAEYAEAEFTYLEGCELLRLRYLNGKETLQADPPKAAVHAHPISDHEATLR 180
Db 166 TORVEAEYAEAEFTYLEGCELLRLRYLNGKETLQADPPKAAVHAHPISDHEATLR 225
QY 191 CWALGFYPAETLTWQRDGEQTQDTLVETRPAG 215
Db 226 CWALGFYPAETLTWQRDGEQTQDTLVETRPAG 260
RESULT 4
1B27_HUMAN STANDARD; PRT; 362 AA.
ID 1B27_HUMAN

AC SEQUENCE FROM N.A. (B*2701).
AC Q29961;
DT 23-OCT-1986 (Rel. 02, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-27 alpha chain precursor
DE (MHC class I antigen B*27).
DE HLA-B OR HLA-B*27.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*2701).
RP MEDLINE=86138405; PubMed=3912316;
RA Weiss E.H., Kuon W., Doerner C., Lang M., Rietmueller G.;
RT "Organization, sequence and expression of the HLA-B*27 gene: a
molecular approach to analyze HLA and disease associations.";
RL Immunobiology 170:367-380(1985).
RN [2]
RP SEQUENCE OF 25-361 FROM N.A. (B*2701).
RP MEDLINE=86149317; PubMed=3485286;
RA Szoets H., Rietmueller G., Weiss E., Meo T.;
RT "Complete sequence of HLA-B*27 cDNA identified through the
characterization of structural markers unique to the HLA-A, -B, and
-C allelic series.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
RN [3]
RP SEQUENCE OF 25-295 (B*2701).
RP MEDLINE=85226361; PubMed=2408663;
RA Ezquerro A., Bragado R., Vega M.A., Strominger J.L., Woody J.,
RA Lopez de Castro J.A.;
RT "Primary structure of papain-solubilized human histocompatibility
antigen HLA-B*27.";
RL Biochemistry 24:1733-1741(1985).
RN [4]
RP SEQUENCE FROM N.A. (B*2701 AND B*2702).
RP MEDLINE=86220133; PubMed=3011411;
RA Seemann G.H.A., Rein R.S., Brown C.S., Floegh H.L.;
RT "Gene conversion-like mechanisms may generate polymorphism in human
class I genes.";
RL EMBO J. 5:547-552(1986).
RN [5]
RP SEQUENCE FROM N.A. (B*2702).
RP MEDLINE=96086486; PubMed=7482496;
RA Moses J.H., Marsh S.G.E., Arnett K.L., Adams E.J., Bodmer J.G.,
RA Parham P.;
RT "On the nucleotide sequences of B*2702 and B*2705.";
RL Tissue Antigens 46:50-53(1995).
RN [6]
RP SEQUENCE OF 86-107 AND 171-181 (B*2702).
RP MEDLINE=86042671; PubMed=2414775;
RA Vega M.A., Ezquerro A., Rojo S., Aparicio P., Bragado R.,
RA Lopez de Castro J.A.;
RT "Structural analysis of an HLA-B*27 functional variant: identification
of residues that contribute to the specificity of recognition by
cytolytic T lymphocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
RN [7]
RP SEQUENCE FROM N.A. (B*2703).
RP MEDLINE=88227491; PubMed=3286582;
RA Choo S.Y., St John T., Orr H.T., Hansen J.A.;
RT "Molecular analysis of the variant alloantigen HLA-B*27d (HLA-B*2703).
It identifies a unique single amino acid substitution.";
RL Hum. Immunol. 21:209-219(1988).
RN [8]
RP SEQUENCE FROM N.A. (B*2704 AND B*2706).
RP MEDLINE=96134006; PubMed=8550101;
RA Rudwaleit M., Bowness P., Wordsworth P.;
RT "The nucleotide sequence of HLA-B*2704 reveals a new amino acid
substitution in exon 4 which is also present in HLA-B*2706.";
RL Immunogenetics 43:160-162(1996).
RN [9]


```
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC_I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 363 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT 25 363 B-73 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 333
FT DOMAIN 334 363
FT CARBOHYD 110 110 CYTOPLASMIC TAIL.
FT DISULFID 125 188 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 363 AA; 40435 MW; 04522E97C1E11C40 CRC64;

Query March 79.5%; Score 932; DB 1; Length 363;
Best Local Similarity 80.5%; Pred. No. 9.7e-72;
Matches 173; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

QY 1 IAVEYVDVDTQFLRPSDAAIPRMEPRFVWEGQPGYQWWTGYAKANAQTDVLRNLL 60
DB 47 ITVGVDVDTQFVRDSDAASPREPRAPWLEQEGPEYWDNRNTQICKAKAQTDVLRNLR 106
QY 61 RRYNQSEAGSHTLQMGNGCDMPDGRLLRGHQHAWGDKYIISNEDLRSWTAADTVAQI 120
DB 107 GYINQSEAGSHTLQMGNGCDMPDGRLLRGYINQPAYDKGYIALNEDLRSWTAADTAAQI 166
QY 121 TORFVEAEVYAEERPTVLEGGCLLRYLLENGKETIQRADPPKARVAHHPISDEATLR 180
DB 157 TORKWEARVAEQRAYLEGGCVLRRHLENGKETIQRADPPKTHVTHHPISDEATLR 226
QY 181 CWALGFYPAEITLTWQRDGBEQTDTELVTETRPAG 215
DB 227 CWALGFYPAEITLTWQRDGBEQTDTELVTETRPAG 261

RESULT 6
1B39 HUMAN
ID 1B39 HUMAN STANDARD; PRT; 362 AA.
AC P30475; Q02960; Q78217; P30476; P79504; Q29665; Q29697; Q29749;
AC Q29847; Q29852; Q29858; Q8HWF0; Q9TPQ7;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-39 alpha chain precursor
DE (MHC class I antigen B*39).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*3901 AND B*3902).
RX MEDLINE=93131294; PubMed=8420828;
RA Kato N., Karaki S., Kashiwase K., Mueller C., Akaza T., Juji T.,
RA Kano K., Takiguchi M.
RT "Molecular analysis of HLA-B39 subtypes."
RL Immunogenetics 37:212-216(1993).
RN [2]
RP SEQUENCE FROM N.A. (B*3902 AND B*3905).
RX MEDLINE=95242308; PubMed=7725307;
RA Adams E.J., Martinez-Naves E., Arnett K.L., Little A.-M.,
RA Tyman D.B., Parham P.
RT "HLA-B*6 antigens: sequence of the B*6 antigen, further definition
RT of two B*6 subtypes and evidence for convergent evolution of
RT B*3902."
RL Tissue Antigens 45:18-26(1995).
RN [3]
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RESULT 5
1B73 HUMAN
ID 1B73 HUMAN STANDARD; PRT; 363 AA.
AC Q316T2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE HLA class I histocompatibility antigen, B-73 alpha chain precursor
DE (MHC class I antigen B*73).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*7301).
RX MEDLINE=95026796; PubMed=7504186;
RA Parham P., Arnett K.L., Adams E.J., Barber L.D., Domina J.D.,
RA Stewart D., Hildebrand W.H., Little A.-M.;
RT "The HLA-B*73 antigen has a most unusual structure that defines a
RT second lineage of HLA-B alleles."
RL Tissue Antigens 43:302-313(1994).
RN [2]
RP SEQUENCE FROM N.A. (B*7301).
RX MEDLINE=94299292; PubMed=7517915;
RA Vilches C., de Pablo R., Herrero M.J., Moreno M.E., Kreisler M.;
RT "HLA-B*73: an atypical HLA-B molecule carrying a Bw6-epitope motif
RT variant and a B pocket identical to HLA-B*27."
RL Immunogenetics 40:166-166(1994).
RN [3]
RP SEQUENCE FROM N.A. (B*7301).
RX MEDLINE=96164742; PubMed=8547229;
RA Hoffmann H.J., Kristensen T.J., Jensen T.G., Graugaard B., Lamm L.U.;
RT "Antigenic characteristics and cDNA sequences of HLA-B*73."
RL Eur. J. Immunogenet. 22:231-240(1995).
RN [4]
RP SEQUENCE FROM N.A. (B*7301).
RC TISSUE=Blood;
RX MEDLINE=22512041; PubMed=12622774;
RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
RA Madrigal J.A., Little A.-M.;
RT "Cloning and sequencing full-length HLA-B and -C genes."
RL Tissue Antigens 61:20-48(2003).
CC -I- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -I- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
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CC
CC ENBL; U04787; AAS53175.1; -
CC ENBL; X77658; AAS4739.1; -
CC ENBL; L24373; AAA96733.1; -
CC ENBL; AJ311601; CAC35319.1; -
CC PIR; I37512; S42102.
CC HSP; P03989; IHSA.
CC Genew; HGNC:4932; HLA-B.
CC MTM; 142830. -
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig-cl.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00129; MHC_I; 1.
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Fernandez-Vina M.A., Stastny P.;
"Evolution of HLA-class I compared to HLA-class II polymorphism in
Terena, a South-American Indian tribe."
Hum. Immunol. 60:1138-1149(1999).
[14]
SEQUENCE OF 26-206 FROM N.A. (B*3923).
MEDLINE=21160452; PubMed=11260515;
Akasaka T., Kashiwase K., Ishikawa Y., Tanaka H., Shimizu M.,
Kawai T., Akaza T., Takanashi T., Juji T.;
"Allele frequency of HLA-B*39 in the Japanese population and
identification of a novel B39 allele, B*3923."
Tissue Antigens 57:169-172(2001).
[15]
SEQUENCE OF 60-196 FROM N.A. (B*3907).
MEDLINE=95317819; PubMed=7797264;
Garber T.L., Butler L.M., Trachtenberg E.A., Erlich H.A., Rickards O.,
De Stefano G., Watkins D.I.;
"HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles."
Immunogenetics 42:19-27(1995).
-I- FUNCTION: Involved in the presentation of foreign antigens to the
immune system.
-I- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- POLYMORPHISM: The following alleles of B-39 are known: B*3901
(B39.1), B*3902 (B9.2), B*3903, B*3904 (B39N), B*3905 (ST-16),
B*3906 (B39G), B*3907 (B39uw3), B*3909, B*3910, B*3912 (B3901v),
B*3923 (B39022v1) and B*3924. The sequence shown is that of
B*3901.

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EMBL; M94052; AAA52658.1; -
EMBL; M94051; AAA52660.1; -
EMBL; M94053; AAA52659.1; -
EMBL; U04243; AAA87396.1; -
EMBL; L36318; AAA73942.1; -
EMBL; L22649; AAA93861.1; -
EMBL; U29480; AAC50392.1; -
EMBL; L42024; AAB59484.1; -
EMBL; U29083; AAC32741.1; -
EMBL; U56246; AAB01985.1; -
EMBL; Y09058; CAA70261.1; -
EMBL; AB091216; BAC11810.1; -
EMBL; AB091218; BAC11811.1; -
EMBL; AF428252; AAN63555.1; -
EMBL; L42280; AAB51452.1; -
EMBL; U76395; AAB39108.1; -
EMBL; U76394; AAB39108.1; JOINED.
EMBL; AB032097; BAA84116.1; -
EMBL; U15640; AAA74047.1; -
PIR; I38876; I38876.
PIR; I54314; I54314.
PIR; I54505; I54505.
PIR; I68850; I68850.
PIR; I84488; I84488.
HSSP; P30460; IAGD.
Genew; HGNC:4932; HLA-B.
MIM; 142830; -
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0030106; F:MHC class I receptor activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPRO07110; Ig-like.
InterPro; IPRO03597; Ig cl.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO01039; MHC_I.
Pfam; PF00047; Ig; 1.

DR PFAM: PF00129; MHC_I.1;
 DR PRINTS: PR01638; MHCCLASSI.
 DR PRODOM: PD000050; MHC_I.1;
 DR SMART: SM00407; IGC1.1;
 DR PROSITE: PS00835; IG_LIKE.1;
 DR PROSITE: PS00290; IG_MHC.1;
 KW MHC_I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-39 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 309 332 CONNECTING PEPTIDE.
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 Y -> D (in allele B*3912).
 FT VARIANT 33 33 Y -> A (in allele B*3904 and allele
 FT VARIANT 35 35 S -> A (in allele B*3912).
 FT VARIANT 35 35 /FTID=VAR_016421.
 FT VARIANT 35 35 /FTID=VAR_016421.
 Query Match 79.0%; Score 927; DB 1; Length 362;
 Best Local Similarity 79.5%; Pred. No. 2.6e-71;
 Matches 171; Conservative 15; Mismatches 29; Indels 0; Gaps 0;
 OY 1 IAVEYDDTQFLRFDSDAI PRMEPREPWVREGPOYEWITTCYAKANQTDVRLNLL 60
 DB 47 ISGVYDDTQFLRFDSDAASPREPRAPWIEQGEYDNRNTQICKNTQTDRSLNLR 106
 OY 61 RYVNSQSEASHTIQGMNGCDMGDPGLRLRGYHCHAWDGKDYISLNEELRSWTAADTVAQI 120
 DB 107 GYVNSQSEASHTIQGMNGCDMGDPGLRLRGYHCHAWDGKDYISLNEELRSWTAADTVAQI 166
 OY 121 TCRFYAEYAEFFRYLEGECELELLRYLNGKETLQADPPKARVHHPISDHEATLR 180
 DB 167 TCRKWEARVAEQLRYLEGTCEVRLRYLNGKETLQADPPKRVTHTHPISDHEATLR 226
 OY 181 CVALGYPFAEITLTWQDGEEOQDTVELVETRPAG 215
 DB 227 CVALGYPFAEITLTWQDGEEOQDTVELVETRPAG 261
 RESULT 7
 ID 1B67_HUMAN STANDARD; PRT; 362 AA.
 AC Q29836; Q29878; Q6SNC5; Q95IA6; Q9BD38;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-67 alpha chain precursor
 DE (MHC class I antigen B*67).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*6701).
 RX MEDLINE=94294981; PubMed=7517584;
 RA Little A.-M., Domene J.-D., Hildebrand W.H., Shen S.Y., Barber L.D.,
 RA Marsh S.G.E., Bias W.B., Parham P.;
 RT "HLA-B*67: a member of the HLA-B*67 family that expresses the M51
 epitope";
 RL Tissue Antigens 43:38-43 (1994).
 RP [2]
 RP SEQUENCE OF 26-205 FROM N.A. (B*6701).
 RC TISSUE=Blood;
 RA Petersdorf E.;
 RT "Molecular diversity of HLA-B.";

Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A. (B*6702).
 RP Iglehart B.A., Lefell M.S.;
 RT "HLA-B*6702 (Promoter-3'UTR).";
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE OF 26-206 FROM N.A. (B*6702).
 RP Baldassarre L.A., Hurley C.K.;
 RT "Novel HLA-B allele (HLA-B*67012 variant).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- POLYMORPHISM: The following alleles of B-67 are known: B*6701
 CC (B-67LAV) and B*6702. The sequence shown is that of B*6701.

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 CC or send an email to license@sib-sib.ch).

 CC EMBL: L17005; AAC37548.1; --
 DR EMBL: L1789; AAB60360.1; --
 DR EMBL: AF487379; AAL93257.1; --
 DR EMBL: AF321835; AAK09378.1; --
 DR EMBL: AF321834; AAK09378.1; JOINED.
 DR EMBL: AY050196; AAL18235.1; --
 DR EMBL: AY050195; AAL18235.1; JOINED.
 DR PIR: I59645; I59645.
 DR HSSP: P30460; IAGD.
 DR Genew: HGNC:4932; HLA-B.
 DR MIM: 142830; --
 DR InterPro: IPR001110; IG-like.
 DR InterPro: IPR003597; IG.cl.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR PRODOM: PD000050; MHC_I; 1.
 DR SMART: SM00407; IGC1; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW MHC_I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-67 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
 FT DOMAIN 333 362 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 E -> G (in allele B*6702).
 FT DISULFID 227 283 I -> V (in allele B*6702).
 FT VARIANT 69 69 /FTID=VAR_016536.
 FT VARIANT 76 76 I -> V (in allele B*6702).
 FT VARIANT 87 87 N -> E (in allele B*6702).
 FT VARIANT 90 90 /FTID=VAR_016537.
 FT VARIANT 93 93 /FTID=VAR_016538.
 FT VARIANT 93 93 I -> K (in allele B*6702).
 FT VARIANT 97 97 /FTID=VAR_016539.
 FT VARIANT 97 97 A -> R (in allele B*6702).
 FT VARIANT 97 97 /FTID=VAR_016540.
 FT VARIANT 97 97 T -> A (in allele B*6702).

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FT FT VARIANT 100 100 /FTID=VAR 016541.
FT E -> V (in allele B*6702).
FT /FTID=VAR 016542.
SQ SEQUENCE 362 AA; 40342 MW; 3F6A17FC10230F70 CRC64;

Query Match 79.0%; Score 927; DB 1; Length 362;
Best Local Similarity 80.0%; Pred. No. 2.6e-71;
Matches 172; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPVEQPGQYWEWTTGYAKANAQTDRLVALRNL 60
DB 47 ISVGVDVDTQFVRFDSDAASPEERAPWIEQGEYWDNRNTQIYKAQAQTDRESLRNL 106

QY 61 RRYNQSEAGSHTLQGMNGCDMGDPDGRLLRGYHQHAWDKDYISLNEDLRSWTAADTVAQI 120
DB 107 GYINQSEAGSHTLQGMNGCDMGDPDGRLLRGYHQHAWDKDYISLNEDLRSWTAADTVAQI 166

QY 121 TORFYAEYAEAEFTYLEGCELELLRRLYENGKETLQORADPPKAVHAHPIISDHEATLR 180
DB 167 TQKWEARVAEQRLTYLEGTCVWLRRLYENGKETLQORADPPKAVHAHPIISDHEATLR 226

QY 181 CWALGFYPAEITLTWQRGEQTDTELVEPTRPAG 215
DB 227 CWALGFYPAEITLTWQRGEQTDTELVEPTRPAG 261

RESULT 8
1B42 HUMAN STANDARD; PRT; 362 AA.
ID 1B42 HUMAN STANDARD; PRT; 362 AA.
AC P30480; P79555;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-42 alpha chain precursor
DE (MHC class I antigen B*42).
GN HLA-B OR HLAB
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*4201).
RX MEDLINE=89235215; PubMed=2715640;
RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
RT "Diversity and diversification of HLA-A,B,C alleles.";
RL J. Immunol. 142:3937-3950(1989).
[2]
RP SEQUENCE FROM N.A. (B*4202).
RX MEDLINE=97387746; PubMed=9243763;
RA Lardy N.M., Otting N., van de Weerd M.J., van de Horst A.R.,
RT "Full-length cDNA nucleotide sequence of the HLA-B*4202 allele.";
RL Tissue Antigens 50:83-84(1997).
[3]
RP SEQUENCE FROM N.A. (B*4201).
RC TISSUE=Blood;
RX MEDLINE=22512041; PubMed=12622774;
RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
RT "Cloning and sequencing full-length HLA-B and -C genes.";
RL Tissue Antigens 61:20-48(2003).
CC -1- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- POLYMORPHISM: The following alleles of B-42 are known: B*4201
CC (Bw-42) and B*4202. The sequence shown is that of B*4201.
CC -----
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DR EMBL; M24034; AAA59667.1; -
DR EMBL; U88407; AAC16437.1; -
DR EMBL; AJ309194; CAC38393.1; -
DR PIR; I61865; I61865.
DR HSP; P30460; IAGD.
DR Genew; HGNC:4932; HLA-B.
DR MM; 142830.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-CL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig_1.
DR PRINTS; PF00129; MHC_I_1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I_1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IGLIKE; 1.
DR PROSITE; PS00290; IGMHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-42 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED (GLNAC. . .) (BY SIMILARITY).
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT VARIANT 33 33 Y -> H (in allele B*4202).
FT /FTID=VAR 016460.
SQ SEQUENCE 362 AA; 40333 MW; C9155AB015DEA1BE CRC64;

Query Match 78.8%; Score 924; DB 1; Length 362;
Best Local Similarity 79.1%; Pred. No. 4.6e-71;
Matches 170; Conservative 18; Mismatches 27; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPVEQPGQYWEWTTGYAKANAQTDRLVALRNL 60
DB 47 ISVGVDVDTQFVRFDSDAASPEERAPWIEQGEYWDNRNTQIYKAQAQTDRESLRNL 106

QY 61 RRYNQSEAGSHTLQGMNGCDMGDPDGRLLRGYHQHAWDKDYISLNEDLRSWTAADTVAQI 120
DB 107 GYINQSEAGSHTLQGMNGCDMGDPDGRLLRGYHQHAWDKDYISLNEDLRSWTAADTVAQI 166

QY 121 TORFYAEYAEAEFTYLEGCELELLRRLYENGKETLQORADPPKAVHAHPIISDHEATLR 180
DB 167 TQKWEARVAEQRLTYLEGTCVWLRRLYENGKETLQORADPPKAVHAHPIISDHEATLR 226

QY 181 CWALGFYPAEITLTWQRGEQTDTELVEPTRPAG 215
DB 227 CWALGFYPAEITLTWQRGEQTDTELVEPTRPAG 261

RESULT 9
1B47 HUMAN STANDARD; PRT; 362 AA.
ID 1B47 HUMAN STANDARD; PRT; 362 AA.
AC P30485; O19555; O77933; Q95392; Q9GIL3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-47 alpha chain precursor
DE (MHC class I antigen B*47) (Bw-47).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A. (B*4701).
 RX MEDLINE=88152906; PubMed=3257938;
 RA Zemmour J., Ennis P.D., Parham P., Dupont B.;
 RT "Comparison of the structure of HLA-Bw47 to HLA-B13 and its
 RL relationship to 21-hydroxylase deficiency."; Immunogenetics 27:281-287(1988).
 RP SEQUENCE FROM N.A. (B*4701).
 RX MEDLINE=22512041; PubMed=12622774;
 RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
 RL Madrigal J.A., Little A.-M.;
 RT "Cloning and sequencing full-length HLA-B and -C genes."; Tissue Antigens 61:20-48(2003).
 RP SEQUENCE OF 1-302 FROM N.A. (B*4702).
 RX TISSUE=peripheral blood;
 RA Fischer G.F., Broer E., Fae I., Leitner D., Mayr W.R.;
 RL "Nucleotide sequence analysis of an HLA-B47 variant (HLA-B*4702)."; Tissue Antigens 49:540-542(1997).
 RP SEQUENCE OF 26-206 FROM N.A. (B*4703).
 RX MEDLINE=20548605; PubMed=11098929;
 RA Ellis J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H.,
 RL Hurley C.K.;
 RT "Diversity is demonstrated in class I HLA-A and HLA-B alleles in Cameroon, Africa: description of HLA-A*03012, *2612, *3006 and HLA-B*1403, *4703."; Tissue Antigens 56:291-302(2000).
 RP SEQUENCE OF 26-206 FROM N.A. (B*4703).
 RX Kosman C.A., Hurley C.K.;
 RA "Novel HLA class I B locus alleles"; Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases
 CC -1- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
 CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- POLYMORPHISM: The following alleles of B-47 are known: B*4701, B*4702 and B*4703. The sequence shown is that of B*4701.
 CC
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 CC
 CC EMBL; M19756; AAA52664.1; -
 CC EMBL; AJ308398; CAC33087.2; -
 CC EMBL; AJ295141; CAC17463.2; -
 CC EMBL; Y09118; CAA70335.1; -
 CC EMBL; AF016843; AAB70513.1; -
 CC EMBL; AF016842; AAB70513.1; JOINED.
 CC EMBL; AF071764; AAC23752.1; -
 CC EMBL; AF071763; AAC23752.1; JOINED.
 CC PIR; I68724; I68724.
 CC HSSP; P03989; 1HSA.
 CC Genew; HGNC:4932; HLA-B.
 CC MIM; 142830; -
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig cl.
 CC InterPro; IPR003006; Ig MHC.
 CC InterPro; IPR001039; MHC_I.
 CC Pfam; PF00047; ig; 1.
 CC Pfam; PF00129; MHC_I; 1.
 CC PRINTS; PR01638; MHCCLASSI.
 CC ProDom; PD000050; MHC_I; 1.

DR SMART; SMO0407; IGc1; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT CHAIN 25 362 B-47 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 323
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT VARIANT 101 101 D -> S (in allele B*4702 and allele B*4703).
 FT /FTID=VAR_016474.
 FT T -> N (in allele B*4702 and allele B*4703).
 FT /FTID=VAR_016475.
 FT LR -> RG (in allele B*4702).
 FT /FTID=VAR_016476.
 FT E3D3B4CBF8C15EAE CRC64;
 SQ SEQUENCE 362 AA; 40571 MW; E3D3B4CBF8C15EAE CRC64;
 Query Match 78.7%; Score 923; DB 1; Length 362;
 Best Local Similarity 79.5%; Pred. No. 5.6e-71;
 Matches 171; Conservative 12; Mismatches 32; Indels 0; Gaps 0;
 QY 1 IAVEVDVDTQFLRFDSDAAIPRMEPREPVEQEGPQYWEWTTGVAKANAQTDRAVALRNL 60
 DB 47 ITVGVDVDTLFRFDSDATSPKPRAPWIEQEGPEYWDRETOISKTKTQIVREDLRLL 106
 QY 61 RRYNQSEAGSHTLQGMNCDMPDGRLLRGVYHQHAWDKYISLNEDLRSWTAATVAQI 120
 DB 107 RRYNQSEAGSHTLQRMFGCDVGPDRLLRGVYHQDAVDGKYIALNEDLSWTAATAAQI 166
 QY 121 TORFVEAEYEAEPTYLEGCLLRRYLENGKTELQRAADPPKAAHVAHPISDHEATLR 180
 DB 167 TORKWEARVAQLRAYLEGECEVWRRLRYLENGKTELQRAADPPKTHVTHHFIISDHEATLR 226
 QY 181 CWALGFYPAEITLTWQRDGEQQTQTELVTETRPAG 215
 DB 227 CWALGFYPAEITLTWQRDGEQQTQTELVTETRPAG 261
 RESULT 10
 ID 1B08 HUMAN STANDARD; PRT; 362 AA.
 AC P30460; O62901; Q95730; Q98140; P79542; Q95369; Q95J00; Q9GJ20;
 AC Q9MY78; Q9MYF4; Q9TQ86; Q9TCM2; Q9UQT0;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-8 alpha chain precursor
 GN (MHC class I antigen B*8).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*0801).
 RX MEDLINE=89235215; PubMed=2715640;
 RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."; J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (B*0801).
 RX TISSUE=Blood;
 RC MEDLINE=22512041; PubMed=12622774;
 RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,

RA Madrigal J.A., Little A.-M.;
RT "Cloning and sequencing full-length HLA-B and -C genes";
RL Tissue Antigens 61:20-48(2003).
RN [3]
RP SEQUENCE FROM N.A. (B*0801).
RA Shiina S., Tamiva G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 26-206 FROM N.A. (B*0804).
RX MEDLINE=97473039; PubMed=9331954;
RA Hoyer R.J., Bratlie A., Schreuder G.M., Hurley C.K.;
RT "Characterization of a novel HLA-B allele, B*0804, in a Norwegian family";
RL Tissue Antigens 50:308-310(1997).
RN [5]
RP SEQUENCE OF 33-257 FROM N.A. (B*0804).
RA Eberle M., Lorentzen D., Iwanaga K.K., Watkins D.I.;
RT "Identification of a new HLA-B*08 variant, B*08NEW";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 26-206 FROM N.A. (B*0806).
RA Marcos C.Y., Lazaro A.M., Noreen H., Stastny P.;
RT "New HLA-B locus allele.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 26-206 FROM N.A. (B*0807 AND B*0809).
RX MEDLINE=20336961; PubMed=1077103;
RA Kennedy C.T., Dodd R., Le T., Wallace R., Ng G., Greville W.D.,
RA Kennedy A., Taverntiti A., Moses J.H., Clow N., Watson N.,
RA Dunkley H.;
RT "Routine HLA-B genotyping with PCR-sequence-specific oligonucleotides (PCR-SSO) detects eight new alleles: B*0807, B*0809, B*1551, B*3529, B*3532, B*4025, B*5304 and B*5508";
RL Tissue Antigens 55:266-270(2000).
RN [8]
RP SEQUENCE OF 116-206 FROM N.A. (B*0809).
RX MEDLINE=20166355; PubMed=10703615;
RA Elsner H.A., Blasczyk R.;
RT "Identification of the novel allele HLA-B*0809 in a Caucasian individual: estimation of allelic potential between B*08 variants";
RL Tissue Antigens 55:74-77(2000).
RN [9]
RP SEQUENCE OF 26-206 FROM N.A. (B*0809; B*0812; B*0813 AND B*0814).
RX MEDLINE=21276061; PubMed=11380951;
RA Steiner N.K., Gans C.P., Kosman C., Baldassarre L.A., Edson S.,
RA Jones P.F., Rizzuto G., Pimantothai N., Koester R., Mitton W., Ng J.,
RA Hartman R.J., Hurley C.K.;
RT "Novel HLA-B alleles associated with antigens in the 8C CREG";
RL Tissue Antigens 57:373-375(2001).
RN [10]
RP SEQUENCE OF 26-206 FROM N.A. (B*0810).
RA Day S.;
RT "A new B*08 variant allele.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-300.
RX MEDLINE=97130420; PubMed=8976183;
RA Reid S.W., McAdam S., Smith K.J., Klennerman P., O'Callaghan C.A.,
RA Harlos K., Jakobsen B.K., McMichael A.J., Bell J.I., Stuart D.I.,
RA Jones E.V.;
RT "Antagonist HIV-1 Gag peptides induce structural changes in HLA B8";
RL J. Exp. Med. 184:2279-2286(1996).
CC CC -/- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
CC CC -/- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
CC CC -/- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -/- POLYMORPHISM: The following alleles of B-8 are known: B*0801, B*0804, B*0806, B*0807 (B*NV), B*0809 (B*HM; B*08HO), B*0810, B*0812, B*0813 and B*0814. The sequence shown is B*0801.
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DR PDB; IAGY; 16-JUN-97.
DR PDB; IAGZ; 16-JUN-97.
DR PDB; IAGA; 16-JUN-97.
DR PDB; IAGB; 16-JUN-97.
DR PDB; IAGC; 16-JUN-97.
DR PDB; IAGD; 16-JUN-97.
DR PDB; IAGE; 16-JUN-97.
DR PDB; IAGF; 16-JUN-97.
DR PDB; IAGG; 16-JUN-97.
DR PDB; IAGH; 16-JUN-97.
DR PDB; IAGI; 16-JUN-97.
DR PDB; IAGJ; 16-JUN-97.
DR PDB; IAGK; 16-JUN-97.
DR PDB; IAGL; 16-JUN-97.
DR PDB; IAGM; 16-JUN-97.
DR PDB; IAGN; 16-JUN-97.
DR PDB; IAGO; 16-JUN-97.
DR PDB; IAGP; 16-JUN-97.
DR PDB; IAGQ; 16-JUN-97.
DR PDB; IAGR; 16-JUN-97.
DR PDB; IAGS; 16-JUN-97.
DR PDB; IAGT; 16-JUN-97.
DR PDB; IAGU; 16-JUN-97.
DR PDB; IAGV; 16-JUN-97.
DR PDB; IAGW; 16-JUN-97.
DR PDB; IAGX; 16-JUN-97.
DR PDB; IAGY; 16-JUN-97.
DR PDB; IAGZ; 16-JUN-97.
DR PDB; IAGA; 16-JUN-97.
DR PDB; IAGB; 16-JUN-97.
DR PDB; IAGC; 16-JUN-97.
DR PDB; IAGD; 16-JUN-97.
DR PDB; IAGE; 16-JUN-97.
DR PDB; IAGF; 16-JUN-97.
DR PDB; IAGG; 16-JUN-97.
DR PDB; IAGH; 16-JUN-97.
DR PDB; IAGI; 16-JUN-97.
DR PDB; IAGJ; 16-JUN-97.
DR PDB; IAGK; 16-JUN-97.
DR PDB; IAGL; 16-JUN-97.
DR PDB; IAGM; 16-JUN-97.
DR PDB; IAGN; 16-JUN-97.
DR PDB; IAGO; 16-JUN-97.
DR PDB; IAGP; 16-JUN-97.
DR PDB; IAGQ; 16-JUN-97.
DR PDB; IAGR; 16-JUN-97.
DR PDB; IAGS; 16-JUN-97.
DR PDB; IAGT; 16-JUN-97.
DR PDB; IAGU; 16-JUN-97.
DR PDB; IAGV; 16-JUN-97.
DR PDB; IAGW; 16-JUN-97.
DR PDB; IAGX; 16-JUN-97.
DR PDB; IAGY; 16-JUN-97.
DR PDB; IAGZ; 16-JUN-97.
DR PDB; IAGA; 16-JUN-97.
DR PDB; IAGB; 16-JUN-97.
DR PDB; IAGC; 16-JUN-97.
DR PDB; IAGD; 16-JUN-97.
DR PDB; IAGE; 16-JUN-97.

FT VARIANT 101 101 S -> N (in allele B*0806).
 FT FTID=VAR_016504.
 FT VARIANT 119 119 L -> W (in allele B*0809).
 FT FTID=VAR_016505.
 FT VARIANT 121 121 S -> R (in allele B*0812).
 FT FTID=VAR_016506.
 FT VARIANT 121 121 S -> T (in allele B*0809).
 FT FTID=VAR_016507.
 FT VARIANT 137 138 HN -> YH (in allele B*0814).
 FT FTID=VAR_016519.
 FT VARIANT 138 138 N -> D (in allele B*0807).
 FT FTID=VAR_016508.
 FT VARIANT 140 140 Y -> D (in allele B*0814).
 FT FTID=VAR_016520.
 FT VARIANT 176 176 V -> E (in allele B*0806).
 FT FTID=VAR_016509.
 FT VARIANT 180 180 D -> L (in allele B*0813).
 FT FTID=VAR_016510.
 FT VARIANT 180 180 D -> R (in allele B*0806).
 FT FTID=VAR_016511.
 FT STRAND 27 36
 FT TURN 39 40
 FT STRAND 45 52
 FT TURN 53 54
 FT STRAND 55 61
 FT TURN 62 63
 FT STRAND 70 71
 FT TURN 74 76
 FT HELIX 77 78
 FT HELIX 81 108
 Query Match 78.6%; Score 922; DB 1; Length 362;
 Best Local Similarity 78.6%; Pred. No. 6.8e-71;
 Matches 169; Conservative 18; Mismatches 28; Indels 0; Gaps 0;
 Qy 1 IAVEYDDTQFLRPSDAALPRMEPREPWVQEQPGQWETTCYAKANAQTDVVALRNLL 60
 Db 47 ISVGIVDDTQVFRFSDAASPREPRAPWTEQEQPEYMDRNTQIFKNTQTDRESLRNL 106
 Qy 61 RRYNOSAGSHLLGMMGDMGPDGRLRGYHOGANDKDYISLNEDLSRWTAAQI 120
 Db 107 GYNNOSAGSHLLQSMYGCVDGPDGRLRGYHOGANDKDYISLNEDLSRWTAAQI 166
 Qy 121 TORPYAEVABEPTVLEGCELELLRRLYENKEILQADPPKAVHAPIISCHAEATLR 180
 Db 167 TQRKWEARVAEQDRAYLEGTCVLEWRLRYLNGKDTLERADPPKTHVTHPIISCHAEATLR 226
 Qy 181 CWALGFYPAETTLTWQDGEQOTDTELVTETPAG 215
 Db 227 CWALGFYPAETTLTWQDGEQOTDTELVTETPAG 261
 RESULT 11
 1B07 HUMAN STANDARD; PRT; 362 aa.
 AC P01889; Q29638; Q29681; Q29854; Q29861; Q31613; Q9GIX1; Q9TF95;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-7 alpha chain precursor
 DE (MHC class I antigen B*7).
 GN HLA-B OR HLAB
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*0702).
 RX MEDLINE=90207291; PubMed=2320591;
 RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;
 RT "Rapid cloning of HLA-A,B cDNA by using the polymerase chain
 RT reaction: frequency and nature of errors produced in amplification.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).

[2]
 RN SEQUENCE FROM N.A. (B*0702).
 RP MEDLINE=90315860; PubMed=2700944;
 RX Parham P., Benjamin R.J., Chen B.P., Clayberger C., Ennis P.D.,
 RA Kresky A.M., Lawlor D.A., Littman D.R., Norment A.M., Orr H.T.,
 RA Salter R.D., Zemmour J.;
 RT "Diversity of class I HLA molecules: functional and evolutionary
 RT interactions with T cells.";
 RL Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989).
 RN [3]
 RP SEQUENCE FROM N.A. (B*0702).
 RX MEDLINE=85287366; PubMed=2993161;
 RA Sood A.K., Pan J., Biro P.A., Pereira D., Srivastava R., Reddy V.B.,
 RA Ducean B.W., Weissman S.M.;
 RT "Structure and polymorphism of class I MHC antigen mRNA";
 RL Immunogenetics 22:101-121(1985).
 RN [4]
 RP SEQUENCE FROM N.A. (B*0702).
 RX Ellexson M.E., Zhang L., Hildebrand W.H.;
 RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (B*0703).
 RX MEDLINE=94148707; PubMed=8106270;
 RA Bergmans A., Tijssen H., Lardy J., Reekers P.;
 RT "Complete nucleotide sequence of HLA-B*0703, a B7-variant (BPOT).";
 RL Hum. Immunol. 38:159-162(1993).
 RN [6]
 RP SEQUENCE FROM N.A. (B*0704).
 RX MEDLINE=95381233; PubMed=7652739;
 RA Kubens B.S., Arnett K.L., Adams E.J., Parham P., Grosse-Wilde H.;
 RT "Definition of a new HLA-B7 subtype (B*0704) by isoelectric focusing,
 RT family studies and DNA sequence analysis.";
 RL Tissue Antigens 45:322-327(1995).
 RN [7]
 RP SEQUENCE FROM N.A. (B*0705).
 RX MEDLINE=95184211; PubMed=7878658;
 RA Arnett K.L., Adams E.J., Domena J.D., Parham P.;
 RT "Structure of a novel subtype of B7 (B*0705) isolated from a Chinese
 RT individual.";
 RL Tissue Antigens 44:318-321(1994).
 RN [8]
 RP SEQUENCE FROM N.A. (B*0703 AND B*0705).
 RX MEDLINE=96128250; PubMed=8537119;
 RA Smith K.D., Epperson D.F., Lutz C.T.;
 RT "Alloreactive cytotoxic T-lymphocyte-defined HLA-B7 subtypes differ in
 RT peptide antigen presentation.";
 RL Immunogenetics 43:27-37(1996).
 RN [9]
 RP SEQUENCE FROM N.A. (B*0706).
 RX MEDLINE=96369317; PubMed=8773323;
 RA Sanz L., Vilches C., de Pablo R., Bunce M., Moreno M.E., Kreisler M.;
 RT "Haplotypic association of two new HLA class I alleles: Cw*15052 and
 RT B*0706: evolutionary relationships of HLA-Cw*15 alleles.";
 RL Tissue Antigens 47:329-332(1996).
 RN [10]
 RP SEQUENCE FROM N.A. (B*0718).
 RX Bettinotti M.P., Hadzikadic L., Dhillon G., Barracchini K.,
 RA Marincola F.M.;
 RT "A new HLA-B allele.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A. (B*0702).
 RX Marsh S.G.E.;
 RT "Intron sequences of HLA class I";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A. (B*0702).
 RX TISSUE=Blood;
 RL MEDLINE=22512041; PubMed=12622774;
 RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
 RA Madrigal J.A., Little A.-M.;
 RT "Cloning and sequencing full-length HLA-B and -C genes.";
 RL Tissue Antigens 61:20-48(2003).

[13] SEQUENCE OF 26-206 FROM N.A. (B*0724).
 RN TISSUE=Peripheral blood;
 RC MEDLINE=2142086; PubMed=11556973;
 RA Middleton D., Curran M.D., Anholts J.D., Reilly E.R., Schreuder G.M.;
 RT "Characterisation of a new HLA-B allele, HLA-B*0724.";
 RL Tissue Antigens 57:471-473(2001).
 [14] SEQUENCE OF 25-295 (B*0702).
 RN MEDLINE=8008278; PubMed=518865;
 RA Orr H.T., Lopez de Castro J.A., Lancet D., Strominger J.L.;
 RT "Complete amino acid sequence of a papain-solubilized human
 histocompatibility antigen, HLA-B*7. 2. Sequence determination and
 search for homologies.";
 RL Biochemistry 18:5711-5720(1979).
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
 immune system.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 microglobulin).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- POLYMORPHISM: The following alleles of B-7 are known: B*0702
 (B*7.2), B*0703 (BPOT), B*0704, B*0705, B*0706 (B*7L79), B*0718 and
 B*0724. The sequence shown is B*0702.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M32317; AAA36230.1; -;
 DR EMBL; M16102; AAA59622.1; ALT_SEQ.
 DR EMBL; U29087; AAA91229.1; -;
 DR EMBL; X64454; CAA45785.1; -;
 DR EMBL; U04245; AAA87398.1; -;
 DR EMBL; L33922; AAA65639.1; -;
 DR EMBL; U21052; AAA92563.1; -;
 DR EMBL; U21053; AAA92564.1; -;
 DR EMBL; X91749; CAA62864.1; -;
 DR EMBL; AF189017; AAF01052.1; -;
 DR EMBL; AJ309047; CAC35468.1; -;
 DR EMBL; AJ292075; CAC33440.1; -;
 DR EMBL; AJ401222; CAC10402.1; -;
 DR PIR; B35997; HLHUB7.
 DR PIR; I59651; I59651.
 DR HSSP; P30460; IAGD.
 DR Genew; HGNC:4932; HLA-B.
 DR MIM; 142830; -;
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0030106; F:MHC class I receptor activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASS1.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGCL; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 262
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 B-7 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206
 FT EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298
 FT EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309
 FT CONNECTING PEPTIDE.

TRANSMEM 330 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .).
 FT DISULFID 125 168
 FT DISULFID 127 283
 FT VARIANT 93 95
 FT VARIANT 118 119
 FT VARIANT 121 121
 FT VARIANT 138 138
 FT VARIANT 180 180
 FT VARIANT 187 187
 FT VARIANT 306 306
 FT CONFLICT 15 18
 FT CONFLICT 266 266
 FT CONFLICT 268 268
 FT CONFLICT 297 297
 FT CONFLICT 314 315
 SQ SEQUENCE 362 AA; 40460 MW; 5E5A7BDE031403D6 CRC64;
 Query Match 78.5%; Score 921; DB 1; Length 362;
 Best Local Similarity 79.1%; Pred. No. 8.2e-71;
 Matches 170; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
 QY 1 IAVEYVDDTQFLRSDAAIPEMEPEPWEQSGPQWETTCYAKANAQTDVALRNLL 60
 DB 47 ISVGIVDDTQFVRPDSDAAPREPRAPFWEQSGPQWETTCYAKANAQTDVALRNLL 106
 QY 61 RRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAMDGKDYIISINEDLRSWTAADTVAQI 120
 DB 107 GYINQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAMDGKDYIISINEDLRSWTAADTVAQI 166
 QY 121 TORPYEAEVABEPTTYLEGECELLRRLYENKGTQLORADPPKAVAHHPISDHEATLR 180
 DB 167 TQKWEAAREAEQRRAYLEGECEVLEWLYLENGKOKLERADPPKAVAHHPISDHEATLR 226
 QY 181 CWALGFYPAEITLTWQRDGBEQTDQTELVTETRPAG 215
 DB 227 CWALGFYPAEITLTWQRDGBEQTDQTELVTETRPAG 261
 RESULT 12
 1B14 HUMAN
 ID 1B14 HUMAN STANDARD; PRT; 362 AA.
 AC P30462; O02862; P30463;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-14 alpha chain precursor
 DE (MHC class I antigen B*14).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*1401 AND B*1402).
 RX MEDLINE=89235215; PubMed=2715640;
 RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles.";
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (B*1402).
 RC TISSUE=Blood;
 RX MEDLINE=22512041; PubMed=12622774;
 RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,

Madrigal J.A., Little A.-M.;
 "Cloning and sequencing full-length HLA-B and -C genes.";
 Tissue Antigens 61:20-48(2003).
 [3]
 SEQUENCE OF 26-206 FROM N.A. (B*1403).
 MEDLINE=20548605; PubMed=11098929;
 Ellis J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H.,
 Hurley C.K.;
 "Diversity is demonstrated in class I HLA-A and HLA-B alleles in
 Cameroon, Africa: description of HLA-A*03012, *2612, *3006 and HLA-B*1403, *4016, *4703.";
 Tissue Antigens 56:1291-302(2000).
 CC - FUNCTION: Involved in the presentation of foreign antigens to the
 immune system.
 CC - SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 microglobulin).
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - POLYMORPHISM: The following alleles of B*14 are known: B*1401
 (Bw-64; B-64), B*1402 (Bw-65, B-65) and B*1403. The sequence shown
 is that of B*1401.

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 or send an email to license@isb-sib.ch).

 EMBL; M24040; AAA59661.1; -;
 EMBL; M24032; AAA59664.1; -;
 EMBL; AJ301657; CAC20461.1; -;
 EMBL; U91331; AAB61335.1; -;
 EMBL; U91330; AAB61335.1; JOINED.
 PIR; I61859; I61859.
 HSP; P30460; IAGD.
 Genew; HGNC:4932; HLA-B.
 MIM; 142830; -;
 GO; GO:0005887; C: integral to plasma membrane; NAS.
 GO; GO:0030106; F: MHC class I receptor activity; NAS.
 GO; GO:0006955; P: immune response; NAS.
 InterPro; IPR007110; IG-like.
 InterPro; IPR003597; IG cl.
 InterPro; IPR003006; IG_MHC.
 InterPro; IPR001039; MHC_I.
 Pfam; PF00047; IG; 1.
 Pfam; PF00129; MHC_I; 1.
 PRINTS; PR01638; MHCCLASSI.
 PRODOM; PD000050; MHC_I; 1.
 SMART; SM00407; IGcl; 1.
 PROSITE; PS00835; IG_LIKE; 1.
 PROSITE; PS00290; IG_MHC; 1.
 MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 SIGNAL 1 24
 CHAIN 25 362
 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 B-14 ALPHA CHAIN.
 DOMAIN 25 114
 EXTRACELLULAR ALPHA-1.
 DOMAIN 115 206
 EXTRACELLULAR ALPHA-2.
 DOMAIN 207 298
 DOMAIN 299 309
 EXTRACELLULAR ALPHA-3.
 TRANSMEM 310 333
 CONNECTING PEPTIDE.
 DOMAIN 334 362
 CYTOPLASMIC TAIL.
 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 BY SIMILARITY.
 BY SIMILARITY.
 S -> A (in allele B*1402 and allele
 B*1403).
 /FTID=VAR_016364.
 L -> R (in allele B*1403).
 /FTID=VAR_016654.
 SEQUENCE 362 AA; 40358 MW; 9039122C400337F CRC64;
 Query Match 78.5%; Score 921; DB 1; Length 362;

Best local similarity 79.1%; Pred. No. 8.2e-71;
 Matches 170; Conservative 15; Mismatches 30; Indels 0; Gaps 0;
 QY 1 IAVEYVDTQFLREDSDAAIPEMEPRBPWVQEGPOYWEWTTGYAKANAQTDVVALRNLL 60
 DB 47 ISVGYVDDTQFVRFDSDAASPREEPFAPWIEQEGFSDWRNTQCKNTQTDRESLNLR 106
 QY 61 RRYNQSEAGSHTLQMGSCDMGPDGRLRLRGYHQHAWDKDYISNEDLRSWTAADTVAQI 120
 DB 107 GYVQSEAGSHTLQWYGVDPDGRLLRGYVQAYDKGYIALNEDLSSTWTAADTAAQI 166
 QY 121 TORFYAEYAEPTVLEGECLLARYLNGKTLQADPPKAAHVAHHPISDHEATLR 180
 DB 167 TQKWEAREAEQLRAYLEGTCVWLRHLENGKETQADPPKTHVTHHPISDHEATLR 226
 QY 181 CWALGFYPAEITLTWQRDCEQTDQTELVEITRPAG 215
 DB 227 CWALGFYPAEITLTWQRDGEDQTDQTELVEITRPAG 261

 RESULT 13
 1B37 HUMAN STANDARD; PRT; 362 AA.
 ID 1B37 HUMAN STANDARD; PRT; 362 AA.
 AC P18453; O19627; Q95HA3; Q95HA8; Q95HM9; Q9GJ31;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-37 alpha chain precursor
 DE (MHC class I antigen B*37).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*3701).
 RX MEDLINE=90207291; PubMed=2320591;
 RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;
 "Rapid cloning of HLA-A,B CDNA by using the polymerase chain
 reaction: frequency and nature of errors produced in amplification.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (B*3704).
 RC TISSUE=Peripheral blood;
 RX MEDLINE=22025782; PubMed=12028544;
 RA Estefania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;
 "Complementary DNA sequence of the novel HLA-B*3704 allele.";
 RL Tissue Antigens 59:142-144(2002).
 RN [3]
 RP SEQUENCE FROM N.A. (B*3705).
 RX MEDLINE=22131942; PubMed=12135437;
 RA Pyo C.-W., Han H., Kim T.G.;
 "Identification of a new HLA-B allele, B*3705 containing a Bw6
 sequence motif.";
 RL Tissue Antigens 59:335-337(2002).
 RN [4]
 RP SEQUENCE OF 1-322 FROM N.A. (B*3701).
 RA Hurley C.K., Bei M., Rodriguez S., Johnson A.;
 Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 26-206 FROM N.A. (B*3704).
 RA Gans C.P., Hurley C.K.;
 "Novel HLA-B allele.";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: Involved in the presentation of foreign antigens to the
 immune system.
 CC - SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 microglobulin).
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - POLYMORPHISM: The following alleles of B-37 are known: B*3701,
 B*3704 and B*3705. The sequence shown is that of B*3701.

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[illegible]

Query Match	78.5%	Score 921;	DB 1;	Length 362;
Best Local Similarity	79.1%	Pred. No. 8.2e-71;		
Matches 170;	Conservative 16;	Mismatches 29;	Indels 0;	Gaps 0;
Qy	1	IAEYVDDTQFLRFDSDAAIPRMPREPPWYEQSGPQWETTCYAKANAQTDQVALRNLL	60	
Db	47	ISGVDDTQFVRFDSDAASPTREPAPWIEQGGPEYWDRETIQISKNTQTYYEDLRLL	106	
Qy	61	RRYNQSEAGSHTLQGMNGCDMPGRLLRGVHAWDGKDYISLNEDLESWTAATVAQI	120	
Db	107	RRYNQSEAGSHTIQRMSCGDVPDGRLLRGVYNQFAYDGDYIALNEDLESWTAATAAQI	166	
Qy	121	TQRFYAEYAEPEFTYLEGSCLELLRRYLLENKETLQRAADPKAHVAHPISDHEATLR	180	
Db	167	TQKWEARFARVADODRAYLEGFCVLEWLRYLENKETLQRAADPKPIVYTHPISDHEATLR	226	
Qy	181	CWALGFYPAEITLTWQDGEQOTDTELVTETPAG	215	
Db	227	CWALGFYPAEITLTWQDGEOTDTELVTETPAG	261	

```

RESULT 14
ID B46_HUMAN STANDARD; PRT; 362 AA.
AC P30484; Q9TPR2;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-46 alpha chain precursor
DE (MHC class I antigen B*46) (Bw-46).
GN HLA-B OR HLAB
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (B*4601).
RP MEDLINE=89235215; PubMed=2715640;
RA Parham P, Lawlor D.A., Lomen C.E., Ennis P.D.;
RT university and diversification of HLA-A,B,C alleles." ;
RN J. Immunol. 142:3937-3950(1989).
[2]
RN SEQUENCE FROM N.A. (B*4601).
RP TISSUE=Blood;
RC MEDLINE=22512041; PubMed=12622774;
RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
RA Madrigal J.A., Little A.-M.;
RT "Cloning and sequencing full-length HLA-B and -C genes." ;
RN Tissue Antigens 61:20-48(2003).
[3]
RN SEQUENCE OF 26-206 FROM N.A. (B*4602) .
RP MEDLINE=20340078; PubMed=10885569;
RA Akesaka T., Kashiwase K., Shimamura M., Ishikawa Y., Tanaka H.,
RA Fujii M., Akaza T., Honda K., Yuasa S., Takahashi T., Juji T.;
RT "Identification of a novel HLA-B46 allele, B*4602, in Japanese." ;
RN Tissue Antigens 55:460-462(2000).
CC -I- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -I- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- POLYMORPHISM: The following alleles of B-46 are known: B*4601
CC and B*4602. The sequence shown is that of B*4601.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collabora-
CC tion between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC		ENBL; M2403; AAA5965;.1; -.	
DR	DR	ENBL; A310508; CAC34573.1; -	
DR	DR	ENBL; AB03291; BAA8411.1; -	
DR	DR	P1R; I61863; IG1863.	
DR	DR	HSP; P30683; LA95.	
DR	DR	Gnew; H42830; -	
DR	DR	MIM; 149830; -	
DR	DR	InterPro; IPR007110; IG-like.	
DR	DR	InterPro; IPR003597; IG_C1.	
DR	DR	InterPro; IPR003006; IG_MHC.	
DR	DR	InterPro; IPR001039; MHC_I.	
DR	DR	Fram; PF00047; IG; 1.	
DR	DR	Fram; PF00139; MHC_I; 1.	
DR	DR	PRINTS; PR01638; MHC_CLASSI.	
DR	DR	PfDom; PD00050; MHC_I; 1.	
DR	DR	SMART; SMC0407; IGc1; 1.	
DR	DR	PROSITE; PS00835; IG_LIKE; 1.	
DR	DR	PROSITE; PS00230; IG_MHC; 1.	
KW	KW	MHC_I; Transmembrane; Glycopr	
FT	FT	SIGNAL	1 24
FT	FT	CHAIN	25 362

HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-46 ALPHA CHAIN.

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OM protein - protein search, using sw model

Run on: June 18, 2004, 09:53:52 ; Search time 66 Seconds
(without alignments)
1027.824 Million cell updates/sec

Title: US-09-819-371-6

Perfect score: 1173
Sequence: 1 TAVEYVDTQFLRFSDAAI.....QRDGEQTDTELVEVPAG 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1164	99.2	324	7	Q861F0
2	1164	99.2	324	7	Q861E9
3	1164	99.2	346	7	Q8MGQ1
4	1164	99.2	346	7	Q8WLP5
5	1164	99.2	362	7	Q9TP68
6	1164	99.2	442	7	Q9SHC0
7	1150	98.0	346	7	Q95IT2
8	1150	98.0	362	6	Q7VR27
9	945	80.6	362	7	Q8MXK1
10	939	80.1	273	7	Q8SNC9
11	939	80.1	274	7	Q19692
12	939	80.1	362	7	P79612
13	939	80.1	362	7	Q78189
14	938	80.0	362	4	Q29705
15	935	79.7	354	7	Q95530
16	935	79.7	354	7	Q9MW41

17	935	79.7	359	7	Q29934
18	935	79.7	362	7	Q9MXI2
19	934	79.6	362	7	Q9MXD1
20	933	79.5	341	7	O19589
21	933	79.5	362	7	Q86017
22	932	79.5	362	7	Q9TPW6
23	931	79.4	298	7	Q9GJF1
24	931	79.4	362	7	Q7YQB0
25	928	79.1	326	7	Q861E8
26	928	79.1	362	7	Q9MXI0
27	928	79.1	362	7	Q9MXL8
28	927	79.0	338	7	Q95HL2
29	926	78.9	354	7	Q95412
30	926	78.9	362	7	Q9MXM2
31	925	78.9	363	7	Q8MEG3
32	924	78.8	362	7	Q9MXK5
33	924	78.7	362	7	Q9TFL5
34	923	78.7	273	7	Q9GJ38
35	923	78.7	273	7	Q95IH9
36	922	78.6	350	7	O19691
37	922	78.6	354	7	Q9MXK4
38	922	78.6	362	7	Q30933
39	922	78.6	362	7	Q9GIX2
40	922	78.6	362	7	Q31602
41	922	78.6	363	7	Q30988
42	921	78.5	273	7	Q8HML6
43	921	78.5	273	7	Q7YQ36
44	921	78.5	336	7	O19782
45	921	78.5	359	7	Q30711

ALIGNMENTS

RESULT 1
Q861F0 PRELIMINARY; PRT; 324 AA.
ID Q861F0
AC Q861F0; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nonclassical MHC class I antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., Liu Y., Zeng Y.; He X.; Xu L.;
RA "Nonclassical MHC class I HLA-F.";
RT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY216682; AAC37689.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;
Query Match 99.2%; Score 1164; DB 7; Length 324;


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Best Local Similarity 99.5%; Pred. No. 1.9e-99; Mismatches 0; Indels 0; Gaps 0;
Matches 214; Conservative 1;

QY 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 60
DB 40 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 99

QY 61 RRYNOSEAGSHTLQGMNCGDMPDGLRLRGYHQHAWDGKDYISLNEDLSWTAAADTVAQI 120
DB 100 RRYNOSEAGSHTLQGMNCGDMPDGLRLRGYHQHAWDGKDYISLNEDLSWTAAADTVAQI 159

QY 121 TORFYAEYAEAEPRTYLGECELELLRRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 180
DB 160 TORFYAEYAEAEPRTYLGECELELLRRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 219

QY 181 CWALGFYPAEITLTWQDGEQGTQDTTELVTETRPAG 215
DB 220 CWALGFYPAEITLTWQDGEQGTQDTTELVTETRPAG 254

RESULT 2
Q861E9 PRELIMINARY; PRT; 324 AA.
ID Q861B9
AC Q861B9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Xu L., Zeng Y., He X.;
RT "A new polymorphism in non-classical MHC class I HLA-F.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY221102; AAC34407.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2715F4 CRC64;

Query Match 99.2%; Score 1164; DB 7; Length 324;
Best Local Similarity 99.5%; Pred. No. 1.9e-99;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 60
DB 40 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 99

QY 61 RRYNOSEAGSHTLQGMNCGDMPDGLRLRGYHQHAWDGKDYISLNEDLSWTAAADTVAQI 120
DB 100 RRYNOSEAGSHTLQGMNCGDMPDGLRLRGYHQHAWDGKDYISLNEDLSWTAAADTVAQI 159

QY 121 TORFYAEYAEAEPRTYLGECELELLRRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 180
DB 160 TORFYAEYAEAEPRTYLGECELELLRRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 219

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QY 181 CWALGFYPAEITLTWQDGEQGTQDTTELVTETRPAG 215
DB 220 CWALGFYPAEITLTWQDGEQGTQDTTELVTETRPAG 254

RESULT 3
Q8MGQ1 PRELIMINARY; PRT; 346 AA.
ID Q8MGQ1
AC Q8MGQ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class Ib antigen.
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; AF523284; AAU74979.1; -
CC EMBL; AF523291; AAU74986.1; -
CC EMBL; AF523292; AAU74987.1; -
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0006955; P:immune response; IEA.
CC InterPro; IPR001064; Crystallin.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig-cl.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00129; MHC_I; 1.
CC PRINTS; PR01638; MHCCLASSI.
CC ProDom; PD000050; MHC_I; 1.
CC SMART; SM00407; IGcl; 1.
CC PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 346 AA; 39061 MW; D4782968A67E9B7D CRC64;

Query Match 99.2%; Score 1164; DB 7; Length 346;
Best Local Similarity 99.5%; Pred. No. 2.1e-99;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 60
DB 44 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRAVALRNLL 103

QY 61 RRYNOSEAGSHTLQGMNCGDMPDGLRLRGYHQHAWDGKDYISLNEDLSWTAAADTVAQI 120
DB 104 RRYNOSEAGSHTLQGMNCGDMPDGLRLRGYHQHAWDGKDYISLNEDLSWTAAADTVAQI 163

QY 121 TORFYAEYAEAEPRTYLGECELELLRRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 180
DB 164 TORFYAEYAEAEPRTYLGECELELLRRYLENGKETLQRAADPPKAAHVAHPISDHEATLR 223

QY 181 CWALGFYPAEITLTWQDGEQGTQDTTELVTETRPAG 215
DB 224 CWALGFYPAEITLTWQDGEQGTQDTTELVTETRPAG 258

RESULT 4
Q8WLP5

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QWLP5 PRELIMINARY; PRT; 346 AA.

AC QBLP5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE MHC class Ib antigen.
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP Ishigami A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation
RT spanning the nonclassical class I genes."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP He X., Liu Y., Xu L., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 2 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 3 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 4 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 5 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 6 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 7 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 8 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 9 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 10 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 11 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 12 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 13 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 14 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [16]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 15 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [17]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 16 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [18]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 17 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [19]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 18 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [20]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 19 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [21]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 20 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [22]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 21 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [23]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 22 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [24]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 23 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [25]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 24 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [26]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 25 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [27]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 26 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [28]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 27 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [29]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 28 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [30]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y., Zeng Y.;
RA "Cloning of full-length HLA-F*0101 variant 29 cDNA from Han Chinese."; <http://www.ncbi.nlm.nih.gov/pubmed/12511111>
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [31]
RP SEQUENCE FROM N.A.
RP He X., Xu L., Liu Y

224 CWALGFFPAEITLTWQDGEQQTDELVETRPAG 258

RESULT 5

Q9TP68 PRELIMINARY; PRT; 362 AA.

AC Q9TP68

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE DJ377H14.9 (Major histocompatibility complex, class I, F (CD412)).

DE HLA-F.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_taxid=9606;

OX (1)

FP SEQUENCE FROM N.A.

RA Williams S.

RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.

CC -! FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE

CC -! IMMUNE SYSTEM (BY SIMILARITY).

CC -! SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).

CC EMBL; AL022723; CAB46623.1; -.

DR HSP; Q30201; 1A6Z.

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0006955; P: immune response; IEA.

DR InterPro; IPR001064; Crystalin.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003066; Ig MHC.

DR InterPro; IPR001039; MHC_I.

DR Pfam; PF00047; Ig; 1.

DR Pfam; PF00129; MHC_I; 1.

DR PRINTS; PR01638; MHCCLASSI.

DR ProDom; PD000050; MHC_I; 1.

DR SMART; SM00407; IGcl; 1.

DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.

DR PROSITE; PS00835; IG LIKE; 1.

DR PROSITE; PS00290; IG MHC; 1.

KW Glycoprotein; Transmembrane.

SQ SEQUENCE 362 AA; 40578 MW; 970D072C813A07B2 CFC64;

Query Match 99.5%; Score 1164; DB 7; Length 362;

Best Local Similarity 99.5%; Pred. No. 2.2e-99;

Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVSYVDVDTQFLRDSAAIPRMSPRPWVEQGPQYWEITGYAKANAQTDVVALRNLL 60

DB 44 IAVSYVDVDTQFLRDSAAIPRMSPRPWVEQGPQYWEITGYAKANAQTDVVALRNLL 103

QY 61 RRYNQSEAGSHTLQMGNGCDMPDGRLLRGVYQHAWDKGYISLNSDLRSWTAADTVAQI 120

DB 104 RRYNQSEAGSHTLQMGNGCDMPDGRLLRGVYQHAWDKGYISLNSDLRSWTAADTVAQI 163

QY 121 TORPYEAEYAEERPTVLEGCELLRRYLENGKETIQRADPPPKAHVAHHPISDHEATLR 180

DB 164 TORPYEAEYAEERPTVLEGCELLRRYLENGKETIQRADPPPKAHVAHHPISDHEATLR 223

QY 181 CWALGFFPAEITLTWQDGEQQTDELVETRPAG 215

DB 224 CWALGFFPAEITLTWQDGEQQTDELVETRPAG 258

RESULT 6

Q95HCO PRELIMINARY; PRT; 442 AA.

AC Q95HCO

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Similar to major histocompatibility complex, class I, F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009260; AA09260.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01638; MHC_I; 1.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS003597; Ig cl.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01638; MHC_I; 1.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 442 AA; 50427 MW; 6459D3B5F4B5704A CRC64;

Query Match 99.2%; Score 1164; DB 7; Length 442;
Best Local Similarity 99.5%; Pred. No. 2.9e-99;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYWEWTTGYAKANAQTDRAVALRNL 60
DB 44 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYWEWTTGYAKANAQTDRAVALRNL 103

QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLRGYHQHAWDGKDYISLNEDLSRSTAADTVAQI 120
DB 104 RRYNQSEAGSHTLQGMNGCDMGDPGRLRGYHQHAWDGKDYISLNEDLSRSTAADTVAQI 163

QY 121 TORFYAEAEYAEFRITYLEGECELELLRRYLENGKETLQRAADPPKAVHHPISDHEATLR 180
DB 164 TORFYAEAEYAEFRITYLEGECELELLRRYLENGKETLQRAADPPKAVHHPISDHEATLR 223

QY 181 CWALGFYPAEITLTWQDGEEOQDTDELVETRPAG 215
DB 224 CWALGFYPAEITLTWQDGEEOQDTDELVETRPAG 258

RESULT 7
ID Q95IT2 PRELIMINARY; PRT; 346 AA.
AC Q95IT2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21291697; PubMed=11398964;
RA Adams E.J., Farham P.;
RT "Genomic analysis of common chimpanzee major histocompatibility complex class I genes."
RL Immunogenetics 53:200-208(2001).
DR EMBL; AF338355; AA07479.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01638; MHC_I; 1.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;

Query Match 98.0%; Score 1150; DB 7; Length 346;
Best Local Similarity 99.1%; Pred. No. 4.1e-98;
Matches 213; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYWEWTTGYAKANAQTDRAVALRNL 60
DB 44 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYWEWTTGYAKANAQTDRAVALRNL 103

QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLRGYHQHAWDGKDYISLNEDLSRSTAADTVAQI 120
DB 104 RRYNQSEAGSHTLQGMNGCDMGDPGRLRGYHQHAWDGKDYISLNEDLSRSTAADTVAQI 163

QY 121 TORFYAEAEYAEFRITYLEGECELELLRRYLENGKETLQRAADPPKAVHHPISDHEATLR 180
DB 164 TORFYAEAEYAEFRITYLEGECELELLRRYLENGKETLQRAADPPKAVHHPISDHEATLR 223

QY 181 CWALGFYPAEITLTWQDGEEOQDTDELVETRPAG 215
DB 224 CWALGFYPAEITLTWQDGEEOQDTDELVETRPAG 258

RESULT 8
ID QYR27 PRELIMINARY; PRT; 362 AA.
AC QYR27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Class Ib.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22709134; PubMed=12799463;
RA Anzai T., Shiina T., Kimura N., Yanagita K., Kohara S., Shigenari A.,
RA Yamagata T., Kuleki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT "Comparative sequencing of human and chimpanzee MHC class I regions unveils insertions/deletions as the major path to genomic divergence."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
DR EMBL; AB100087; BAC78191.1; --
SQ SEQUENCE 362 AA; 40625 MW; BA5699D08181A1PF CRC64;

Query Match 98.0%; Score 1150; DB 6; Length 362;
Best Local Similarity 99.1%; Pred. No. 4.4e-98;
Matches 213; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYWEWTTGYAKANAQTDRAVALRNL 60
DB 44 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYWEWTTGYAKANAQTDRAVALRNL 103

QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLRGYHQHAWDGKDYISLNEDLSRSTAADTVAQI 120

```
Db 104 RRYNQSAGSHLTQGMNGCDMPDGLLRGYHQHAYDGDYISLNEDLSRWTAADTVAQI 163
QY 121 TORFYAEYAEFRYLYEGECLELLRRLRYLNGKETLQADPPKAAHVAHPISDHEATLR 180
Db 164 TORFYAEYAEFRYLYEGECLELLRRLRYLNGKETLQADPPKAAHVAHPISDHEATLR 223
QY 181 CWAALGYPAEITLTWQDGEQGTQDTTELVTETPAG 215
Db 224 CWAALGYPAEITLTWQDGEQGTQDTTELVTETPAG 258

RESULT 9
ID Q9MXK1 PRELIMINARY; PRT; 362 AA.
AC Q9MXK1;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE MHC class I antigen.
GN Pan troglodytes (Chimpanzee).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20322475; PubMed=10866106;
RA de Groot N.G., Oetting J.N., Arguello R., Watkins D.I., Doxiadis G.G.M.,
RA Madrigal J.A., Bontrop R.E.;
RT "Major histocompatibility complex class I diversity in a West African
RT chimpanzee population: implications for HIV research.";
RL Immunogenetics 51:398-409(2000).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF168410; AAF72791.1; -.
DR HSPB; P03988; IHSB.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40442 MW; 4E1A081945D3A4F3 CRC64;

Query Match 80.6%; Score 945; DB 7; Length 362;
Best Local Similarity 81.4%; Pred. No. 4.1e-79;
Matches 175; Conservative 12; Mismatches 28; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTRVALRNLL 60
Db 47 IAVGYVDDTQFVRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTRVALRNLL 106
QY 61 RRYNQSAGSHLTQGMNGCDMPDGLLRGYHQHAYDGDYISLNEDLSRWTAADTVAQI 120
Db 107 RRYNQSAGSHLTQGMNGCDMPDGLLRGYHQHAYDGDYISLNEDLSRWTAADTVAQI 166
QY 121 TORFYAEYAEFRYLYEGECLELLRRLRYLNGKETLQADPPKAAHVAHPISDHEATLR 180
Db 167 TORKWEARVAEQRLAYLEGECEVLEWLRRLRYLNGKETLQADPPKTHVTHHPISDHEATLR 226
QY 181 CWAALGYPAEITLTWQDGEQGTQDTTELVTETPAG 215
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Db 227 CWAALGYPAEITLTWQDGEQGTQDTTELVTETPAG 261

RESULT 10
Q8SNC9 PRELIMINARY; PRT; 273 AA.
ID Q8SNC9
AC Q8SNC9;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Garcia-Sanchez F., Vicario J.L., Alonso M., Balas A., Lillo R.;
RT "Four new HLA class I alleles in Caucasoids.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF480612; AAL87223.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 273
SQ SEQUENCE 273 AA; 31602 MW; 0C8731F012089A7E CRC64;

Query Match 80.1%; Score 939; DB 7; Length 273;
Best Local Similarity 80.9%; Pred. No. 1e-78;
Matches 174; Conservative 11; Mismatches 30; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTRVALRNLL 60
Db 22 ITVGYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWEWTTGYAKANAQTRVALRNLL 81
QY 61 RRYNQSAGSHLTQGMNGCDMPDGLLRGYHQHAYDGDYISLNEDLSRWTAADTVAQI 120
Db 82 RRYNQSAGSHLTQGMNGCDMPDGLLRGYHQHAYDGDYISLNEDLSRWTAADTVAQI 141
QY 121 TORFYAEYAEFRYLYEGECLELLRRLRYLNGKETLQADPPKAAHVAHPISDHEATLR 180
Db 142 TORKWEARVAEQRLAYLEGECEVLEWLRRLRYLNGKETLQADPPKTHVTHHPISDHEATLR 201
QY 181 CWAALGYPAEITLTWQDGEQGTQDTTELVTETPAG 215
Db 202 CWAALGYPAEITLTWQDGEQGTQDTTELVTETPAG 236

RESULT 11
O19692 PRELIMINARY; PRT; 274 AA.
ID O19692
AC O19692;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
```

DE HLA-B protein (Fragment).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87009855; PubMed=3489755;
RA Coppin H.L., McDewitt H.O.;
RT "Absence of polymorphism between HLA-B*27 genomic exon sequences
RT isolated from normal donors and ankylosing spondylitis patients.";
RL J. Immunol. 137:2168-2172(1986).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; M14013; AAA59643.1; -;
DR HSSP; P03989; IHSA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 274
SQ SEQUENCE 274 AA; 31659 MW; 0C9A7A4902383219 CRC64;
Query Match 80.1%; Score 939; DB 7; Length 274;
Best Local Similarity 80.9%; Pred. No. 1e-78;
Matches 174; Conservative 11; Mismatches 30; Indels 0; Gaps 0;
QY 1 IAVEYDDTQFLRFDSDAAIPRMEPRPWEQSGPQYWEWTTGYAKANAQTDRLVALRNL 60
DB 23 ITGVYDDTLFVRFDSDAASPREEPRAPWIEQEGPEYWDRETQICKAKAQTDRESLRLL 82
QY 61 RRYNQSAGSHTLQNMGCDMPDGLLRGYHQHAWDKDYISLNEDLSRWTAADTVAQI 120
DB 83 RRYNQSAGSHTLQNMGCDMPDGLLRGYHQHAWDKDYISLNEDLSRWTAADTVAQI 142
QY 121 TQRYEAEYAEFRFTYLEGECLELLRRLRYLENGKETLQRADPPKAVHAHPISDHEATLR 180
DB 143 TQKWEARVAEQRLAYLEGECVWLRVLENGKETLQRADPPKTHVTHHPISDHEATLR 202
QY 181 CWALGFYPAETTLTWQDGEQOTDTLVELTRPAG 215
DB 203 CWALGFYPAETTLTWQDGEQOTDTLVELTRPAG 237
RESULT 12
F79612 PRELIMINARY; PRT; 362 AA.
AC F79612
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE HLA-B protein.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
TISSUE=Blood;
RA Haegawa T., Sugahara Y., Moriyama Y., Nanzai H., Ogawa A., Tawara K.,
RA Kondo S., Tokunaga K.;
RT "Molecular characterization of a novel HLA-B*27 allele.";
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; D83043; BAA11753.1; -;
DR HSSP; P03989; IHSA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40441 MW; 3CA65547E63FDF84 CRC64;
Query Match 80.1%; Score 939; DB 7; Length 362;
Best Local Similarity 80.5%; Pred. No. 1.5e-78;
Matches 173; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 IAVEYDDTQFLRFDSDAAIPRMEPRPWEQSGPQYWEWTTGYAKANAQTDRLVALRNL 60
DB 47 ITGVYDDTLFVRFDSDAASPREEPRAPWIEQEGPEYWDRETQICKAKAQTDRESLRLL 106
QY 61 RRYNQSAGSHTLQNMGCDMPDGLLRGYHQHAWDKDYISLNEDLSRWTAADTVAQI 120
DB 107 RRYNQSAGSHTLQNMGCDMPDGLLRGYHQHAWDKDYISLNEDLSRWTAADTVAQI 166
QY 121 TQRYEAEYAEFRFTYLEGECLELLRRLRYLENGKETLQRADPPKAVHAHPISDHEATLR 180
DB 167 TQKWEARVAEQRLAYLEGECVWLRVLENGKETLQRADPPKTHVTHHPISDHEATLR 226
QY 181 CWALGFYPAETTLTWQDGEQOTDTLVELTRPAG 215
DB 227 CWALGFYPAETTLTWQDGEQOTDTLVELTRPAG 261
RESULT 13
O78189 PRELIMINARY; PRT; 362 AA.
ID O78189
AC O78189
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE MHC class I antigen.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98427840; PubMed=9756409;
RA Seurnyck K., Baxter-Lowe L.A.;
RT "Novel polymorphism detected in exon 1 of HLA-B*2713.";
RL Tissue Antigens 52:187-189(1998).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; AF026218; AAC42275.1; -;
DR HSSP; P03989; IHSA.

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Glycoprotein; Transmembrane.
 KW Glycoprotein; Transmembrane.
 SQ SEQUENCE 362 AA; 40479 MW; 148B56561595A505 CRC64;
 Query Match 80.1%; Score 939; DB 7; Length 362;
 Best Local Similarity 80.9%; Pred. No. 1.5e-78;
 Matches 174; Conservative 11; Mismatches 30; Indels 0; Gaps 0;
 QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVQEGPQYWEWTGYAKANAQTDRAVALRNLL 60
 DB 47 ITGVYVDDTLFVRFDSDAASPPEPRAPWTEQSGPEYWDRETQICKAKACTDREDLRTLL 106
 QY 61 RRYNQSEAGSHTLQGMGCDMGDPGRLLRGYHQHAWGKDYISLNEDLSRSTAAADTVAQI 120
 DB 107 RYTNQSEAGSHTLQNMVYGCYVDPGRLLRGYHQDAYDYGKDYIALNEDLSSTAAADTAAQI 166
 QY 121 TORFYEAEEYAEFRTYLEGCELLRRYLENGKETLQADPPPKAHVAHPHISDHEATLR 180
 DB 167 TQKWEARVAEQRLAYLEGCEVWLRRLYLENGKETLQADPPKTHVTHHPISDHEATLR 226
 QY 181 CWALGFYPAEITLTWQDGEQOTDTLVELTRPAG 215
 DB 227 CWALGFYPAEITLTWQDGEDQDTLVELTRPAG 261
 RESULT 15
 Q95530 PRELIMINARY; PRT; 354 AA.
 AC Q95530
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Class I histocompatibility antigen (Fragment).
 GN HLA-B.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Teppie;
 RX MEDLINE=94286544; PubMed=8016085;
 RA McAdam S.N., Boyson J.E., Liu X., Garber T.L., Hughes A.L.,
 RA Bontrou R.E., Watkins D.I.;
 RT "A uniquely high level of recombination at the HLA-B locus."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897 (1994).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 CC IMMUNE SYSTEM (BY SIMILARITY).
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).
 DR EMBL; J05581; AAA50184.1; -.
 DR PIR; I80170; I80170.
 DR HSP; P30685; I432.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Glycoprotein; Transmembrane.
 KW Glycoprotein; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 354 AA; 39555 MW; 61942B24D173786F CRC64;
 Query Match 79.7%; Score 935; DB 7; Length 354;
 Best Local Similarity 80.5%; Pred. No. 3.4e-78;
 Matches 173; Conservative 14; Mismatches 28; Indels 0; Gaps 0;
 QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVQEGPQYWEWTGYAKANAQTDRAVALRNLL 60

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Glycoprotein; Transmembrane.
 KW Glycoprotein; Transmembrane.
 SQ SEQUENCE 362 AA; 40486 MW; BC00FC372955711D CRC64;
 Query Match 80.1%; Score 939; DB 7; Length 362;
 Best Local Similarity 80.9%; Pred. No. 1.5e-78;
 Matches 174; Conservative 11; Mismatches 30; Indels 0; Gaps 0;
 QY 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWPVQEGPQYWEWTGYAKANAQTDRAVALRNLL 60
 DB 47 ITGVYVDDTLFVRFDSDAASPPEPRAPWTEQSGPEYWDRETQICKAKACTDREDLRTLL 106
 QY 61 RRYNQSEAGSHTLQGMGCDMGDPGRLLRGYHQHAWGKDYISLNEDLSRSTAAADTVAQI 120
 DB 107 RYTNQSEAGSHTLQNMVYGCYVDPGRLLRGYHQDAYDYGKDYIALNEDLSSTAAADTAAQI 166
 QY 121 TORFYEAEEYAEFRTYLEGCELLRRYLENGKETLQADPPPKAHVAHPHISDHEATLR 180
 DB 167 TQKWEARVAEQRLAYLEGCEVWLRRLYLENGKETLQADPPKTHVTHHPISDHEATLR 226
 QY 181 CWALGFYPAEITLTWQDGEQOTDTLVELTRPAG 215
 DB 227 CWALGFYPAEITLTWQDGEDQDTLVELTRPAG 261
 RESULT 14
 Q29705 PRELIMINARY; PRT; 362 AA.
 AC Q29705
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE MHC class I antigen HLA-B precursor.
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Balas A., Santos S., Vicario J.L.;
 RT "Gerological and molecular characterization of a novel HLA-B allele."
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U31971; AAA98506.1; -.
 DR HSP; P03989; I45A.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Glycoprotein; Transmembrane.
 KW Glycoprotein; Transmembrane.
 FT SIGNAL 1
 FT CHAIN 25 362
 MHC CLASS I ANTIGEN HLA-B.

Db	39	IAVGYYDDTQFVRPDSDAIPEMEPRAPWIEQEGEPEYWDRETQISKTNQAQTYRVGLRNL	98
Qy	61	RRYNQSEAGSHTLQGNMGCDMGPDGRLLRGYHGHAWDKDYISINEDLSWTAADTVAQI	120
Db	99	GYYNQSEAGSHTWQTMYGCDVGPGRLLRGYRQFAYDKGYIALNKOLSSWTAADTAAQI	158
Qy	121	TORFEYAEBEYAEFFRYLEGECELELLRRYLENGKETLQRADPPKAHVAHPHISDHEATLR	180
Db	159	TORKWENARWAEQLRAYLEGTCEWLRVYLENGKETLQRADPPKTHVTHHPISDHEATLR	218
Qy	181	CWALGFYPAEITLTWQDGEETQDTELVEHPAG	215
Db	219	CWALGFYPAEITLTWQDGEDQDTELVEHPAG	253

Search completed: June 18, 2004, 10:51:52
Job time : 67 secs

29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Run on: June 18, 2004, 07:40:40 ; Search time 2501 Seconds (without alignments)
2567.121 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 1173
Sequence: 1 IAVEYVDTRFLRFDSDAAI.....QRDGEQOTDELVETRPAG 215

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09819371/runat_16062004.170028.7855/app_query.fasta_1.391
-DB=EST -OPMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DUALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09819371 @CGN 1.1 3437 @runat_16062004.170028.7855 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DESBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*

ALIGNMENTS

RESULT 1	BO707312	926 bp	mRNA	linear	EST 16-JUL-2002
BO707312	AGENCY	8354575	NIH_MGC_113	Homo sapiens	cDNA clone IMAGE:6281285
LOCUS	5', mRNA	sequence.			
DEFINITION	BO707312	1	GI:21846211		
ACCESSION	BO707312				
VERSION	BO707312.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 926)				

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2473 row: n column: 06
 High quality sequence stop: 628.

FEATURES source
 1..926
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6281285"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1 41e-119 Length: 926
 Score: 1164.00 Matches: 214
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.53% Mismatches: 0
 Query Match: 99.23% Indels: 0
 DB: 13 Gaps: 0
 US-09-819-371-6 (1-215) x BQ07312 (1-926)

Qy 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaLalle 20
 Db 129 ATCGCGGTGGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCCCGGATT 188
 Qy 21 ProArgMetGluProArgGluProTTPValGluGlnGluGlyProGlnTyrTrpGluTrp 40
 Db 189 CCAGAGNTGAGCGCGGGGCGCGTGGTGGACAGAGGGCGCGAGTATTGGGAGTGG 248
 Qy 41 ThrThrGlyTyrAlaLysAlaAenAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
 Db 249 ACCACAGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 308
 Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 Db 309 CGCGCGTACAAACAGAGCGAGGTGGGTCTCACACCTCCAGGGAATGATGGCTCGGAC 368
 Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
 Db 369 ATGGGGCCGACGAGCGCTCTCCGCGGTATCACAGCACGCGTACGACGCGCAAGGAT 428
 Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
 Db 429 TACATCTCCCTGACAGGAGGACCTCCGCTCTGACCGCGCGGACACCGGTGCTCAGATC 488
 Qy 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
 Db 489 ACCAGCGCTTCTATGAGGCGAGGAGATATGACAGAGGATTCAGGACCTACCTGGAGGCG 548
 Qy 141 GluCysLeuGlnLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 Db 549 GAGTGCCTGGAGTGTCTCCGAGATCTTGGAGATGGGAGGAGACGCTACAGCGCGCA 608

Qy 161 AspProProlYsAlaHisValAlaHisHisProlIserAspHisGluAlaThrLeuArg 180
 Db 609 GATCCTCCAAAGGCACACGTTGCCACCCCATCTCTGACCATGAGGCCACCTTGAGG 668
 Qy 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
 Db 669 TGTGGGCTTGGCTTCTACCTGCGGATCAGCTGACCTGACCTGGCAGCGGATGGGAG 728
 Qy 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 Db 729 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGCGCTGCAGGG 773

RESULT 2
 BQ962778 875 bp mRNA linear EST 21-AUG-2002
 LOCUS AGENCOURT 9820719 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6380038
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ962778
 VERSION BQ962778.1 GI:22378256
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 875)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2567 row: p column: 23
 High quality sequence stop: 673.

FEATURES source

1..875
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6380038"
 /tissue_types="epithelioid carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_42"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1 03e-117 Length: 875
 Score: 1147.00 Matches: 212
 Percent Similarity: 99.07% Conservative: 1
 Best Local Similarity: 98.60% Mismatches: 2
 Query Match: 97.78% Indels: 0
 DB: 13 Gaps: 0
 US-09-819-371-6 (1-215) x BQ962778 (1-875)

Qy 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaLalle 20
 Db 133 ATCGCGGTGGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCGCGGATT 192

QY 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTrpGluTrp 40
 Db 193 CCGAGGATGAGCGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGG 252
 QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
 Db 253 ACCACAGGAGTACGCCAAGCCCAACGACAGATGACCGAGTGGCCCTGAGGAACCTGCTC 312
 QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 Db 313 CGCGGCTACACACGAGCGAGGTGGTCTCACACCCCTCCAGGGAATGAATGGCTGCAGC 372
 QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
 Db 373 ATGGGCGCGGACGAGCGCTCTCCCGGGTATACACGACGCGGTACAGCGCAAGGAT 432
 QY 101 TyrIleSerLeuAsnGlnAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
 Db 433 TACATCTCTGACGAGGACCTGGCTCTCTGGACCGCGCGGACACCGCTGGCTCAGATC 492
 QY 121 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGluPheArgThrTyrLeuGluGly 140
 Db 493 ACCACGCGCTTATGAGGCGAGGAATATGACAGAGAGTTCAGGACCTTACCTGGAGGCG 552
 QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 Db 553 GAGTGGCTGGAGTGTCTCCGAGATACTTGGAGATGGGAAGAGAGCGCTACAGCGCGCA 612
 QY 161 AspProProlysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
 Db 613 GATCTCTCAAAGGACACACGCTGGCCACCCATCTCTGACCATGAGGCCACCTGAGG 672
 QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
 Db 673 TCGTGGCGCTTACCTACCTCGGAGATCACGCTGAGTGGCAGCGGATGGGGAG 732
 QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 Db 733 GAACACCCGACGACAGAGCTTGGAGACCGAGCGCTGCAGG 777

RESULT 3
 BM561951
 LOCUS
 DEFINITION AGENCOURT 6593.72 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5484505
 5', mRNA sequence.

ACCESSION BM561951
 VERSION 1
 KEYWORDS EST.
 SOURCE BM561951.1 GI:18807627
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 N-H-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: csapbs-x@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM2013 row: o column: 02
 High quality sequence stop: 682.

FEATURES
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 1. .949
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

/clone="IMAGE:5484505"
 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_106"
 /note="Organ: blood; Vector: pOTE7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores: 1.52e-117 Length: 949
 Pred. No.: 1146.00 Matches: 211
 Score: 99.07% Conservative: 2
 Percent Similarity: 98.14% Mismatches: 0
 Best Local Similarity: 97.70% Indels: 0
 Query Match: 12 Gaps: 0
 DB:

US-09-819-371-6 (1-215) x BM561951 (1-949)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
 Db 156 ATCCGCGTGGAGTACGTAGACGACACCAATTCCTGGCGTTCGACGACGCGCGGAT 215
 QY 21 ProArgMetGluProArgGluProTyrValGluGlnGlyProGlnTrpGluTrp 40
 Db 216 CCGAGGATGGAGCGCGGAGCGCGTGGTGGAGCAAGGGCGCGAGTATGGAGTGG 275
 QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
 Db 276 ACCACGCGTACGCGCAAGGCCACACGACAGTACCGAGTGGCGCTGAGGAACCTGCTC 335
 QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
 Db 336 CGCGCTACAAACGAGCGAGCGGTGGGTCTCACACCTCCAGAGAAATGAATGGCTGCAGC 395
 QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
 Db 396 ATGGGCGCGGACGAGCGCTCTCCCGGGTATCACGACGACGCGTACGACGCAAGGAT 455
 QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
 Db 456 TACATCTCTGACGAGGACCTCGCTCTCTGGACCGCGCGGACACCGCTGCTCAGATC 515
 QY 121 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGluPheArgThrTyrLeuGluGly 140
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 QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
 Db 576 GAGTGGCTGGAGTGTCTCCGAGATATCTGGAGAATGGGAAGGACGCTACAGCGCGCA 635
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 Db 636 GATCTCTCAAAGGACACGCTTGGCCACCCATCTCTGACCATGAGGCCACCTGAGG 695
 QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
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 QY 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
 Db 756 GAACACCCGACGACAGAGCTTGGGAGAGACCAAGCGCTGCAGG 800

RESULT 4

CD514705
 LOCUS
 DEFINITION

CD514705 829 bp mRNA linear EST 06-JUN-2003
 AGENCOURT 14394444 NIH_MGC_181 Homo sapiens cDNA clone
 IMAGE:30408575 5', mRNA sequence.

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ACCESSION      CD514705
VERSION        CD514705.1  GI:31446423
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens (human)
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 829)
JOURNAL        NIH-MGC http://mgi.nci.nih.gov/.
COMMENT        National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
                Contact: Daniela S. Gerhard, Ph.D.
                Office of Cancer Genomics
                National Cancer Institute / NIH
                Bldg. 31 Rm10A07 Bethesda, MD 20892
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: Dr. Michael Brownstein
                cDNA Library Preparation: Invitrogen Corp
                DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
                Cloned (Scovv) site is destroyed upon cloning. Average
                insert size 1.42 kb. Library was constructed by
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: NDAM491 row: 1 column: 24
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                /dev_stage="Unknown"
                /lab_host="DH10B-Ton A ( T1 and T5 phage resistances )"
                /clone_lib="NIH_MGC_181"
                /notes="Vector: pCMV-Sport6.1; Site 1: NotI; Site 2: EcoRV
                (destroyed); Library is oligo-dt primed and directionally
                cloned (Scovv) site is destroyed upon cloning). Average
                insert size 1.42 kb. Library was constructed by
                (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:      1.59e-117      Length:      829
Score:          1145.00      Matches:     213
Percent Similarity: 99.07%      Conservative: 1
Best Local Similarity: 98.61%      Mismatches:  1
Query Match:    97.61%      Indels:      1
DB:             14          Gaps:        0
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Qy      21  ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 40
Db      202 CCGAGGATGAGCGCGGAGCCGCTGGTGGTGGACAGAGCGGCGCGAGTATTGGGAGTGG 261
Qy      41  ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db      262 ACCACAGGTTACGCCAGGCGCACGACAGACTGACCGAGTGGCCCTGAGAACCTGCTC 321
Qy      61  ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db      322 CGCGGTACAAACAGAGCGAGGCTGGTCTTCACACCTCCAGGGAATGATGCTCGCAC 381
Qy      81  MetClyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db      382 ATGGGGCCCGACGACGCCCTCTCCCGGGGTATCACCAGCAGCGGTACGACGCGAAGAT 441
Qy      101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120

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Db      442 TACATCTCCCTGAACAGGACCTGCCTCTGGAGCCGCGGACACCGCTGGCTCAGATC 501
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Db      502 ACCCAGCGCTTCTATGAGGACAGAGGAATATGCAGAGGAGTTCAGGACCTACCTGGAGGGC 561
Qy      141 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db      562 GAGTGGCTCGAGTGTCTCCGAGATCTTGGAGATGGAGAGGAGAGCGGTACAGCGCGCA 621
Qy      161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Db      622 GATCTCTCAAAGGCACACAGCTTGCCACCCACCCCATCTCTGACCATGAGGCCACCTGAGG 681
Qy      181 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 200
Db      682 TGCTGGGCCCTTGCGCTTCTACCTTGGGAGATCACGCTGACCTGACCTGGCAGCGGATGGGAG 741
Qy      201 GluGlnThrGlnAspThrGluLeuValGluThr-ArgProAlaGly 215
Db      742 GACAGACCCAGGACACAGAGCTTGTGGAGCCANNNGCCTGCAGGG 787

RESULT 5
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LOCUS      AGENCOURT 8064678 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206180
DEFINITION 5', mRNA sequence.
ACCESSION  BO688194
VERSION    BO688194.1 GI:21813510
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 886)
JOURNAL     NIH-MGC http://mgi.nci.nih.gov/.
COMMENT     National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2360 row: d column: 21
            High quality sequence stop: 677.
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            /lab_host="DH10B (phage-resistant)"
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            /notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
            Site 2: EcoRI; cDNA made by oligo-dt priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCAGGAG(G). Library constructed by
            Ling Hong in the laboratory of Gerald M. Rubin (University
            of California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:      8.3e-117      Length:      886
Score:          1139.00      Matches:     212
Percent Similarity: 98.61%      Conservative: 1

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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2469 row: d column: 13
High quality sequence stop: 647.

FEATURES
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/clone_lib="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN
Alignment Scores:
Pred. No.: Length: 928
Score: 1138.00 Matches: 212
Percent Similarity: 98.61% Conservative: 1
Best Local Similarity: 98.15% Mismatches: 2
Query Match: 97.02% Indels: 1
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x BQ710481 (1-928)

QY 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 20
Db 142 ATCGCGTGGAGTACGTAGACGACACGCAATTCCTCGGTTCCAGACGCGCGCGATT 201
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr 40
Db 202 CCGAGGATGGAGCGCGCGGAGCGCGTGGTGGAGCAGAGGGCGCGCATTTCCGAGTGG 261
QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 262 ACCACAGGTTACGCCAAGGCCAACGACACGACGACGAGTGGCGCTCGAGAACCTGCTC 321
QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 322 CGCGCTACAAACAGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAATGCTCGGAC 391
QY 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 382 ATGGGGCCCGAGCGAGCGCTCTCCGCGGGTATCACCCAGACGCGTACGACGCAAGGAT 441
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 442 TACATCTCCCTGAACAGGAGACCTCGCTCTCGGACCGCGCGACACCGTGGCTCAGATC 501
QY 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 502 ACCACAGCTTCTATGAGCGAGAGATATGACAGAGGATTCAGGACCTACCTGGAGGGC 561
QY 141 GluCysLeuLeuLeuLeuArgArgTyrLeuGluAsnGlyLysGlnThrLeuGlnArgAla 160
Db 562 GAGTGGCTGGAGTTGCTCCGCGAGATACTTCGAGAAATGGGAGAGAGCGCTACAGCGCGCA 621
QY 161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Db 622 GATCTCTCAAAGGCACACGTTGGCCACACACCCCATCTCTGACCATGAGGCCACCTTGAG 681
QY 181 CysTrpAlaLeuLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 682 TGCTGGGCCCTGGGCTTCTACCTCGCGAGATCACTGCTGACCTGCGAGCGCGGATGGGAG 741
QY 201 GluGlnThrGlnAspThrGlu-LeuValGluThrArgProAlaGly 215

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2469 row: d column: 13
High quality sequence stop: 647.

Location/Qualifiers
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/note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 116-116 Length: 928
Score: 1138.00 Matches: 212
Percent Similarity: 98.61% Conservative: 1
Best Local Similarity: 98.15% Mismatches: 2
Query Match: 97.02% Indels: 1
DB: 13 Gaps: 0

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Db 142 ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCACAGCAGCGCGCGATT 201
QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr 40
Db 202 CCGAGGATGGAGCCCGGAGCGCGTGGTGGAGCAAGAGGGCGCGAGTATTGGAGTGG 261
QY 41 ThrThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60
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QY 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 322 CGCGCGTACACACAGAGGAGCTGGCTCTCACCCCTCCAGGGAATGAATGGCTGGCGAC 381
QY 81 MetGlyProAspGlyVarGluLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Db 382 ATGGGGCCCGACGAGCGCTCTCTCGGGTATCACACGACGCGTACGACGCGCAAGGAT 441
QY 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Db 442 TACATCTCCCTGAACGAGGACCTGGCTCTCGAGCCGCGCGGACACCGCTGGCTCAGATC 501
QY 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrTrpLeuGluGly 140
Db 502 ACCACGCGCTCTATGAGCAGAGGAATATGAGGAGGAGTTCAGGACCTACCTGGAGGGC 561
QY 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGlnThrLeuGlnArgAla 160
Db 562 GAGTGGCTGGAGTGGCTCCGCGAGATCTTGGAGAAATGGGAGGAGACGCTACAGCGCGCA 621
QY 161 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 180
Db 622 GATCTCTCAAGGACACAGCTTGGCCACACCCCATCTCTGACCATGAGGCCACCTTGANG 681
QY 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Db 682 TGTGGGCCCTGGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 741
QY 201 GluGlnThrGlnAspThrGlu-LeuValGluThrArgProAlaGly 215

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742 GAACAGACCAGCACAGAGCGCTGGTGAGACCGGGCTGCAGGG 787
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AGENCOURT_8343876 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248481
5', mRNA sequence.
BQ690438
BQ690438.1 GI:21815754
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2388 row: 9 column: 10
High quality sequence stop: 623.
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/db_xref="taxon:9606"
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/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 2,45e-114 Length: 892
Score: 1117.00 Matches: 210
Percent Similarity: 98.14% Conservative: 1
Best Local Similarity: 97.67% Mismatches: 2
Query Match: 95.23% Indels: 2
DB: 13 Gaps: 0

US-09-819-371-6 (1-215) x BQ690438 (1-892)

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QY 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr 40
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QY 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 249 ACCACAGGGTACCGCAAGGCCACGACAGCTACCGAGTGGCCCTCGAGGACCTGCTC 308
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ORIGIN		NIH_MGC Library."	
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Pred. No.:	2,67e-114	Matches:	208
Score:	1117.00	Conservative:	1
Best Similarity:	98.58%	Mismatches:	2
Best Local Similarity:	98.11%	Indels:	1
Query Match:	95.23%	Gaps:	0
DB:	13		
US-09-819-371-6 (1-215) x BQ711764 (1-941)			
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Db	139	ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCACAGCGCGCGGAT	198
Qy	21	ProArgMetGlnProArgGluProTyrValGluGlnGluGluProGlnTyrTrpGluTrp	40
Db	199	CCGAGGATGAGCGCGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTATGGGAGTG	258
Qy	41	ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu	60
Db	259	ACCACAGGATACGCCAAGGCCACGACAGCTGACGAGTGCGCTGAGAACCTGCTC	318
Qy	61	ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp	80
Db	319	CGCGCGTACACACAGACGAGCGGTGGGTCTCACACCTCCAGGGAATGAATGGCTCGAC	378
Qy	81	MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp	100
Db	379	ATGGGGCCCGACGCGCTCTCTCCGGGGTATCACCGACGCGGTACGACGCGCAAGGAT	438
Qy	101	TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle	120
Db	439	TACATCTCCCTGAAACGAGGACCTCGCTCTCGACCGCGCGGACCGTGGGTCTGATC	498
Qy	121	ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluPheArgThrTyrLeuGluGly	140
Db	499	ACCCAGCGCTTCTATGAGGACAGAGATATGACAGAGGTTTACGACCTACCTGGAGGGC	558
Qy	141	GluCysLeuGluLeuLeuLeuArgTyrTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla	160
Db	559	GAGTGCCTGGAGTTGCTCCGCGAGTACTTGGAGAAATGGAGAGAGCGCTACAGCGGCA	618
Qy	161	AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThr-LeuAr	180
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Db	679	GTGCTGGGCCCTGGGCTTCTACCTTGGGAGTACGCTGACCTGCGAGCGGGATGGGA	738
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BQ926296			
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VERSION			
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 931)			
NIH-MGC http://mgi.nci.nih.gov/ .			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2604 row: e column: 14 High quality sequence stop: 638.	
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ORIGIN		US-09-819-371-6 (1-215) x BQ926296 (1-931)	
Alignment Scores:		Length:	931
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Score:	1093.50	Conservative:	1
Percent Similarity:	98.14%	Mismatches:	4
Best Local Similarity:	97.67%	Indels:	3
Query Match:	93.22%	Gaps:	0
DB:	13		
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Db 144 ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCGCGGAT 203			
Qy 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 40			
Db 204 CCGAGGATGAGCGCGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGG 263			
Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60			
Db 264 ACCACAGGATACGCCAAGGCCAACGACAGCTGACCGAGTGGCGCTGAGGAACCTGCTC 323			
Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80			
Db 324 CGCGGCTCAACACGAGCGAGGCTGGGTCTCACCTCCAGGGAATGATGGCTGGCAG 383			
Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100			
Db 384 ATGGGGCCCGACGCGCTCTCCGGGGTATCACCGACGCGGTACGACGCGCAAGGAT 443			
Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120			
Db 444 TACATCTCCCTGAACGAGGACCTCGCTCTCGACCGCGCGGACACCGCTGCTGATC 503			
Qy 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluPheArgThrTyrLeuGluGly 140			
Db 504 ACCACGGCTTCTATGAGGACAGGGAATATGACAGGAGTTCAGGACCTTACCTGGAGGGC 563			
Qy 141 GluCysLeuGluLeuLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160			
Db 564 GAGTGCCTGGAGTTCCTCCGCGAGTACTTGGAGAAATGGAGAGAGCGGTACAGCGGCA 623			
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ORIGIN				MMH_MSC Library:			
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Pred. No.:		1073.00	Matches:		208		
Score:		96.35%	Conservative:	3			
Percent Similarity:		94.98%	Mismatches:	4			
Best Local Similarity:		91.47%	Indels:	4			
Query Match:		12	Gaps:	0			
DB:							
US-09-819-371-6 (1-215) x BM917072 (1-1130)							
QY	1	IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaIaIle	20				
DB	138	ATCGCGGTGGAGTACGTAGCACACGCAATTCCTGCGGTTCCGACGACGCCCGGATT	197				
QY	21	ProArgMetGluProArgGluProTyrPheValGluGlnGluGlyProGlnTyrTrpGluTrp	40				

/clone_lib="NCI_CGAP_Skn4"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:
Pred. No.: 2.06e-105 Length: 718
Score: 1036.00 Matches: 190
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.48% Mismatches: 0
Query Match: 88.32% Indels: 0
DB: 12 Gaps: 0

US-09-819-371-6 (1-215) x BG679105 (1-718)

Qy 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAilaile 20
Db 144 ATCCCGTGGAGTACGTAGACACACGCAATCTCGGTTCGACAGCGCGCGCAT 203
Qy 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyrp 40
Db 204 CCGAGGATGAGCGCGGAGCGGTGGTGGAGCAAGAGGCGCGCGCATTTGGAGTGG 263
Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 264 ACCAGAGGTAGCCAGCCACACGACACTGACCGAGTGGCGCTGAGGAACTGCTC 323
Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 324 CGCGCTACACACAGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAATGGCTGGAC 383
Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyVysAsp 100
Db 384 ATGGGGCGCGAGCGAGCGCTCTCCGCGGGTATCACACAGCGCGGTACGACGGCAAGAT 443
Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
Db 444 TACATCTCTCCGACAGAGACTGGCTCTGGACCGCGCGGACACCGTGGCTCAGATC 503
Qy 121 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 504 ACCAGCGCTTCTATGAGCGAGGATATGACAGAGGATTCAGGACCTACCTCGAGGCGC 563
Qy 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 564 GAGTGCCTGGAGTTGCTTCGCGAGTACTTGGAGATGGAGAGGACGCTACAGCGCGCA 623
Qy 161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Db 624 GATCTCCCAAGGCACAGCTTGCCACACACCCCATCTCTGACCATGAGGCGCACCTGAGG 683
Qy 181 CysTrpAlaLeuGlyPheTyrProAlaGluIle 191
Db 684 TGCTGGCGCTGGGTCTTACCTCGGAGATC 716

RESULT 12
BG762711
LOCUS 602734620F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4859957 5',
DEFINITION mRNA sequence.
ACCESSION BG762711
VERSION BG762711.1 GI:14073364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 745)
AUTHORS NIH-MGC <http://mgi.nhl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCDP/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
Plate: LLCMI716 row: h column: 06
High quality sequence stop: 745.

FEATURES

source

1..745
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4859957"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Alignment Scores:
Pred. No.: 4.84e-104 Length: 745
Score: 1024.00 Matches: 196
Percent Similarity: 97.52% Conservative: 1
Best Local Similarity: 97.03% Mismatches: 5
Query Match: 87.30% Indels: 2
DB: 12 Gaps: 0

US-09-819-371-6 (1-215) x BG762711 (1-745)

Qy 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAilaile 20
Db 140 ATCCCGTGGAGTACGTAGACACACGCAATCTCGGTTCGACAGCGCGCGCAT 199
Qy 21 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyrp 40
Db 200 CCGAGGATGAGCGCGGAGCGGTGGTGGAGCAAGAGGCGCGCGCATTTGGAGTGG 259
Qy 41 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Db 260 ACCAGCGGTACCCAGGCGCACACGACACTGACCGAGTGGCGCTGAGGAACTGCTC 319
Qy 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Db 320 CGCGCTACACACAGAGCGAGGCTGGGTCTCACACCTCCA-GGAATGAATGGCTGGAC 378
Qy 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyVysAsp 100
Db 379 ATGGGGCGCGAGCGCGCTCTCCGCGGGTATCACACGACGACGCGTACGACGGCAAGAT 438
Qy 101 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 120
Db 439 TACATCTCTCCGACAGGACCTTGGCTCTCGAGCGCGCGGACACCGTGGCTCAGATC 498
Qy 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Db 499 ACCAGCGCTTCTATGAGCGAGGAAATATGACAGAGGATTCAGGACCTACCTCGAGGCGC 558
Qy 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Db 559 GAGTGCCTGGAGTTGCTTCGCGAGTACTTGGAGATGGGAGGAGCGCTACAGGCGCA 618

22

.....

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 18, 2004, 06:00:43 ; Search time 63.5 seconds
(without alignments)
5739.941 Million cell updates/sec

Title: US-09-819-371-3
Perfect score: 1183
Sequence: 1 atcgccgtggagtactagtaga.....tggagaccaggcctgcagg 645

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2 1/USPTO spool/US09819371/runat 16062004.165855 7353/app query.fasta_1.839
-DS=A_Geneseq_29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09819371 @CGN 1 1 101 @runat 16062004.165855 7353 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Match Length	Description
1	1156	97.7	215 4 AAG64619 Human can
2	1156	97.7	271 3 AAB3986 Human can
3	1156	97.7	274 4 AAG64618 Human can
4	1156	97.7	362 4 AAG64617 Human can
5	1156	97.7	362 4 ABB50296 HLA-Cw ov
6	1156	97.7	677 4 ABG326726 Novel hum
7	932	78.8	274 1 AAP80911 Consensus
8	919	77.7	362 1 AAP70155 Sequence
9	918.5	77.6	337 1 AAP70590 Sequence
10	914	77.3	369 4 AAU32882 Novel hum

11	914	77.3	374	4	AAO06772	Aao06772 Human pol
12	913	77.2	322	7	AAm23760	Am23760 Human EST
13	897	75.8	362	7	ADe64171	De64171 Human pro
14	897	75.8	362	7	ADe64175	De64175 Human pro
15	896	75.7	366	2	AAy07033	Y07033 Breast ca
16	895	75.7	366	2	AAr12465	Ar12465 HLA-C exo
17	893	75.5	362	2	AAO31142	O31142 Sequence
18	892	75.4	374	4	AAO313073	O313073 Human pol
19	891	75.3	362	2	AAO31144	O31144 Sequence
20	885	74.8	366	2	AAr12466	Ar12466 HLA-C exo
21	883	74.6	362	2	AAr12464	Ar12464 HLA-B35 a
22	879	74.3	362	2	AAr12463	Ar12463 HLA-BW53
23	878	74.2	380	4	AAU32883	Au32883 Novel hum
24	861	72.8	326	5	AAU79454	Au79454 HLA-G rec
25	861	72.8	338	7	ADD46572	Ad46572 Human pro
26	851.5	72.0	379	5	ABP70087	Bp70087 Human NOV
27	851.5	72.0	379	7	ADe40254	De40254 Human NOV
28	849	71.8	365	3	AAy68272	Y68272 Human leu
29	849	71.8	365	3	AAy52926	Y52926 HLA-A2/A2
30	849	71.8	365	4	AAb58687	Ab58687 HLA-A2/A2
31	849	71.8	368	4	AAm24017	Am24017 Human EST
32	848	71.7	365	3	AAy52922	Y52922 HLA-A2/A2
33	848	71.7	365	4	AAb58683	Ab58683 HLA-A2/A2
34	848	71.7	365	4	AAy68267	Y68267 Human leu
35	845	71.4	365	3	AAy52921	Y52921 HLA-A2/A2
36	845	71.4	365	4	AAb58682	Ab58682 HLA-A2/A2
37	845	71.4	365	4	AAy68275	Y68275 Human leu
38	844	71.3	274	3	AAy68276	Y68276 Human leu
39	844	71.3	274	3	AAy52930	Y52930 HLA-A2/A2
40	844	71.3	274	3	AAy52929	Y52929 HLA-A2/A2
41	844	71.3	274	4	AAb58690	Ab58690 HLA-A2/A2
42	844	71.3	274	4	AAb58691	Ab58691 HLA-A2/A2
43	844	71.3	274	4	ABP70088	Bp70088 Human NOV
44	844	71.3	364	5	ABP70088	Bp70088 Human NOV
45	843	71.3	365	3	AAy68271	Y68271 Human leu

ALIGNMENTS

RESULT 1
AAG64619
ID AAG64619 standard; protein; 215 AA.
XX
AC AAG64619;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human cancer cell specific HLA-F antigen SEQ ID 6.
XX
KW HLA-F antigen; cancer cell specific; human.
XX
OS Homo sapiens.
XX
PN JP2001095584-A.
XX
PD 10-APR-2001.
XX
PF 30-SEP-1999; 95JP-00279566.
XX
PR 30-SEP-1999; 99JP-00279566.
XX
PA (EGAW/) EGAWA K.
PA (MEDI-) MEDINET KK.
PA (KIMU/) KIMURA K.
XX
DR WPI; 2001-360493/38.
XX
DR N-PSDB; AAH45557.
XX
PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX
PS Claim 1; Page 11-12; 12pp; Japanese.
XX
CC This invention relates to a cancer cell specific HLA-F antigen. The

CC invention includes DNA encoding the antigen, and a method for the
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC used in a method to diagnose cancer, in which the protein is used to
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC sequence represents the cancer cell-specific HLA-F antigen of the
CC invention
XX
SQ Sequence 215 AA;

Alignment Scores: 6.39e-92 Length: 215
Pred. No.: 1156.00 Matches: 213
Score: 1156.00
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-3 (1-645) x AAG64619 (1-215)

QY 1 ATCCCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCCCGCGGATT 60
Db 1 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaIle 20
QY 61 CCAGAGTGGAGCGCGGGAGCGTGGTGGAGCAGAGAGCGCGCGAGTATGGAGTGG 120
Db 21 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTrpGluTrp 40
QY 121 ACCACGGGTACCGCAAGGCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGTC 180
Db 41 ThrThrGlyTyrAlaValAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 60
QY 181 CGCGGTACACACAGAGCGAGGTGGGTCTCACSCCTCCAGGGAATGAATGGCTGGAC 240
Db 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
QY 241 ATGGGCGCGACGAGCGCTCTCCCGGGTATCACACGACGCGTACGACGCGCAAGGAT 300
Db 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 100
QY 301 TACATCTCCGTGAACGAGGACCTCGCTCTCGACCGCGCGGACACCGTGTGATC 360
Db 101 TyrIleSerLeuAsnGluLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
QY 361 ACCACGGCTTCATGAGGAGGAGGATATGACAGAGGATTCAGGACCTACCTGGAGGC 420
Db 121 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluPheArgThrTyrLeuGluGly 140
QY 421 GAGTGGCTGGAGTGTCTCCGACATACCTGGAGATGGGAAGGAGACGCTACGCGCGCA 480
Db 141 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
QY 481 GATCCTCCAAAGGACACAGCTTGGCCACCCACCCATCTGACCATGAGCGCCACCTGAG 540
Db 161 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
QY 541 TGTGGGCGCTGGCTTCTACCTGGCGGAGATCACGCTGACCTGGCGGAGATGGGAG 600
Db 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
QY 601 GAACAGCCAGACACAGAGCTTGTGGAGACACCGCCCTGCGAGG 645
Db 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215

RESULT 2

AAB43986
ID AAB43986 standard; protein; 271 AA.

XX AAB43986;

XX 08-FEB-2001 (first entry)

XX Human cancer associated protein sequence SEQ ID NO:1431.

KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
KW dermatological; neuroprotective; thrombolytic; coagulant; neutropenic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
XX Homo sapiens.
OS WO200055350-A1.
PN 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US005882.
XX 12-MAR-1999; 99US-0124270P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
FI WPI; 2000-587533/55.
DR N-PSDB; AAC78195.
XX Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer.
XX Claim 11; Page 2115-2116; 2352pp; English.
PS AAC77607 to AAC78448 encode the human cancer associated proteins given in
CC AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerable; immunomodulator;
CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
CC neutropenic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease, and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention
XX SQ Sequence 271 AA;

Alignment Scores: 6.77e-92 Length: 271
Pred. No.: 1156.00 Matches: 213
Score: 1156.00
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 3 Gaps: 0

US-09-819-371-3 (1-645) x AAB43986 (1-271)

QY 1 ATCCCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCCCGCGGATT 60
Db 50 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaIle 69
QY 61 CCAGAGTGGAGCGCGGGAGCGTGGTGGAGCAGAGCGCGCGAGTATGGAGTGG 120

Db 70 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 89
QY 121 ACCACGGGTACCCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 90 ThrThrGlyTyrAlaValAlaValAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 109
QY 181 CGCCGCTACAAACAGACGAGCGCTGGTCTCAGCCCTCAGGGAATGAATGCTGCGAC 240
Db 110 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 129
QY 241 ATGGGGCCGACGACGCTCCCTCCGGGTATCACCAGACGCGTACAGCGCAAGGAT 300
Db 130 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 149
QY 301 TACATCTCCCTGACACGAGGACCTGCGCTCTGAGCCGCGGACACCTGCGTCAATC 360
Db 150 TyrIleSerLeuAsnGluLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 169
QY 361 ACCACGCTCTATGAGCAGAGGATATGACAGAGTTCAGGACCTACCTGAGGAGGC 420
Db 170 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGlyPheArgThrTyrLeuGluGly 189
QY 421 GAGTGGCTGAGTGTCTCCGACAGATCTTGAGAAATGGGAAGAGACGCTACAGCGCGCA 480
Db 190 GluCysLeuGluLeuLeuArgTyrTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 209
QY 481 GATCTCTCAAAGGACACGCTTGGCCACCCACCTCTCTGACCATGAGGCCACCTGAGG 540
Db 210 AspProGlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 229
QY 541 TGCTGGCCCTGGCTCTACCTCGGAGATCACGCTGACCTGGAGCGGGATGGGGAG 600
Db 230 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 249
QY 601 GAACAGACCCAGACACAGAGCTTGTGGAGACCAAGCGCTGCAGG 645
Db 250 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 264

RESULT 3
AAG64618 standard; protein; 274 AA.
XX AC AAG64618;
XX DT 12-SEP-2001 (first entry)
XX DE Human cancer cell specific HLA-F antigen SEQ ID 5.
XX DE HLA-F antigen; cancer cell specific; human.
XX OS Homo sapiens.
XX PN JP2001095584-A.
XX PD 10-APR-2001.
XX PF 30-SEP-1999; 99JP-00279566.
XX PR 30-SEP-1999; 99JP-00279566.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA K.
XX DR WPI; 2001-360493/38.
XX DR N-PSDB; RAH45556.
XX FT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX FS Claim 2; Page 10-11; 12pp; Japanese.
XX CC This invention relates to a cancer cell specific HLA-F antigen. The
XX CC invention includes DNA encoding the antigen, and a method for the

CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC used in a method to diagnose cancer, in which the protein is used to
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC sequence represents the cancer cell-specific HLA-F antigen of the
CC invention
XX SQ Sequence 274 AA;
Alignment Scores:
Pred. No.: 6.79e-92 Length: 274
Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 4 Gaps: 0
US-09-819-371-3 (1-645) x AAG64618 (1-274)
QY 1 ATCGCGTGGAGTACGTAGACGACACGCAATTCCTGGGTTCGACAGCGCGCGCGATT 60
Db 23 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 42
QY 61 CCGAGGATGGAGCCCGGAGCCCGTGGTGGAGCAAGAGGGCGCGAGTATGGAGTGG 120
Db 43 ProArgMetGluProArgGluProTrpValGluGlnGlyProGlnTyrTrpGluTrp 62
QY 121 ACCACGGGTACGCGCAAGGCCAACGACACGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 63 ThrThrGlyTyrAlaValAlaAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 82
QY 181 CGCCGCTACAAACAGGAGCGAGCTGGTCTCACCCCTCCAGGGAATGAATGCTGCGAC 240
Db 83 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 102
QY 241 ATGGGGCCGAGGAGCGCTCTCGCGGGTATCACAGACGCGTACAGCGCGCAAGGAT 300
Db 103 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 122
QY 301 TACATCTCCCTGACACGAGGACCTGCGCTCTCGGAGCGCGGAGCACCGCTGAGGATC 360
Db 123 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 142
QY 361 ACCACGCTCTATGAGCAGAGATATGACAGAGTTCAGGACCTACCTGAGGAGGC 420
Db 143 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGluPheArgThrTyrLeuGluGly 162
QY 421 GAGTGGCTGAGTGTCTCCGACAGATCTTGAGAAATGGGAAGAGACGCTACAGCGCGCA 480
Db 163 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 182
QY 481 GATCTCTCAAAGGACACGCTTGGCCACCCACCTCTGAGCAATGAGCGCGCTGCAGG 540
Db 183 AspProGlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 202
QY 541 TGCTGGCCCTGGCTCTACCTCGGAGATCACGCTGACCTGGAGCGGGATGGGGAG 600
Db 203 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 222
QY 601 GAACAGACCCAGACACAGAGCTTGTGGAGACCAAGCGCTGCAGG 645
Db 223 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 237

RESULT 4
AAG64617
ID AAG64617 standard; protein; 362 AA.
XX AC AAG64617;
XX DT 12-SEP-2001 (first entry)
XX DE Human cancer cell specific HLA-F antigen SEQ ID 4.
XX DE HLA-F antigen; cancer cell specific; human.
KW

XX Homo sapiens.
 XX JP2001095584-A.
 XX
 XX 10-APR-2001.
 XX
 XX 30-SEP-1999; 99JP-00279566.
 XX
 XX 30-SEP-1999; 99JP-00279566.
 XX
 XX (EGAW/) EGAWA K.
 XX (MEDI-) MEDINET KK.
 XX (KIMU/) KIMURA K.
 XX
 XX WPI; 2001-360493/38.
 XX N-PSDB; AAH45555.
 XX
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
 XX
 XX Disclosure; Page 9-10; 12pp; Japanese.
 XX
 XX This invention relates to a cancer cell specific HLA-F antigen. The
 CC invention includes DNA encoding the antigen, and a method for the
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
 CC used in a method to diagnose cancer, in which the protein is used to
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
 CC sequence represents the cancer cell-specific HLA-F antigen of the
 CC invention
 XX
 XX SQ Sequence 362 AA;
 Alignment Scores:
 Pred. No.: 7.29e-92 Length: 362
 Score: 1156.00 Matches: 213
 Percent Similarity: 99.07% Conservative: 0
 Best Local Similarity: 99.07% Mismatches: 2
 Query Match: 97.72% Indels: 0
 DB: 4 Gaps: 0
 US-09-819-371-3 (1-645) x AAG64617 (1-362)
 QY 1 ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTGACAGCGCGCGGATT 60
 DB 44 ILAAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaIle 63
 QY 61 CCGAGGATGAGCGCGGGAGCCGCTGGTGGAGCAAGAGCGCGCGGATTTGGAGTGG 120
 DB 64 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 83
 QY 121 ACCACSGGTACGCCAAGGCCAAGCCACACACTGACCGAGTGGCGCTGAGGACCTGCTC 180
 DB 84 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 103
 QY 181 CGCGCGCTACACACAGACGAGGCTGGGTCTCACSCCTCCAGGGAATGAATGCTCGGAC 240
 DB 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
 QY 241 ATGGGGCCGACGACGCCCTCTCCGGGGTATCACACACCGCTACGACGCGCAAGGAT 300
 DB 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
 QY 301 TACATCTCCCTGACGAGGACCTGCGCTCTCGGACCGCGCGGACACCGGCGCTCAGATC 360
 DB 144 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
 QY 361 ACCACGCGCTTCTATGAGGACGAGGAATATGCGAGAGTTCAGGACCTACCTGGAGGCG 420
 DB 164 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTrpLeuGluGly 183
 QY 421 GAGTGGCTGGAGTTGCTCCGACAGATCTTGGAGATGGGAGGAGAGCTACAGCGGCA 480
 DB 184 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 203

QY 481 GATCTCCAAAGGACACACTTGGCCACCCACCCATCTCTGACCATGAGGCCACCTGAGG 540
 DB 204 AspProProlysAlaHisValAlaHisIleProlSerAspHisGluAlaThrLeuArg 223
 QY 541 TGCTGGGCGCTTGTCTTCTACCTCGCGAGATCACGCTGACCTGCGACGGGATGGCGAG 600
 DB 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCGCTGCAGG 645
 DB 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258
 RESULT 5
 ABB50296
 ID ABB50296 standard; protein; 362 AA.
 XX
 AC ABB50296;
 DT 08-FEB-2002 (first entry)
 XX
 DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.
 KW Ovarian tumour marker gene; human; overexpression; upregulation;
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
 KW identification; serous cystadenoma; borderline serous tumour;
 KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
 KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
 KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
 KW immune response pathway; cell proliferation regulation; protein folding;
 KW membrane localised; secreted; therapeutic target; cytostatic;
 KW gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX WO200175177-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010947.
 XX
 PR 03-APR-2000; 2000US-0194336P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
 XX
 DR WPI; 2001-626450/72.
 XX N-PSDB; ABA83122.
 XX
 PT Detecting and identifying ovarian tumor, identifying increased risk for
 PT developing ovarian cancer, and determining effectiveness of ovarian
 PT cancer treatment, by measuring expression level of ovarian tumor marker
 PT gene.
 XX
 PS Claim 23; Page 126-127; 140pp; English.
 XX
 CC The invention relates to methods for diagnosing and prognosing ovarian
 CC tumors in an individual via the detection and measurement of the
 CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183). The methods of the invention are useful for
 CC detecting an ovarian tumour in a patient, for identifying an individual
 CC at increased risk for developing ovarian cancer, in prognostic tests for
 CC assessing the relative severity of ovarian cancer, in tests for
 CC monitoring a patient in remission from ovarian cancer and in tests for
 CC monitoring disease status in a patient being treated for ovarian cancer.
 CC The methods can additionally be used to identify a particular tumour as
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
 CC mucinous cystadenoma, borderline mucinous tumour, mucinous
 CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,

CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes or their encoded
CC proteins may be used as therapeutic targets for the treatment and
CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent
CC proteins encoded by ovarian tumour marker genes of the invention
XX
SQ Sequence 362 AA;

Alignment Scores:
Pred. No.: 7, 29e-92 Length: 362
Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservatives: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-3 (1-645) x ABB50296 (1-362)

QY 1 ATCGCGGTGGAGTACGTAGACACGCAATTCCTCGGTTCCGACAGCGCGCGCGATT 60
DB 44 ILeAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 63
QY 61 CGAGAGTACGCGCGGAGCGGTGGTGGAGCAAGAGGGCGCCAGTATTGGGAGTGG 120
DB 64 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr 83
QY 121 ACCACGGGTACGCCAAGCCCAACACACAGACTGACCGAGTGGCCCTCAGGAACCTGTC 180
DB 84 ThrThrGlyTyrAlaAlaValAlaAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
QY 181 CACCGCTACACACAGAGCGAGCTGGTCTCACCCCTCCAGGGATGAATGGCTGGCCAC 240
DB 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
QY 241 ATGGGGCCCGCAGCGGCGCTCTCCGGGGTATCACCAGACGCGTACGAGCGCAAGAT 300
DB 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
QY 301 TACATCTCCCTGAACGAGACCTGGCTCTCGAGCGCGGCGGACACCGTGGCTCAGATC 360
DB 144 TyrlleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
QY 361 ACCACGGCTTCTATCAGCAGAGGAATATGACAGAGGAGTTCAGGACCTACCTGAGGCG 420
DB 164 ThrGlnArgPheTyrGlnAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 183
QY 421 GAGTGCCTGAGTGTCTCCGCGATACCTTGGAGATGGGAAGAGACGCTACAGCGCGCA 480
DB 184 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 203
QY 481 GATCTCTCCAAAGCACACGTGTCACCCACCCATCTCTGACCATGAGCCACCTGAGG 540
DB 204 AspProProlAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 223
QY 541 TGTGTGGCGCTGGGCTTCTACCTCGGAGATCACCTGAGTGGCGAGCGGATGGGAG 600
DB 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
QY 601 GACACGCCACGACACAGCTTGTGGAGACCGAGCGCTGCAGG 645
DB 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258

RESULT 6
ABG26726
ID ABG26726 standard; protein; 677 AA.
XX

AC ABG26726;
XX 18-FEB-2002 (first entry)
DT
XX Novel human diagnostic protein #26717.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX WO200175067-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
FA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
XX
DR N-PSDB; AAS90913.
DR
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 57085; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 677 AA;

Alignment Scores:
Pred. No.: 8, 54e-92 Length: 677
Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservatives: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 4 Gaps: 0

US-09-819-371-3 (1-645) x ABG26726 (1-677)

QY 1 ATCGCGGTGGAGTACGTAGACACGCAATTCCTCGGTTCCGACAGCGCGCGCGATT 60
DB 353 ILeAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 372
QY 61 CGAGAGTACGCGCGGAGCGCGTGGTGGAGCAAGAGGGCGCCAGTATTGGGAGTGG 120

Db 223 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 237

RESULT 8

AAP70155 ID AAP70155 standard; protein; 362 AA.

XX AC AAP70155;

XX 25-MAR-2003 (revised)

DT 10-MAR-1993 (revised)

DT 03-APR-1991 (first entry)

XX DE Sequence encoded by genomic DNA encoding human histocompatibility antigen HLA-B 27.

XX DE Ankylosing spondylitis; rheumatic disorder; diagnosis.

XX KW Homo sapiens.

XX OS EP226069-A.

XX PN 24-JUN-1987.

XX PD 21-NOV-1986; 86EP-00116139.

XX PF 30-NOV-1985; 85DE-00542024.

XX PR 21-DEC-1985; 85DE-03545576.

XX XX (BEHW) BEHRINGWERKE AG.

XX PI Szots H, Weiss E, Dornier C, Lang M, Meo T, Riethmulle G;

XX DR WPI; 1987-171469/25.

XX DR N-PSDB; AAN70225.

XX PT DNA coding for human histocompatibility antigen HLA-B 27 - useful for

XX PT diagnosis and antigen and antibody prodn.

XX PS Disclosure; Page 6; 13pp; German.

XX CC The DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis. (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 362 AA;

Alignment Scores:

Pred. No.: 2,96e-71 Length: 362
Score: 919.00 Matches: 171
Percent Similarity: 84.19% Conservative: 10
Best Local Similarity: 79.53% Mismatches: 34
Query Match: 77.68% Indels: 0
DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x AAP70155 (1-362)

Qy 1 ATCCCGTGGAGTACGTAGACACACGAATTCCTCGGTTCCACAGCGCGCGCGGAT 60

Db 47 ILeThrValGlyTyrValAspThrLeuPheValArgPheAspSerAspAlaAAser 66

Qy 61 CCAGAGTGGAGCGCGGAGCCGTCGTGGAGCAAGAGGGCGCGAGTATTGGAGTGG 120

Db 67 ProArgGluGluProAArgAlaProTrpIleGluGluGlyProGluTyrTrpAspArg 86

Qy 121 ACCACSGGGTACGCCAAGGCCACACAGACTGACCGAGTGGCCCTCAGAGAACCTGCTC 180

Db 87 GluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGluAspLeuA-gThrLeuLeu 106

Qy 181 CGCGCTACACACAGAGCGAGTGGTCTCACSCCTCCAGGAATGAATGGCTGGAC 240

Db 107 ArgTyrTyrAenGlnSerGluAlaAAserHisThrLeuGlnAenMetTyrAlaCysAsp 126

Qy 241 ATGGGGCCGACGACGCGCTCTCCGCGGGTATCACCAGCACGCGTACGACGCAAGGAT 300
Db 127 ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp 146
Qy 301 TACATCTCCCTGAACGAGGACCTCGCTCTCGACCGCGCGGACACCGTGGCTCAGATC 360
Db 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
Qy 361 ACCCAGCGCTTCTATGAGGCGAGAGGAATATCAGAGGAGTTTCAGGACCTACCTGAGGGC 420
Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
Qy 421 GAGTCCCTGGAGTTCCTCCGCGAGATCTTGAGAAATGGAGAGACGCTACAGCGCGCA 480
Db 187 GluCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
Qy 481 GATCTCCAAAGGCACACGTTGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 207 AspProProlLysThrHisValThrHisProLysSerAspHisGluAlaThrLeuArg 226
Qy 541 TGCTGGCGCTGGGCTTCTACCTCGCGAGATCAGCTGACCTGCGACGGGATGGGAG 600
Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAGCGCTGAGG 645
Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 9

AAP70590 ID AAP70590 standard; protein; 337 AA.

XX AC AAP70590;

XX DT 10-APR-1991 (first entry)

XX DE Sequence of the human histocompatibility antigen HLA B27.

XX KW Rheumatic disorder; genetic screening; diagnosis; ankylosing spondylitis.

XX OS Homo sapiens.

XX PN DE3542024-A.

XX XX 04-JUN-1987.

XX PF 28-NOV-1985; 85DE-03542024.

XX PR 21-DEC-1985; 85DE-03545576.

XX PA (BEHW) BEHRINGWERKE AG.

XX PI Riethmulle G, Meo T, Weiss E, Szots H;

XX DR WPI; 1987-157893/23.

XX DR N-PSDB; AAN70935.

XX PT DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA, antigen or antibody.

XX PS Disclosure; Page 5; 5pp; German.

XX CC The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, eg for assessing susceptibility to rheumatic disorders such as ankylosing spondylitis, or may be used to transform cells for prodn of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in immunoassay

XX SQ Sequence 337 AA;

Alignment Scores:

Pred. No.:	3,22e-71	Length:	337
Score:	918.50	Matches:	172
Percent Similarity:	84.65%	Conservative:	10
Best Local Similarity:	80.00%	Mismatches:	32
Query Match:	77.64%	Indels:	1
DB:	1	Gaps:	1

US-09-819-371-3 (1-645) x AAP70590 (1-337)			
QY	1	ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCGACAGCGCCGCGGATT	60
DB	23	IleThrValGlyTyrValAspAspThrLeuPheValArgPheAspSerAspAlaAlaSer	42
QY	61	CGAGAGTGGAGCGCGGAGCGTGGTGGACAAAGAGCGCGCGAGATTGGAGTGG	120
DB	43	ProArgGluGluProArgAlaProTrpIleGluGluGluProGlyTrpAspArg	62
QY	121	ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC	180
DB	63	GluThrGlnIleCysIysAlaLysAlaGlnThrAspArgGluAspLeuArgThrLeuLeu	82
QY	181	CGCGCTTACACGAGCGAGGCTGGTCTCACSCCTCCAGGGAATGATGGCTCGAC	240
DB	83	---ArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnAsnMetTyrGlyCysAsp	101
QY	241	ATGGGCGCCGACGAGCGCTCTCCGCGGGTATCACGACGCGTACGAGCGCAAGGAT	300
DB	102	ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp	121
QY	301	TACATCTCCCTGACGAGGACCTCGCTCTCGGACCGCGCGGACACCGTGGCTCAGATC	360
DB	122	TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle	141
QY	361	ACCAGCGCTTCTATGAGGAGGAGGATATGACAGAGGTTTCAGGACCTACCTGGAGGC	420
DB	142	ThrGlnArgIleTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly	161
QY	421	GAGTGGCTGGAGTGTCTCCGACAGTACTTGGAGAATGGGAAGGAGAGCTTACAGCGCGCA	480
DB	162	GluCysValGluTrpLeuArgGlyTyrLeuGluAsnGlyLysGluThrLeuGlnArgVal	181
QY	481	GATCTCCAAAGGACACAGCTTGGCCACCCATCTCTGACCATGAGGCCACCTGAGG	540
DB	182	AspProProLysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg	201
QY	541	TGCTGGGCGCTTCTACCTCGGAGATCACGCTGACCTGGAGCGGATGGGAG	600
DB	202	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu	221
QY	601	GAACAGACCCAGGACACAGAGCTTGTGGAGACACGAGCTTCAGGG	645
DB	222	AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	236

RESULT 10			
ID	AAU32882	standard; protein; 369 AA.	
XX	AC	AAU32882;	
XX	AC	(first entry)	
DT	18-DEC-2001	Novel human secreted protein #3373.	
XX	DE	Human; vaccination; gene therapy; nutritional supplement;	
XX	KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;	
XX	KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.	
XX	OS	Homo sapiens.	
XX	FN	WO200179449-A2.	
XX	XX	25-OCT-2001.	

Pf	16-APR-2001;	2001WO-US008656.
XX	18-APR-2000;	2000US-00552929.
PR	26-JAN-2001;	2001US-00770160.
XX	(HYSE-) HYSEQ INC.	
XX	Tang YT, Liu C, Drmanac RT;	
XX	WPI; 2001-611725/70.	
XX	Nucleic acids encoding a range of human polypeptides, useful in genetic	
PT	vaccination, testing and therapy.	
XX	Claim 20; Page 583; 765pp; English.	
XX	The invention relates to novel human secreted polypeptides. The	
CC	polypeptides and antibodies to the polypeptides are useful for	
CC	determining the presence of or predisposition to a disease associated	
CC	with altered levels of polypeptide. The polypeptides are also useful for	
CC	identifying agents (agonists and antagonists) that bind to them. Cells	
CC	expressing the proteins are useful for identifying a therapeutic agent	
CC	for use in treatment of a pathology related to aberrant expression or	
CC	physiological interactions of the polypeptide. Vectors comprising the	
CC	nucleic acids encoding the polypeptides and cells genetically engineered	
CC	to express them are also useful for producing the proteins. The proteins	
CC	are useful in genetic vaccination, testing and therapy, and can be used	
CC	as nutritional supplements. They may be used to increase stem cell	
CC	proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon	
CC	and/or nerve tissue growth or regeneration; immune suppression and/or	
CC	stimulation; as anti-inflammatory agents; and in treatment of leukaemias.	
CC	AAU29510-AAU33304 represent the amino acid sequences of novel human	
CC	secreted proteins of the invention	
XX	SQ	Sequence 369 AA;

Alignment Scores:			
Pred. No.:	8.1e-71	Length:	369
Score:	914.00	Matches:	168
Percent Similarity:	86.05%	Conservative:	17
Best Local Similarity:	78.14%	Mismatches:	30
Query Match:	77.26%	Indels:	0
DB:	4	Gaps:	0

US-09-819-371-3 (1-645) x AAU32882 (1-369)			
QY	1	ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCGACAGCGCCGCGGATT	60
DB	50	IleSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaSer	69
QY	61	CGAGAGTGGAGCGCGGAGCGTGGTGGACAAAGAGCGCGCGAGTATGGAGTGG	120
DB	70	ProArgGluGluProArgAlaProTrpIleGluGluGluProGlyTrpAspArg	89
QY	121	ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC	180
DB	90	AsnThrGlnIlePheLeuThrAsnThrGlnThrAspArgGluSerLeuArgAsnLeuArg	109
QY	181	CGCGCTTACACGAGCGAGGCTGGTCTCACSCCTCCAGGGAATGATGGCTCGAC	240
DB	110	GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnSerMetTyrGlyCysAsp	129
QY	241	ATGGGCGCCGACGAGCGCTCTCCGCGGGTATCACGACGCGTACGAGCGCAAGGAT	300
DB	130	ValGlyProAspGlyArgLeuLeuArgGlyHisGlnThrAlaTyrAspGlyLysAsp	149
QY	301	TACATCTCCCTGACGAGGACCTCGCTCTCGGACCGCGCGGACACCGTGGCTCAGATC	360
DB	150	TyrIleAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle	169
QY	361	ACCAGCGCTTCTATGAGGAGGAGGATATGACAGAGGTTTCAGGACCTACCTGGAGGC	420
DB	170	ThrGlnArgIleTrpGluAlaAlaArgValAlaGluGlnAspArgAlaTyrLeuGluGly	189

QY	421	GAGTGGCTGGAGTTGCTCGCAGATACCTTGAGAAATGGGAGAGACCTTACAGCCGCA	480
Db	190	ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysAspThrLeuGluArgAla	209
QY	481	GATCTCCAAAGSCACAGTGTGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG	540
Db	210	AspProProlYthrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg	229
QY	541	TGCTGGCCCTGGGCTTCTACCTGCGGATACGCTGACCTGGCAGCGGATGGGAG	600
Db	230	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu	249
QY	601	GAACAGACCCAGACACAGAGCTTGTGAGACCAAGGCTGCAGG	645
Db	250	AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	264
RESULT 11			
AA006772			
ID	AA006772 standard; protein; 374 AA.		
AC	AA006772;		
XX			
DT	06-NOV-2001 (first entry)		
XX			
DE	Human polypeptide SEQ ID NO 20664.		
XX			
KW	Human; cytokines; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorders; arthritis; inflammation.		
OS	Homo sapiens.		
XX			
PN	WO200164835-A2.		
XX			
PD	07-SEP-2001.		
XX			
PF	26-FEB-2001; 2001WO-US004927.		
XX			
PR	28-FEB-2000; 2000US-00515126.		
FR	18-MAY-2000; 2000US-00577409.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YT, Liu C, Drmanac RT;		
XX			
DR	WPI; 2001-514838/56.		
DR	N-PSDB; AAI86703.		
XX			
PT	Isolated nucleic acids and polypeptides, useful for preventing diagnosing		
PT	and treating e.g. leukemia, inflammation and immune disorders.		
XX			
PS	Claim 20; SEQ ID NO 20664; 1399pp + Sequence Listing; English.		
XX			
CC	The invention relates to human polynucleotides (AI79941-AI93841) and		
CC	the encoded proteins (AA00010-AA013910) that exhibit activity relating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activin/inhibin activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and		
CC	inflammation. Note: The sequence data for this patent did not form part		
CC	of the printed specification, but was obtained in electronic format		
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences		
XX			
SO	Sequence 374 AA;		

PF	25-JAN-2001; 2001WO-US002687.	XX	481	GATCCTCCAAAGCAGCACGCTTGCCTCCACCCCATCTCTGACCATGAGCCCTCCGAGG	540
PR	25-JAN-2000; 2000US-00491404.	XX	207	AspProProlysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg	226
PR	17-JUL-2000; 2000US-00617746.	XX	541	TGCTGGGCGCTTCTTACCTCGCGGAGATCACCTGACCTGGCAGCGGGATGGGGAG	600
PR	03-AUG-2000; 2000US-00631451.	XX	227	CysTrpAlaLeuGlyPheTyProAlaGluLeThrLeuThrTrpGlnArgAspGlyGlu	246
PR	15-SEP-2000; 2000US-00663870.	XX	601	GAACAGACCCAGGACACAGAGCTTGGAGACCCAGGCTGCAGGG	645
XX	(HYSB-) HYSEQ INC.	XX	247	AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	261
XX	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;	XX	RESULT 13		
PI	Cao Y, Dimaenac RA, Zhang J, Werthman T;	XX	AD664171		
XX	WPI; 2001-476164/51.	XX	ID	AD664171 standard; protein; 362 AA.	
DR	N-PSDB; AAH98419.	XX	AC	AD664171;	
XX	Isolated polypeptide for treatment of diseases, diagnostics, raising	XX	DT	29-JAN-2004 (first entry)	
PT	antibodies and research use.	XX	DE	Human Protein P30474, SEQ ID NO 10123.	
XX	Claim 20; Page 924-925; 1275pp; English.	XX	XX	Human; pain; neuronal tissue; gene therapy;	
XX	The present invention provides the protein and coding sequences of novel	XX	XX	spinal segmental nerve injury; chronic constriction injury; CCI;	
CC	proteins from a variety of organisms, including human, dog, cat, horse,	XX	XX	spared nerve injury; SNI; Chung.	
CC	cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea	XX	OS	Homo sapiens.	
CC	urchin and tomato. These were derived from expressed sequence tags (ESTs)	XX	XX	WO20003016475-A2.	
CC	from the organism of interest. They can be used in diagnostics,	XX	XX	27-FEB-2003.	
CC	forensics, gene mapping, identification of mutations, to assess	XX	XX	14-AUG-2002; 2002WO-US025765.	
CC	biodiversity, and for nutritional purposes. The present sequence is a	XX	XX	14-AUG-2001; 2001US-0312147P.	
CC	product of the invention	XX	XX	01-NOV-2001; 2001US-0346382P.	
XX	Sequence 322 AA;	XX	XX	26-NOV-2001; 2001US-0333347P.	
XX		XX	XX	(GEO) GEN HOSPITAL CORP.	
XX		XX	XX	(FARB) BAYER AG.	
XX		XX	XX	Woolf C, D'urso D, Befort K, Costigan M;	
XX		XX	XX	WPI; 2003-268312/26.	
XX		XX	XX	GENBANK; F30474.	
XX		XX	XX	New composition comprising two or more isolated polypeptides, useful for	
XX		XX	XX	preparing a medicament for treating pain in an animal.	
XX		XX	XX	Claim 1; Page; 1017pp; English.	
XX		XX	XX	The invention discloses a composition comprising two or more isolated rat	
XX		XX	XX	or human polynucleotides or a polynucleotide which represents a fragment,	
XX		XX	XX	derivative or allelic variation of the nucleic acid sequence. Also	
XX		XX	XX	claimed are a vector comprising the novel polynucleotide, a host cell	
XX		XX	XX	comprising the vector, a method for identifying a nucleotide sequence	
XX		XX	XX	which is differentially regulated in an animal subjected to pain and a	
XX		XX	XX	kit to perform the method, an array, a method for identifying an agent	
XX		XX	XX	that increases or decreases the expression of the polynucleotide sequence	
XX		XX	XX	that is differentially expressed in neuronal tissue of a first animal	
XX		XX	XX	subjected to pain, a method for identifying a compound which regulates	
XX		XX	XX	the expression of a polynucleotide sequence which is differentially	
XX		XX	XX	expressed in an animal subjected to pain, a method for identifying a	
XX		XX	XX	compound that regulates the activity of one or more of the	
XX		XX	XX	polynucleotides, a method for producing a pharmaceutical composition, a	
XX		XX	XX	method for identifying a compound or small molecule that regulates the	
XX		XX	XX	activity in an animal of one or more of the polypeptides given in the	
XX		XX	XX	specification, a method for identifying a compound useful in treating	
XX		XX	XX	pain and a pharmaceutical composition comprising the one or more	
XX		XX	XX	polypeptides or their antibodies. The polynucleotide or the compound that	
XX		XX	XX	modulates its activity is useful for preparing a medicament for treating	
XX		XX	XX	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction	
XX		XX	XX	injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene	

Alignment Scores:
 Pred. No.: 9,56e-71 Length: 322
 Score: 913.00 Matches: 169
 Percent Similarity: 86.05% Conservative: 16
 Best Local Similarity: 78.60% Mismatches: 30
 Query Match: 77.18% Indels: 0
 DB: 4 Gaps: 0

US-09-819-371-3 (1-645) x AM23760 (1-322)

QY	1	ATCGCTGAGTACGTAGACGACGCAATTCCTGGTTCGACAGCGCGCGGAT	60
DB	47	IleSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAlaAsp	66
QY	61	CCGAGGATGAGCGCGCGGAGCCGCTGGTGGAGACAGAGCGCGCGGATGG	120
DB	67	ProArgGluGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAsp	86
QY	121	ACACGGGTACGCCAAGGCCAAGCAGACTGACGAGTGGCTGCGCTGAGGAC	180
DB	87	AsnThrGlnIleTyrLysAlaGlnAlaGlnThrAspArgGluSerLeuArgAsn	106
QY	181	CGCGCTACACACGACGAGCGGTGGTCTCACSCCTCCAGGAATGAATGGCT	240
DB	107	GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnSerMetTyrGly	126
QY	241	ATGGGGCCGACGACGCGCTCTCCGCGGTATCACACGACGCGTACGACGCA	300
DB	127	ValGlyProAspGlyArgLeuLeuArgGlyHisAspGlnTyrAlaTyrAsp	146
QY	301	TACATCTCCCTGACGAGGACCTCGCTCTCTGACCGCGGACACCGGTCT	360
DB	147	TyrIleAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAla	166
QY	361	ACCCAGCGCTTCTATGAGCGCAGAGGAATATGACAGAGTTCAGGACCT	420
DB	167	ThrGlnArgLysTrpGluAlaAlaArgGluAlaGluGlnArgAlaTyrLeu	186
QY	421	GAGTCTCGGTGCTCCGCGAGTACTTGGAGATGGGAGGAGACCTACGCG	480
DB	187	GluCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysAspLeuGlu	206

CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 362 AA;

Alignment Scores:
Pred. No.: 2,43e-69 Length: 362
Score: 897.00 Matches: 167
Percent Similarity: 84.19% Conservative: 14
Best Local Similarity: 77.67% Mismatches: 34
Query Match: 75.82% Indels: 0
DB: 7 Gaps: 0

US-09-819-371-3 (1-645) x ADE64175 (1-362)
QY 1 ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTTCAGACGCCCGCCGCGATT 60
DB 47 ILEAlaValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaser 66
QY 61 CCGAGATGAGCGCGGGAGCGTGGTGGAGCAAGAGCGCGCAGTATTGGAGTGG 120
DB 67 ProArgThrGluProArgAlaProTrrPleGluGluGluGlyProGluTyrTrpAspArg 86
QY 121 ACCACGGGTACGCCAAGCCACGACGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
DB 87 AsnThrGlnIlePheLysThrAsnThrGlnThrTyrArgGluSerLeuArgAsnLeuArg 106
QY 181 CGCGGTACACGACGACGAGGTGGTCTCACCCCTCCAGGATGATGGCTCGAC 240
DB 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisIleGlnArgMetTyrGlyCysAsp 126
QY 241 ATGGGGCCCGACGAGCGCTCTCCCGGGTATCACGACGACGACGACGACGACGACGAC 300
DB 127 LeuGlyProAspGlyArgLeuLeuArgGlyHisAspGlnSerAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTGACCGCGCGACACCGTGGCTCAGATC 360
DB 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
QY 361 ACCGAGCGCTCTATGAGGCGAGGAGTATGACGAGGAGTTCAGGACCTACCTGGAGGC 420
DB 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnArgAlaTyrLeuGluGly 186
QY 421 GAGTCCCTGAGTGTCTCCAGATCTTGGAGATGGGAGGAGACGCTACAGCGCGCA 480
DB 187 LeuCysValGluTrpLeuArgGlyTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
QY 481 GATCCTCAAGGACACGCTGCGCCACCCATCTCTGACCATGAGGCGCCCTGAGG 540
DB 207 AspProLysThrHisValThrHisHisProValSerAspHisGluAlaThrLeuArg 226
QY 541 TGCTGGCGCTGCTCTACCTGCGGAGATCACGCTGACCTGCGGAGGATGGGGAG 600
DB 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
QY 601 GAACAGCCAGGACACGAGCTTGTGAGACCGAGCTGCAGG 645
DB 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 14
ADE64175
ID: ADE64175 standard; protein; 362 AA.
XX AC ADE64175;
XX AC
XX DT 29-JAN-2004 (first entry)
XX XX Human Protein P30474, SEQ ID NO 10127.
XX DE Human; pain; neuronal tissue; gene therapy;
KW

KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
XX
XX GENBANK; P30474.
DR
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 362 AA;

Alignment Scores:
Pred. No.: 2,43e-69 Length: 362
Score: 897.00 Matches: 167
Percent Similarity: 84.19% Conservative: 14
Best Local Similarity: 77.67% Mismatches: 34
Query Match: 75.82% Indels: 0
DB: 7 Gaps: 0

US-09-819-371-3 (1-645) x ADE64175 (1-362)
QY 1 ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTTCAGACGCCCGCCGCGATT 60
DB 47 ILEAlaValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaser 66
QY 61 CCGAGATGAGCGCGGGAGCGTGGTGGAGCAAGAGCGCGCAGTATTGGAGTGG 120

Db 67 ProArgThrGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAspArg 86
QY 121 ACCACGGGTACCCCAAGCCACAGACAGTACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 87 AenThrGluIlePheLysThrAenThrGlnThrTyrArgGluSerLeuArgAenLeuArg 106
QY 181 CGCCGCTACACACAGACGAGGTGGTCTCACSCCCTCAGGATGATGCTGCGAC 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisIleGlnArgMetTyrGlyCysAsp 126
QY 241 ATGGGCGCCGACGAGCGCTCTCCGCGGTATCACACAGCAGCGGTACACGCGCAAGAT 300
Db 127 LeuGlyProAspGlyArgLeuLeuArgGlyHisAspGlnSerAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGACCTGCGCTCTGACACCGCGCGGACACCTGCTCAGATC 360
Db 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
QY 361 ACCACGCGTTCATGAGGACAGGAGATATGACAGAGGATTCAGGACCTTACCTGAGGCG 420
Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnArgArgAlaTyrLeuGluGly 186
QY 421 GAGTCTGGAGTGTCTCCGACATCTTGGAGATGGGAAGAGACGCTACAGCGCGCA 480
Db 187 LeuCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
QY 481 GATCCTCCAAAGGACAGCTTGCGCCACCCATCTCTGACCATGAGCCACCTGAGG 540
Db 207 AspProProLysThrHisValThrHisHisProValSerAspHisGluAlaThrLeuArg 226
QY 541 TGTGCGCCCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGGCAGCGGATGGGAG 600
Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
QY 601 GAACAGACCCAGACACAGAGCTTGGAGACCGAGCCGCTGACGG 645
Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 15
AAAY07033
ID AAAY07033 standard; protein; 366 AA.
XX AC AAAY07033;
XX AC AAAY07033;
XX DT 02-JUL-1999 (first entry)
XX DE Breast cancer associated antigen precursor sequence.
XX KW Cancer associated antigen; diagnosis; research; treatment; human;
XX KW Breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX KW prostate cancer.
XX OS Homo sapiens.
XX PN W09904265-A2.
XX PD 28-JAN-1999.
XX PF 15-JUL-1998; 98WO-US014679.
XX PR 17-JUL-1997; 97US-00896164.
XX PR 10-OCT-1997; 97US-0061599P.
XX PR 10-OCT-1997; 97US-0061765P.
XX PR 10-OCT-1997; 97US-00948705.
XX PR 11-OCT-1997; 97GB-00021697.
XX PR 22-JUN-1998; 98US-00102322.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
XX PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sanin U;

WPI; 1999-132448/11.
XX New isolated cancer associated nucleic acids and polypeptides - isolated
PT using sera from cancer patients, used to develop products for the
PT diagnosis, monitoring or treatment of cancers.
XX
PS Disclosure; Page 417-418; 787pp; English.
XX The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the
CC interaction between the agent and the NAM or the expression product as a
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
XX lung cancer
SQ Sequence 366 AA;
Alignment Scores:
Pred. No.: 2,97e-69 Length: 366
Score: 896.00 Matches: 168
Percent Similarity: 85.12% Conservative: 15
Best Local Similarity: 78.14% Mismatches: 32
Query Match: 75.74% Indels: 0
DB: 2 Gaps: 0
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QY 61 CCGAGGATGGAGCGCGGAGCCCTGGGTGGAGCAAGAGCGCGCGAGTATGGAGTGG 120
Db 67 ProArgGlyGluProArgAlaProTrpValGluGlnGluGlyProGluTyrTrpAspArg 86
QY 121 ACCACGGGTACGCGCAAGGCCAACGACAGACTACCGAGTGGCGCTGAGGAACCTGCTC 180
Db 87 GluThrGlnLysTyrLysArgGlnAlaGlnThrAspArgValSerLeuArgAsnLeuArg 106
QY 181 CGCCGCTACACACAGACGAGGTGGTCTCACSCCCTCAGGGAATGATGCTGCGAC 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisIleGlnArgMetTyrGlyCysAsp 126
QY 241 ATGGGCGCCGACGAGCGCTCTCCGCGGTATCACACAGCAGCGGTACGAGCGCAAGAT 300
Db 127 ValGlyProAspGlyArgLeuLeuArgGlyTyrAspGlnTyrAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGACCTGCGCTCTCGGACCCGCGCGGACACCGTGGCTCAGATC 360
Db 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
QY 361 ACCACGCGTTCATGAGGACAGGAGATATGACAGAGGATTCAGGACCTTACCTGAGGCG 420
Db 167 ThrGlnArgLysTrpGluAlaAlaArgGluAlaGluGlnLeuArgAlaTyrLeuGluGly 186
QY 421 GAGTCTGGAGTGTCTCCGACATCTTGGAGATGGGAAGAGAGAGAGCTACAGCGCGCA 480
Db 187 LeuCysValGluTrpLeuArgArgTyrLeuLysAsnGlyLysGluThrLeuGlnArgAla 206
QY 481 GATCCTCCAAAGGACAGCTTGCGCCACCCATCTCTGACCATGAGCCACCTGAGG 540
Db 207 GluHisProLysThrHisValThrHisHisProValSerAspHisGluAlaThrLeuArg 226
QY 541 TGTGCGCCCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGGCAGCGGATGGGAG 600

Db 227 CysTyrAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTyrGlnTyrPaspGlyGlu 246
QY 601 GAACAGACCCAGCACACAGAGCTTGTGAGACACAGCCCTGCAGGG 645
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Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

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Maximum Match 100%
Listing first 45 summaries

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-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_AA.*
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5: /cn2_6/ptodata/2/iaa/PCUTUS COMB.pep.*
6: /cn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	932	78.8	274	1	US-08-222-851-1
2	849	71.8	365	2	US-08-484-905-104
3	849	71.8	365	3	US-08-481-985B-104
4	849	71.8	365	2	US-08-370-476-104
5	848	71.7	365	2	US-08-484-905-100
6	848	71.7	365	3	US-08-481-985B-100
7	848	71.7	365	3	US-08-370-476-100
8	845	71.4	365	3	US-08-484-905-99
9	845	71.4	365	3	US-08-481-985B-99
10	845	71.4	365	3	US-08-370-476-99
11	844	71.3	274	2	US-08-484-905-107
12	844	71.3	274	2	US-08-484-905-108

13	844	71.3	274	3	US-08-481-985B-107	Sequence 107, App
14	844	71.3	274	3	US-08-481-985B-108	Sequence 108, App
15	844	71.3	274	3	US-08-370-476-107	Sequence 107, App
16	844	71.3	274	3	US-08-370-476-108	Sequence 108, App
17	843	71.3	365	2	US-08-484-905-103	Sequence 103, App
18	843	71.3	365	2	US-08-481-985B-103	Sequence 103, App
19	843	71.3	365	3	US-08-370-476-103	Sequence 103, App
20	842	71.2	365	2	US-08-484-905-102	Sequence 102, App
21	842	71.2	365	3	US-08-481-985B-102	Sequence 102, App
22	842	71.2	365	3	US-08-370-476-102	Sequence 97, App
23	841	71.1	365	2	US-08-484-905-97	Sequence 98, App
24	841	71.1	365	2	US-08-481-985B-97	Sequence 97, App
25	841	71.1	365	3	US-08-370-476-97	Sequence 97, App
26	841	71.1	365	3	US-08-481-985B-98	Sequence 98, App
27	841	71.1	365	3	US-08-481-985B-98	Sequence 98, App
28	841	71.1	365	3	US-08-481-985B-98	Sequence 98, App
29	841	71.1	365	3	US-08-481-985B-98	Sequence 98, App
30	841	71.1	365	3	US-08-481-985B-98	Sequence 98, App
31	841	71.1	365	3	US-08-481-985B-98	Sequence 98, App
32	840	71.0	274	2	US-09-503-444A-23	Sequence 105, App
33	840	71.0	274	3	US-08-481-985B-105	Sequence 105, App
34	840	71.0	274	3	US-08-370-476-105	Sequence 105, App
35	840	71.0	341	3	US-08-890-719-38	Sequence 106, App
36	836	70.7	274	2	US-08-484-905-106	Sequence 106, App
37	836	70.7	274	3	US-08-481-985B-106	Sequence 106, App
38	836	70.7	274	3	US-08-370-476-106	Sequence 101, App
39	832	70.3	365	2	US-08-484-905-101	Sequence 101, App
40	832	70.3	365	3	US-08-481-985B-101	Sequence 101, App
41	832	70.3	365	3	US-08-370-476-101	Sequence 101, App
42	801	67.7	361	3	US-08-652-265-22	Sequence 22, App
43	801	67.7	361	3	US-08-834-497A-22	Sequence 22, App
44	801	67.7	361	3	US-09-503-444A-22	Sequence 22, App
45	797	67.4	363	4	US-08-914-372C-37	Sequence 37, App

ALIGNMENTS

RESULT 1

US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 274 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-222-851-1

Alignment Scores:
 Pred. No.: 74e-73 Length: 274
 Score: 932.00 Matches: 172
 Percent Similarity: 86.05% Conservative: 13
 Best Local Similarity: 80.00% Mismatches: 30
 Query Match: 78.78% Indels: 0
 DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x US-08-222-851-1 (1-274)

QY	1	ATCGCGGTGAGTACGAGCAGCAGCAATCTCGGTTCGACGAGCCGCGGATT	60
DB	23	IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAlaAlaSer	42
QY	61	CCGAGGATGAGCCGCGGAGCGTGGTGGAGCAAGAGGCGCGGAGTATGGAGTGG	120
DB	43	ProArgMetGluProArgAlaProTrieGluGlnGluGlyProGluTyrTrpAspArg	62
QY	121	ACCACGGGTACCCCAAGCCCAAGCAGCAGACTGACCGAGTGGCCCTGAGGACCTGCTC	180
DB	63	GluThrGlnIleValIysAlaGlnSerGlnThrAspArgGluAspLeuArgThrLeuArg	82
QY	181	CGCGCGTACACACGAGCAGGAGTGGTCTCACSCCTCCAGGAAATGAATGGCTGCAC	240
DB	83	GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrIleGlnArgMetTyrGlyCysAsp	102
QY	241	ATGGGCGCGAGCGGAGCTCTCCCGGGTATCACGACGCGGTACGACGCGCAAGGAT	300
DB	103	ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp	122
QY	301	TACATCTCCCTGACAGCAGCCTCGCTCTGACCGCGCGCAGCACACCTGCTCAGATC	360
DB	123	TyrIleAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle	142
QY	361	ACCACGCGTCTATGAGCAGCAGGAAATATGACGAGGAGTTCAGGACCTGAGGCGC	420
DB	143	ThrGlnArgIleTrpGluAlaAlaArgValAlaGluLeuArgAlaTyrLeuGluGly	162
QY	421	GAGTGGCTGGGTGCTCCGACATATGGAGATGGGAGGAGGAGCGCTACAGCGCGCA	480
DB	163	ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla	182
QY	481	GATCCTCCAAAGCAGCAGTTCGCCACCCCATCTCTGACCATGAGGCCACCTGAGG	540
DB	183	AspProGlyThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg	202
QY	541	TGCTGGGCGCTGCTTACCTGCGGAGATCACCTGACCTGCGGCGGATGGGAG	600
DB	203	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu	222
QY	601	GAACAGACCCAGCAGCAGCTGTGTGGAGACCCAGGCGCTGCAGG	645
DB	223	AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	237

RESULT 2

US-08-484-905-104
 Sequence 104, Application US/08484905
 Patent No. 5976551
 GENERAL INFORMATION:
 APPLICANT: Motez, Estelle
 APPLICANT: Abastado, Jean-Pierre
 APPLICANT: Kourilsky, Philippe
 TITLE OF INVENTION: An Altered Major Histocompatibility
 Complex (MHC) Determinant and Methods for Using the
 TITLE OF INVENTION: Determinant
 NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,905
 FILING DATE: 07-JUNE-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/801,818
 FILING DATE: 05-DEC-1991
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/792,473
 FILING DATE: 15-NOV-1991
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Potter, Jane E. R.
 REGISTRATION NUMBER: 33,332
 REFERENCE/DOCKET NUMBER: 03495.0106-03000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 104:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-484-905-104

Alignment Scores:
 Pred. No.: 1.23e-65 Length: 365
 Score: 849.00 Matches: 157
 Percent Similarity: 80.93% Conservative: 17
 Best Local Similarity: 73.02% Mismatches: 41
 Query Match: 71.77% Indels: 0
 DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x US-08-484-905-104 (1-365)

QY	1	ATCGCGGTGAGTACGAGCAGCAGCAATCTCGGTTCGACGAGCCGCGGATT	60
DB	47	IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAlaAlaSer	66
QY	61	CCGAGGATGAGCCGCGGAGCGTGGTGGAGCAAGAGGCGCGGAGTATGGAGTGG	120
DB	67	GlnArgMetGluProArgAlaProTrieGluGlnGluGlyProGluTyrTrpAspPhe	86
QY	121	ACCACGGGTACGCCAAGCCCAAGCAGCAGACTGACCGAGTGGCCCTGAGGACCTGCTC	180
DB	87	AsnThrArgAsnValIysAlaGlnSerGlnThrAspArgValAspLeuSerThrLeuArg	106
QY	181	CGCGCGTACACACGAGCAGGAGTGGTCTCACSCCTCCAGGAAATGAATGGCTGCAC	240
DB	107	GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrIleGlnMetTyrGlyCysAsp	126
QY	241	ATGGGCGCGAGCGGAGCTCTCCCGGGTATCACGACGCGGTACGACGCGCAAGGAT	300
DB	127	ValGlySerAspGlyArgPheLeuArgGlyTyrArgGlnAspAlaTyrAspGlyLysAsp	146
QY	301	TACATCTCCCTGACAGGAGGAGTCTGCTGAGACCCGCGGAGCACCGTGGCTCAGATC	360
DB	147	TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr	166


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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-104

Alignment Scores:
Pred. No.: 1.23e-65 Length: 365
Score: 849.00 Matches: 157
Percent Similarity: 80.93% Conservative: 17
Best Local Similarity: 73.02% Mismatches: 41
Query Match: 71.77% Indels: 0
Gaps: 3
DB:

US-09-819-371-3 (1-645) x US-08-370-476-104 (1-365)
Qy 1 ATCCGCTGGAGTACGTAGACGACGCAATTCCTGCGTTCGACAGCGCGCGGATT 60
Db 47 Ilealavalglytyrvalaspthrlnphevargpheaaspaalaser 66
Qy 61 CCGAGGATGAGCGCGGAGCGCGTGGTGAGCAGAGCGCGCGGAGTGGAGTGG 120
Db 67 Glnargmetgluproargalaprotipileglnglulglyproglutyrtrpasp 86
Qy 121 ACCACGGGTACGCCAAGGCCACGACGACTGACGAGTGGCCCTGAGGAACCTGCTC 180
Db 87 AsnThrarganvallysalaGlnSerGlnThrAspargValaspLeuSerThrLeuArg 106
Qy 181 CGCGCTACACACGAGCGAGCGTGGTCTCAGCCCTCCAGGAGTGAATGGCTGGAC 240
Db 107 GlytyrtyrAsnGlnSerGluallaglySerHisThrIleGlnMetTyrGlyCysAsp 126
Qy 241 ATGGGCGCCGACGAGCGCTCTCCGCGGGTATCACCAGCAGCGGTACGACGCGCAAGAT 300
Db 127 ValglyseraspGlyargpHeleuargglytyrargGlnaspalaTyrapGlyLysAsp 146
Qy 301 TACATCTCCCTGAACGAGGACCTCGCTCTCGTGGACCGCGGAGACACCGTGGCTCAGATC 360
Db 147 TyrlleAlaLeuLysGluaspLeuArgSerTrpThrAlaAlaaspMetAlaAlaGlnThr 166
Qy 361 ACCAGCGCTTCTATGAGCGAGAGGAATATGACAGGAGTTTCAGGACCTACCTGGAGGC 420
Db 167 ThrLysHisLysTrpGluAlaHisValalaGluGlnTrpArgAlaTyrlleuGluGly 186
Qy 421 GAGTGCCTGGAGTTCCTCCGAGACACTCTGGAGAATGGAGAGAGAGACGCTACACGCGCA 480

187 ThrCysValGluTrpLeuArgTyrLeuGluAsnGlyLysGlnThrLeuGlnArgThr 206
481 GATCCTCAAAGGCACAGTGTGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 540
207 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 226
541 TGCTGGGCGCTTCTACCTGCGGAGATCACCTGACCTGCGGAGCGGATGGGAG 600
227 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
601 GAACAGACCCGACGACAGAGCTTGTGGAGACGAGCGCTGCAGGG 645
247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 5
US-08-484-905-100
; Sequence 100, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS-/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-100

Alignment Scores:
Pred. No.: 1.51e-65 Length: 365
Score: 848.00 Matches: 157
Percent Similarity: 80.93% Conservative: 17
Best Local Similarity: 73.02% Mismatches: 41
Query Match: 71.68% Indels: 0
Gaps: 2
DB:
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US-09-819-371-3 (1-645) x US-08-484-905-100 (1-365)
QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCTGACAGCGCCGCGGATT 60
Db 47 IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
QY 61 CCGAGATGAGCGCGGAGCGGTGGTGGAGCAAGAGGGCCGCGAGTATGGAGTGG 120
Db 67 GlnArgMetGluProArgAlaProTrrPleGluGlnGluGlyProGluTyrTrpAspGly 86
QY 121 ACCACGGGTACGCCAAGCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGGTC 180
Db 87 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 106
QY 181 CGCGCTACACACGAGCGAGGCTGGGTCTCACSCCTCCAGGGAATGAATGGTGGCAG 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetPheGlyCysAsp 126
QY 241 ATGGGGCCCGAGCGAGCGCTCTCCGCGGGTATCCAGCAGCGGTAGCAGCGCAAGGAT 300
Db 127 ValGlySerAspGlyArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTCGGACCGCGCGGACACCGTGGCTCAGATC 360
Db 147 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 166
QY 361 ACCACGGCTTCTATGAGCGAGAGGAATATGACAGAGAGTTCAGGACCTACCTGGAGGC 420
Db 167 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
QY 421 GAGTGCCTGGAGTGTCTCCGCGAGATACCTGAGAGATGGAGGAGGACGACACGCGCA 480
Db 187 ThrCysValGluTrpLeuArgGlyTrpLeuGluAsnGlyLysGluThrLeuGlnArgThr 206
QY 481 GATCCTCCAAAGGACACGAGTTCGCCACCCACCTCTCTGACCATGAGGCCACCTCAGG 540
Db 207 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 226
QY 541 TCGTGGGCGCTGGGCTTCTACCTCGGAGATTCAGCTGACCTGACCTGGCGGAGTGGGAG 600
Db 227 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246

US-09-819-371-3 (1-645) x US-08-481-985B-100 (1-365)
QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCTGACAGCGCCGCGGATT 60
Db 47 IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
QY 61 CCGAGATGAGCGCGGAGCGGTGGTGGAGCAAGAGGGCCGCGAGTATGGAGTGG 120
Db 67 GlnArgMetGluProArgAlaProTrrPleGluGlnGluGlyProGluTyrTrpAspGly 86
QY 121 ACCACGGGTACGCCAAGCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGGTC 180
Db 87 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 106
QY 181 CGCGCTACACACGAGCGAGGCTGGGTCTCACSCCTCCAGGGAATGAATGGTGGCAG 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetPheGlyCysAsp 126
QY 241 ATGGGGCCCGAGCGAGCGCTCTCCGCGGGTATCCAGCAGCGGTAGCAGCGCAAGGAT 300
Db 127 ValGlySerAspGlyArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTCGGACCGCGCGGACACCGTGGCTCAGATC 360
Db 147 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 166
QY 361 ACCACGGCTTCTATGAGCGAGAGGAATATGACAGAGAGTTCAGGACCTACCTGGAGGC 420
Db 167 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
QY 421 GAGTGCCTGGAGTGTCTCCGCGAGATACCTGAGAGATGGAGGAGGACGACACGCGCA 480
Db 187 ThrCysValGluTrpLeuArgGlyTrpLeuGluAsnGlyLysGluThrLeuGlnArgThr 206
QY 481 GATCCTCCAAAGGACACGAGTTCGCCACCCACCTCTCTGACCATGAGGCCACCTCAGG 540
Db 207 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 226
QY 541 TCGTGGGCGCTGGGCTTCTACCTCGGAGATTCAGCTGACCTGACCTGGCGGAGTGGGAG 600
Db 227 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246

Alignment Scores:
Pred. No.: 1,51e-65 Length: 365
Score: 848.00 Matches: 157
Percent Similarity: 80.93% Conservative: 17
Best Local Similarity: 73.02% Mismatches: 41
Query Match: 71.68% Indels: 0
DB: 3 Gaps: 0

US-09-819-371-3 (1-645) x US-08-481-985B-100 (1-365)
QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCTGACAGCGCCGCGGATT 60
Db 47 IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
QY 61 CCGAGATGAGCGCGGAGCGGTGGTGGAGCAAGAGGGCCGCGAGTATGGAGTGG 120
Db 67 GlnArgMetGluProArgAlaProTrrPleGluGlnGluGlyProGluTyrTrpAspGly 86
QY 121 ACCACGGGTACGCCAAGCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGGTC 180
Db 87 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 106
QY 181 CGCGCTACACACGAGCGAGGCTGGGTCTCACSCCTCCAGGGAATGAATGGTGGCAG 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetPheGlyCysAsp 126
QY 241 ATGGGGCCCGAGCGAGCGCTCTCCGCGGGTATCCAGCAGCGGTAGCAGCGCAAGGAT 300
Db 127 ValGlySerAspGlyArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTCGGACCGCGCGGACACCGTGGCTCAGATC 360
Db 147 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 166
QY 361 ACCACGGCTTCTATGAGCGAGAGGAATATGACAGAGAGTTCAGGACCTACCTGGAGGC 420
Db 167 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
QY 421 GAGTGCCTGGAGTGTCTCCGCGAGATACCTGAGAGATGGAGGAGGACGACACGCGCA 480
Db 187 ThrCysValGluTrpLeuArgGlyTrpLeuGluAsnGlyLysGluThrLeuGlnArgThr 206
QY 481 GATCCTCCAAAGGACACGAGTTCGCCACCCACCTCTCTGACCATGAGGCCACCTCAGG 540
Db 207 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 226
QY 541 TCGTGGGCGCTGGGCTTCTACCTCGGAGATTCAGCTGACCTGACCTGGCGGAGTGGGAG 600
Db 227 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246

RESULT 6
US-08-481-985B-100
; Sequence 100, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garret &
; ADDRESSER: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995

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QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGCAGGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 7
 US-08-370-476-100
 ; Sequence 100, Application US/08370476
 ; Patent No. 6153408
 ; GENERAL INFORMATION:
 ; APPLICANT: Mottez, Estelle
 ; APPLICANT: Abastado, Jean-Pierre
 ; APPLICANT: Kourilsky, Philippe
 ; APPLICANT: Lene, Yu-Chun
 ; APPLICANT: Ojcius, David
 ; APPLICANT: Casrouge, Amanda
 ; TITLE OF INVENTION: Altered Major Histocompatibility Complex
 ; NUMBER OF SEQUENCES: 127
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/370,476
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/117,575
 ; FILING DATE: 07-SEP-1993
 ; APPLICATION NUMBER: US 08/072,787
 ; FILING DATE: 06-JUN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/801,818
 ; FILING DATE: 05-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/792,473
 ; FILING DATE: 15-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Kenneth J.
 ; REGISTRATION NUMBER: 25,146
 ; REFERENCE/DOCKET NUMBER: 05243.0001-01000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 100:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 365 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-370-476-100

Alignment Scores:
 Pred. No.: 1,51e-65 Length: 365
 Score: 848.00 Matches: 157
 Percent Similarity: 80.93% Conservative: 17
 Best Local Similarity: 73.02% Mismatches: 41
 Query Match: 71.68% Indels: 0
 DB: 3 Gaps: 0

US-09-819-371-3 (1-645) x US-08-370-476-100 (1-365)

QY 1 ATCCCGCTGGAGTACGTAGACACACCAATTCCTGGGTTCAGACGCGCGCGATT 60

Db 47 IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaLaser 66
 QY 61 CCAGAGTGGAGCGCGGGAGCGGTGGTGGAGAGAGGGCGCGAGTATTGGAGTGG 120
 Db 67 GlnArgMetGluProArgAlaProTyrPheGluGlnGlyProGluTyrTrpAspGly 86
 QY 121 ACCACSGGTACGCCAAGCGCAACGACAGACTGACCGAGTGGCCCTCGAGGAACCTGCTC 180
 Db 87 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 106
 QY 181 CGCGCTTACAAACGACGAGCGGTGGTTCACSCCCTCCAGGGGAATGANTGGCTCGCAC 240
 Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetPheGlyCysAsp 126
 QY 241 ATGGGCGCCGACGACGCGCTCCCTCCGCGGTATCACACGACGCGCTACGACGCGCAAGGAT 300
 Db 127 ValGlySerAspGlyArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCCTGAACGAGGAGCCTCGCTCTGGACGCGCGCGACACCGCTGGCTCAGATC 360
 Db 147 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 166
 QY 361 ACCCAGCGCTTCTATGAGGAGGAGGAATATGCGAGAGGAGTTCAGGACCTACCTGGAGGGC 420
 Db 167 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
 QY 421 GAGTCTGGAGTGTCTCCGACAGATCTTGGAGATGGAGAGGAGAGCGCTACAGCGCGCA 480
 Db 187 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgThr 206
 QY 481 GATCCTCCAAAGGCACACAGTGTCCACCCACCCCATCTCAGCATGAGGCGCACCTGAGG 540
 Db 207 AspAlaProLysThrHisMetThrHisAlaValSerAspHisGluAlaThrLeuArg 226
 QY 541 TGCTGGCGCTTGTCTTACCTTGGCGAGATCACGCTGACCTGGCAGCGCGGATGGGAG 600
 Db 227 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 245
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGCAGGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 8
 US-08-484-905-99
 ; Sequence 99, Application US/08484905
 ; Patent No. 5576551
 ; GENERAL INFORMATION:
 ; APPLICANT: Mottez, Estelle
 ; APPLICANT: Abastado, Jean-Pierre
 ; APPLICANT: Kourilsky, Philippe
 ; TITLE OF INVENTION: An Altered Major Histocompatibility
 ; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
 ; TITLE OF INVENTION: Determinant
 ; NUMBER OF SEQUENCES: 127
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,905
 ; FILING DATE: 07-JUNE-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/801,818
 ; FILING DATE: 05-DEC-1991

```

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-99

Alignment Scores:
Pred. No.: 2,74e-65 Length: 365
Score: 845.00 Matches: 156
Percent Similarity: 80.93% Conservative: 18
Best Local Similarity: 72.56% Mismatches: 41
Query Match: 71.43% Indels: 0
DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x US-08-484-905-99 (1-365)
QY 1 ATCGCCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCCGCGGATT 60
DB 47 IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAsaSer 66
QY 61 CGAGAGTGTAGCGCGGGAGCGGTGGTGGAGACAGAGGGCGGCGAGTATTCGGAGTGG 120
DB 67 GlnArgMetGluProArgAlaProTrrPileGlnGluGlyProGluTyrTrpAspGly 86
QY 121 ACCACSGGGTACGCCAAGGCCAAGCACACACTGACCGAGTGCCTCGAGGAACCTGCCTC 180
DB 87 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 106
QY 181 CGCGCTTACACACAGACGAGGTGGGTCTCACSCCCTCCAGGAATGATGGCTCGAC 240
DB 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetTyrGlyCysAsp 126
QY 241 ATGGGCGCCGACGACGCTCTCCGCGGTATCACCGACGCGTACGACGCGCAGGAT 300
DB 127 ValGlySerAspGlyArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGGACCTCGCTCCTCGACCGCGCGGACACCGTGGCTCAGATC 360
DB 147 TyrIleAlaLeuLysGluAspLeuArgSerTrrPThrAlaAlaAspMetAlaAlaGlnThr 166
QY 361 ACCAGCGCTTCTATGAGGACAGGAGGATATGACAGAGTTCAGGACCTACCTGGAGGCG 420
DB 167 ThrLysHisLysTrrPThrAlaHisGluAlaGlnTrrPArgAlaTyrLeuGluGly 186
QY 421 GAGTGCCTCGAGTGTCTCCGACAGATCTTGGAGATGGGAGGAGACGCTACACGCGGCA 480
DB 187 ThrCysValGluTrrPLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgThr 206
QY 481 GATCCTCCAAAGGCACACGTTGCCACACCCCATCTCTGACCATGAGGCGCACCTCGAGG 540
DB 207 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 226
QY 541 TGCTGGCCCTGGGCTCTACCTCGCGAGATACGCTGACCTGGCGAGCGGGATGGGAG 600
DB 227 CysTrrPalaLeuSerPheTyrProAlaGluLeuThrLeuThrTrrPThrGlnArgGlyGlu 246
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACACAGGCGCTCGAGG 645
DB 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261
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RESULT 9
US-08-481-985B-99
; Sequence 99, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-99

Alignment Scores:
Pred. No.: 2,74e-65 Length: 365
Score: 845.00 Matches: 156
Percent Similarity: 80.93% Conservative: 18
Best Local Similarity: 72.56% Mismatches: 41
Query Match: 71.43% Indels: 0
DB: 3 Gaps: 0

US-09-819-371-3 (1-645) x US-08-481-985B-99 (1-365)
QY 1 ATCGCCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCCGCGGATT 60
DB 47 IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAsaSer 66
QY 61 CGAGAGTGTAGCGCGGGAGCGGTGGTGGAGACAGAGGGCGGCGAGTATTCGGAGTGG 120
DB 67 GlnArgMetGluProArgAlaProTrrPileGlnGluGlyProGluTyrTrpAspGly 86
QY 121 ACCACSGGGTACGCCAAGGCCAAGCACACACTGACCGAGTGCCTCGAGGAACCTGCCTC 180
DB 87 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 106
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181 CGCCGCTACACAGAGCGAGCTGGTCTACSCCTCCAGGGAATGAATGGCTGCAC 240
107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetTyrGlyCysasp 126
241 ATGGGGCCCGAGGAGCGCTCTCCGCGGTATACACAGAGCGCTAGCGCAAGGAT 300
127 ValGlySerAspAlaArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysasp 146
301 TACATCTCCCTGACAGAGACCTGGCTCTCGAGCGCGCGGACACCGTGGCTCAGATC 360
147 TyrIleAlaLeuLysGlnAspLeuArgSerTrpThrAlaAlaAspMetAlaGlnThr 166
361 ACCACGCGTCTTATCAGGACAGAGGAATATGAGAGGAGTTCAGGACCTTACCTGGAGGC 420
167 ThrLysHisLysTrpGlnThrAlaHisGluAlaGluGlnTrpArgAlaTyrLeuGluGly 186
421 GAGTGGCTGGAGTGTCTCGCAGATCTTGGAGATGGGAAGAGACGCTACAGCGGCA 480
187 ThrCysValGlnTrpLeuArgArgTyrLeuGluAsnGlyLysGlnThrLeuGlnArgThr 206
481 GATCCTCCAAAGGCACACGTTGGCCACCCACCTCTGACCATGAGGCCACCTTGAGG 540
207 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 226
541 TGCTGGCCCTGGCTTACCTCGCGAGATCACGCTGACCTGAGCGGAGATGGGAG 600
227 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGCGCTGCAGG 645
247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

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RESULT 10

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US-08-370-476-99
; Sequence 99, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Castrouge, Armanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991

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; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-99
Alignment Scores:
Pred No.: 2,74e-65 Length: 365
Score: 845.00 Matches: 156
Percent Similarity: 80.93% Conservative: 18
Best Local Similarity: 72.56% Mismatches: 41
Query Match: 71.43% Indels: 0
DB: Gaps: 0
US-09-819-371-3 (11-645) x US-08-370-476-99 (1-365)
QY 1 ATCCGCGTGGAGTACGTAGACGACACGCAATCTCTGGCTTCGACAGCGCGCGCGGAT 60
Db 47 IleAlaValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaLaser 66
QY 61 CGAGGATGGAGCGCGGAGCGCTGGTGGTGGAGACAGAGGGCGCGAGTATTGGAGTGG 120
Db 57 GlnArgMetGluProArgAlaProTIPleGlnGluGlyProGluTyrTrpAspGly 86
QY 121 ACCACGCGGTACGCCAAGGCCACGACAGACTACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 87 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 106
QY 181 CGCGCTACACACAGAGCGAGGCTGGGTCTCACCCCTCCAGGGAATGAATGGCTGGAC 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetTyrGlyCysasp 126
QY 241 ATGGGGCCCGAGGAGCGCTCTCCGCGGTATACACAGAGCGCTAGCGCAAGGAT 300
Db 127 ValGlySerAspGlyArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysasp 146
QY 301 TACATCTCCCTGACAGAGACCTGGCTCTCGAGCGCGGACACCGTGGCTCAGATC 360
Db 147 TyrIleAlaLeuLysGlnAspLeuArgSerTrpThrAlaAlaAspMetAlaGlnThr 166
QY 361 ACCACGCGTCTTATGAGGACAGAGGAATATGAGAGGAGTTCAGGACCTTACCTGGAGGC 420
Db 167 ThrLysHisLysTrpGlnThrAlaHisGluAlaGluGlnTrpArgAlaTyrLeuGluGly 186
QY 421 GAGTGGCTGGAGTGTCTCGCAGATCTTGGAGATGGGAAGAGACGCTACAGCGGCA 480
Db 187 ThrCysValGlnTrpLeuArgArgTyrLeuGluAsnGlyLysGlnThrLeuGlnArgThr 206
QY 481 GATCCTCCAAAGGCACACGTTGGCCACCCACCTCTGACCATGAGGCCACCTTGAGG 540
Db 207 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 226
QY 541 TGCTGGCCCTGGCTTACCTCGCGAGATCACGCTGACCTGAGCGGAGATGGGAG 600
Db 227 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGCGCTGCAGG 645
Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

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RESULT 11

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US-08-484-905-107
; Sequence 107, Application US/08484905
; Patent No. 5976551

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GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-107

Alignment Scores:
Pred. No.: 3.11e-65 Length: 274
Score: 844.00 Matches: 157
Percent Similarity: 80.93% Conservative: 17
Best Local Similarity: 73.02% Mismatches: 41
Query Match: 71.34% Indels: 0
DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x US-08-484-905-107 (1-274)

QY 1 ATCCGCTGGAGTACGTAGACGACGCAATTCCTGGGTTGACAGCGCGCGGATT 60
Db 23 IleaValGlyTyrValAspThrGluPheValargPheAspSerAspAlaAsaSer 42
QY 61 CCGAGATGAGCGCGGAGCGCTGGTGAGCAAGCGGCGCGAGTATTCGGAGTGG 120
Db 43 ArgArgMetGluProArgAlaProTrpIleGluGlnGlyProGluTyrTrpAspGly 62
QY 121 ACCACGGGTACGCCAAGCCACGACACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 63 GluThrArgLysValLysAlaHisSerGluThrHisArgValAspLeuSerThrLeuArg 82
QY 181 CGCGCTACACACGAGAGCGCTGGGTCTCACCCCTCCAGGGAATGAATGGCTCGAC 240
Db 83 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysAsp 102

QY 241 ATGGGCGCCGAGCGAGCGCTCTCTCGCGGGTATCACAGACGCGGTAGCAGCGCAAGAT 300
Db 103 ValGlySerAspTrpArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 122
QY 301 TACATCTCCCTGACGAGGACTGCGCTCTGGACCGCGGCGGACACCGTGGCTCAGATC 360
Db 123 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 142
QY 361 ACCAGCGCTTCTATGAGCGAGAGATATCAGAGGAGTTCAGAGCCTACTCTGGAGGCG 420
Db 143 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnTrpArgAlaTyrLeuGluGly 162
QY 421 GAGTGGCTGGAGTTCCTCGGAGATACCTTGGAGATGGAGGAGACCTACAGCGCGCA 480
Db 163 ThrCysValGluTrpLeuArgTyrLeuGluGlnGlyLysGluThrLeuGlnArgThr 182
QY 481 GATCTCCAAAGGCGACAGCTTGCACACCCACCTCTGACCATGACAGGCGACCTGAGG 540
Db 183 AspAlaProLysThrHisMetThrHisAlaValSerAspHisGluAlaThrLeuArg 202
QY 541 TGCTGGCGCTGGCTTCTACCTGCGGAGATCAGCTGACCTGCGAGCGGATGGGAG 600
Db 203 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 222
QY 601 GAACAGACCCGAGCACAGAGCTTGTGGAGACCCAGCGCTGCGAGG 645
Db 223 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 237

RESULT 12
US-08-484-905-108
Sequence 108, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:

```

;
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 03-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-107
;
; Alignment Scores:
; Pred. No.: 3,11e-65 Length: 274
; Score: 844.00 Matches: 157
; Percent Similarity: 80.93% Conservative: 17
; Best Local Similarity: 73.02% Mismatches: 41
; Query Match: 71.34% Indels: 0
; DB: 3 Gaps: 0
;
; US-09-819-371-3 (1-645) x US-08-481-985B-107 (1-274)
;
; QY 1 ATCCCGCTGGAGTACGTAGACACGCAATCTCGCGTTCGACGAGCGCGCGGATT 60
; DB 23 IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAsp 42
; QY 61 CCGAGGATGAGCGCGCGGAGCCGCGTGGTGGAGCAGAGGCGCGCAGTATTGGAGTGG 120
; DB 43 ArgArgMetGluProArgAlaProTrpIleGluGlnGlyProGluTyrTrpAspGly 62
; QY 121 ACCACGGGTACGCAAGGCGCACACGACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 180
; DB 63 GluThrArgAsnValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 82
; QY 181 GCGCGCTACAAACAGAGGAGGCTGGTCTCAGCCCTCCAGGGAATGATGGTGGCAG 240
; DB 83 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysAsp 102
; QY 241 ATGGGCGCGCGAGCGAGCTCTCCGCGGGTATCACCAGCAGCGTACGACGCGCAAGGAT 300
; DB 103 ValGlySerAspTrpArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 122
; QY 301 TACATCTCCCTGAACAGAGGAGCTGGCTCTGGAGACCGCGCGGACACCGTGGCTCAGATC 360
; DB 123 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 142
; QY 361 ACCACGCTTCTATGAGCAGAGGATATGAGAGGAGTTCAGAGGAGTTCAGAGGAGG 420
; DB 143 ThrLysHisLysTrpGluAlaHisValAlaGluGlnTrpArgAlaTyrLeuGluGly 162
; QY 421 GAGTGGCTGGAGTGTCTCCGCGAGTACTTGGAGATGGGAGAGACGCTACAGCGCGCA 480
; DB 163 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgThr 182
; QY 481 GATCTCCAAAGCACACGTTGGCCACACCCCATCTCTGACATGAGGCGCACCGCTGAGG 540
; DB 183 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 202
; QY 541 TGCTGGCGCTGGCTCTACCTCGCGGAGATCACGCTGACCTGGCAGCGGAGTGGGAG 600
; DB 203 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 222
; QY 601 GAACAGACCCAGACACAGAGCTTGTGGAGACCGAGCCCTGGAGG 645
; DB 223 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 237
;
; RESULT 13
; US-08-481-985B-107
; Sequence 107, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourileky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &

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Db 143 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnTrpArgAlaTyrLeuGluGly 162
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RESULT 14
US-08-481-985B-108
; Sequence 108, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-108

Alignment Scores:
Pred. No.: 3,11e-65 Length: 274
Score: 844.00 Matches: 157
Percent Similarity: 80.93% Conservative: 17
Best Local Similarity: 73.02% Mismatches: 41

Query Match: 71.34% Indels: 0
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Qy 61 CCAGGATGAGCGCGGAGCCGTGGTGGAGCAAGAGGCGCGCGAGTATTGGAGTGG 120
Db 43 ArgArgMetGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAspGly 62
Qy 121 ACCACSGGTTACCCAAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 63 GluThrArgAsnValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg 92
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Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGCGCTGCAGGG 645
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RESULT 15
US-08-370-476-107
; Sequence 107, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ocius, David
; APPLICANT: Castrouge, Armanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Fri Jun 18 14:22:36 2004

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-107

Alignment Scores:
Pred. No.: 3,116-65 Length: 274
Score: 844.00 Matches: 157
Percent Similarity: 80.93% Conservative: 17
Best Local Similarity: 73.02% Mismatches: 41
Query Match: 71.34% Indels: 0
Gaps: 3

US-09-819-371-3 (1-645) x US-08-370-476-107 (1-274)

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Db	63	GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuSerThrLeuArg	82
QY	181	CGCCGCTACACACGAGCGAGGTGGTCTCACCCCTCCAGGGAATGAATGGCTCGAC	240
Db	83	GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysasp	102
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QY	421	GAGTGCCTGGAGTGTCTCCGAGATACCTTGGAGATGGAGAGACGCTTACAGCGCA	480
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QY	601	GAACAGACCCGACACAGAGCTTGTGGAGACACAGCCCTGCAGGG	645
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Job time : 21 secs

GenCore version 5.1.6
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Run on: June 18, 2004, 07:39:04 ; Search time 200 Seconds
(without alignments)
1820.923 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 2327084

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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No. Score Match Length DB ID Description

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2	1156	97.7	274	12	US-09-819-371-5	Sequence 5, Appli
3	1156	97.7	362	12	US-10-257-021-82	Sequence 82, Appl
4	1156	97.7	442	15	US-10-408-765A-1887	Sequence 1887, Ap
5	1151	97.3	215	12	US-09-819-371-6	Sequence 6, Appli
6	1149	97.1	362	12	US-09-819-371-4	Sequence 4, Appli
7	861	72.8	326	12	US-10-380-880-7	Sequence 7, Appli
8	851.5	72.0	379	12	US-10-210-172-160	Sequence 160, App
9	851.5	72.0	379	15	US-10-093-463-78	Sequence 78, Appl
10	844	71.3	364	15	US-10-093-463-80	Sequence 80, Appl
11	841	71.1	365	14	US-10-138-888-23	Sequence 23, Appl
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14	840	71.0	415	14	US-10-073-300-5	Sequence 5, Appli
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16	840	71.0	510	12	US-10-108-511-5	Sequence 5, Appli
17	824	69.7	371	12	US-10-210-172-156	Sequence 156, App
18	824	69.7	371	15	US-10-085-198-72	Sequence 72, Appl
19	820.5	69.4	256	12	US-10-108-511-2	Sequence 2, Appli
20	814	68.8	361	16	US-10-408-765A-247	Sequence 247, App
21	801	67.7	361	14	US-10-138-888-22	Sequence 22, Appl
22	784.5	66.3	452	12	US-10-210-172-152	Sequence 152, App
23	784.5	66.3	452	15	US-10-085-198-68	Sequence 68, Appl
24	763	64.5	421	12	US-10-210-172-174	Sequence 174, App
25	763	64.5	421	15	US-10-138-588-32	Sequence 32, Appl
26	755.5	63.9	289	15	US-10-085-198-70	Sequence 70, Appl
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31	725	61.3	542	14	US-10-015-535-32	Sequence 26, Appl
32	725	61.3	542	14	US-10-015-535-32	Sequence 32, Appl
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35	657	55.5	201	15	US-10-264-049-4199	Sequence 4199, Ap
36	624	52.7	284	15	US-10-104-047-3648	Sequence 3648, Ap
37	613	51.8	184	9	US-09-858-580-21	Sequence 21, Appl
38	613	51.8	184	10	US-09-847-172-21	Sequence 21, Appl
39	573	48.4	181	10	US-09-013-077A-13	Sequence 13, Appl
40	516	43.6	186	15	US-10-264-049-4063	Sequence 4063, Ap
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44	488	41.3	110	14	US-10-040-862-2139	Sequence 2139, App
45	488	41.3	110	15	US-10-057-475B-799	Sequence 799, App

ALIGNMENTS

RESULT 1
US-09-925-301-1431
; Sequence 1431, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1431
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1431

Alignment Scores: 2.72e-82 Length: 271
Pred. No.: 271

Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 9 Gaps: 0

US-09-819-371-3 (1-645) x US-09-925-301-1431 (1-271)

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RESULT 2

US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US2004005344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE OF INVENTION: Using thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-5

Alignment Scores: 2.72e-82 Length: 274
Pred. No.:

Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 12 Gaps: 0

US-09-819-371-3 (1-645) x US-09-819-371-5 (1-274)

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RESULT 3

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; GENERAL INFORMATION:
; APPLICANT: Morin, Patricia J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 362

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-021-82

Alignment Scores:

Pred. No.: 2,81e-82 Length: 362
Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 12 Gaps: 0

US-09-819-371-3 (1-645) x US-10-257-021-82 (1-362)

Qy 1 ATGCGCTGAGTACGTAGACGACGCAATTCCTGGGTTGACAGCCGCCCGCGATT 50
Db 44 ILEAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 63
Qy 61 CCGAGGATGAGCCGCGGAGCGGTGGTGGAGCAAGAGCGCGCGAGATTGGAGTGG 120
Db 64 ProArgMetGluProArgGluProTyrValGluGlnGlyProGlnTyrTrpGluTrp 83
Qy 121 ACCACSGGTACGCCAAGCCACGACGACACTGACGAGTGCCTGAGGAACTGCTC 180
Db 84 ThrThrGlyTyrAlaTyrAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 103
Qy 181 CGCGCTTACCAACAGAGCGGTGGTCTCACSCCTCCAGGGAATGAATGGCTGGC 240
Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
Qy 241 ATGGGGCCGACGACGACCCCTCCCGCGGTATCACACGACGCGCTACGACGCGC 300
Db 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
Qy 301 TACATCTCCCTGACGAGGACCTCGCTCTCGACCGCGCGGACACCTGGCTCAGATC 360
Db 144 TyrlleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGln 163
Qy 361 ACCCAGCGCTTATGAGGACGAGGAATATGAGAGAGTTACGACCTACCTGAGGCG 420
Db 164 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGlnGlyLysGlnGly 183
Qy 421 GAGTGCTGAGTGTCCGACAGTATGAGAGATGGGAGGAGAGCGCTACAGCGCGCA 480
Db 184 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGlnGlnArgAla 203
Qy 481 GATCCTCAAAGGACACGTTGCCACCCACCCATCTGACCATGAGCCACCTGAGG 540
Db 204 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 223
Qy 541 TGCTGGGCGCTTCTACCTCGCGAGATCACGCTGACCTGGCAGCGGATGGGAG 600
Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 243
Qy 601 GAACAGACCCAGGACAGAGCTTGTGGACACGACCGCTGCAGGG 645
Db 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258

RESULT 4

US-10-408-765A-1887
; Sequence 1887, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1887
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1887

Alignment Scores:

Pred. No.: 2,88e-82 Length: 442
Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 16 Gaps: 0

US-09-819-371-3 (1-645) x US-10-408-765A-1887 (1-442)

Qy 1 ATGCGCTGAGTACGTAGACGACGCAATTCCTGGGTTGACAGCCGCCCGCGATT 60
Db 44 ILEAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAla 63
Qy 61 CCGAGGATGAGCCGCGGAGCGGTGGTGGAGCAAGAGCGCGCGAGATTGGAGTGG 120
Db 64 ProArgMetGluProArgGluProTyrValGluGlnGlyProGlnTyrTrpGluTrp 83
Qy 121 ACCACSGGTACGCCAAGCCACGACGACACTGACGAGTGCCTGAGGAACTGCTC 180
Db 84 ThrThrGlyTyrAlaTyrAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 103
Qy 181 CGCGCTTACCAACAGAGCGGTGGTCTCACSCCTCCAGGGAATGAATGGCTGCAC 240
Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
Qy 241 ATGGGGCCGACGACGACCCCTCCCGCGGTATCACACGACGCGCTACGACGCGC 300
Db 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
Qy 301 TACATCTCCCTGACGAGGACCTCGCTCTCGACCGCGCGGACACCTGGCTCAGATC 360
Db 144 TyrlleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGln 163
Qy 361 ACCCAGCGCTTATGAGGACGAGGAATATGAGAGAGTTACGACCTACCTGAGGCG 420
Db 164 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGlnGlyLysGlnGly 183
Qy 421 GAGTGCTGAGTGTCCGACAGTATGAGAGATGGGAGGAGAGCGCTACAGCGCGCA 480
Db 184 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGlnGlnArgAla 203
Qy 481 GATCCTCAAAGGACACGTTGCCACCCACCCATCTGACCATGAGCCACCTGAGG 540
Db 204 AspProProLysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 223
Qy 541 TGCTGGGCGCTTCTACCTCGCGAGATCACGCTGACCTGGCAGCGGATGGGAG 600
Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 243
Qy 601 GAACAGACCCAGGACAGAGCTTGTGGACACGACCGCTGCAGGG 645
Db 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258

RESULT 5

US-09-819-371-6
; Sequence 6, Application US/09819371
; Publication No. US2004005344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815

; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-6

Alignment Scores:
Pred. No.: 6.52e-82 Length: 215
Score: 1151.00 Matches: 212
Percent Similarity: 99.07% Conservative: 1
Best Local Similarity: 98.60% Mismatches: 2
Query Match: 97.30% Indels: 0
DB: 12 Gaps: 0

US-09-819-371-3 (1-645) x US-09-819-371-6 (1-215)

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Qy 1 ATCCCGCTGAGTACGTAGACACGCAATTCCTCGGTTTCGACAGCCGCCCGCGATT 60
Db 1 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 20
Qy 61 CCGAGGATGAGCGCGGGAGCGTGGTGGACCAAGAGGGCGCGAGTATTGGAGAGGG 120
Db 21 ProArgMetGluProArgGluProTyrValGluGlnGlyProGlnTyrTrpGluTrp 40
Qy 121 ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 41 ThrThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 60
Qy 181 CGCGCTACACACAGACGAGGCTGGGTCTCACSCCTCCAGGGAATGATGCTGCGCAC 240
Db 61 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 80
Qy 241 ATGGGGCCGACGACGCCCTCTCCGGGTATACACAGACGCGTACACGCGCAAGGAT 300
Db 81 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 100
Qy 301 TACATCTCCCTGACAGGACCTGCGCTCTGACCGCGCGGACACCTGCTGCTCAGATC 360
Db 101 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 120
Qy 361 ACCAGCGCTTCTATGAGGACAGGAATATGACAGAGGTTTCAGGACCTACCTGAGGCG 420
Db 121 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 140
Qy 421 GAGTGCCTGAGTGTCTCCGACATCTTGGAGATGGGAAGGAGACGCTACAGCGCGCA 480
Db 141 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 160
Qy 481 GATCCTCCAAAGGCACACGTTGCCACCCACCTCTGACATGAGGCCACCTGAGG 540
Db 161 AspProGlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 180
Qy 541 TGTCTGGCCCTGGCTCTACCTCGGAGATCACCTGACCTGACCTGGCGAGGATGGGAG 600
Db 181 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 200
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACAGCCCTGCGAGG 645
Db 201 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 215
```

RESULT 6

US-09-819-371-4
; Sequence 4, Application US/09819371
; Publication No. US2004005344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; TITLE OF INVENTION: Using Thero2
; FILE REFERENCE: 30815

; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-4

Alignment Scores:
Pred. No.: 9.95e-82 Length: 362
Score: 1149.00 Matches: 212
Percent Similarity: 98.60% Conservative: 0
Best Local Similarity: 98.60% Mismatches: 3
Query Match: 97.13% Indels: 0
DB: 12 Gaps: 0

US-09-819-371-3 (1-645) x US-09-819-371-4 (1-362)

```
Qy 1 ATCCCGCTGAGTACGTAGACACGCAATTCCTCGGTTTCGACAGCCGCCCGCGATT 60
Db 44 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 63
Qy 61 CCGAGGATGAGCGCGGGAGCGTGGTGGACCAAGAGGGCGCGAGTATTGGAGAGGG 120
Db 64 ProArgMetGluProArgGluProTyrValGluGlnGlyProGlnTyrTrpGluTrp 83
Qy 121 ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 84 ThrThrGlyTyrAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
Qy 181 CGCGCTACACACAGACGAGGCTGGGTCTCACSCCTCCAGGGAATGATGCTGCGCAC 240
Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
Qy 241 ATGGGGCCGACGACGCCCTCTCCGGGTATACACAGACGCGTACACGCGCAAGGAT 300
Db 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTrpAspGlyLysAsp 143
Qy 301 TACATCTCCCTGACAGGACCTGCGCTCTGACCGCGCGGACACCTGCTGCTCAGATC 360
Db 144 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
Qy 361 ACCAGCGCTTCTATGAGGACAGGAATATGACAGAGGTTTCAGGACCTACCTGAGGCG 420
Db 164 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 183
Qy 421 GAGTGCCTGAGTGTCTCCGACATCTTGGAGATGGGAAGGAGACGCTACAGCGCGCA 480
Db 184 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLeuGluThrLeuGlnArgAla 203
Qy 481 GATCCTCCAAAGGCACACGTTGCCACCCACCTCTGACATGAGGCCACCTGAGG 540
Db 204 AspProGlyAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 223
Qy 541 TGTCTGGCCCTGGCTCTACCTCGGAGATCACCTGACCTGACCTGGCGAGGATGGGAG 600
Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACAGCCCTGCGAGG 645
Db 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258
```

RESULT 7

US-10-380-880-7
; Sequence 7, Application US/10380880
; Publication No. US20040044182A1
; GENERAL INFORMATION:
; APPLICANT: Hunt, Joan S.
; APPLICANT: Morales, Pedro J.
; APPLICANT: Petroff, Margaret G.
; TITLE OF INVENTION: EXPRESSION, PREPARATION, USES, AND SEQUENCE OF RECOMBINANTLY-DERI

```

; TITLE OF INVENTION: SOLUBLE HLA-G
; FILE REFERENCE: Docket No. US20040044182A1 30772
; CURRENT APPLICATION NUMBER: US/10/380.880
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/232,761
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-880-7

```

```

Alignment Scores:
Pred. No.: 3,75e-59 Length: 326
Score: 861.00 Matches: 160
Percent Similarity: 82.79% Conservative: 18
Best Local Similarity: 74.42% Mismatches: 37
Query Match: 72.78% Indels: 0
DB: 12 Gaps: 0

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US-09-819-371-3 (1-645) x US-10-380-880-7 (1-326)

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QY 1 ATCGCGTGGAGTACGACGACGCAATCTCGCGTTCGACAGCGCGCGCGATT 60
DB 54 IleaMetGlyTyrValAspThrGlnPheValArgPheAspSerAlaCys 73
QY 61 CGAGGATGGAGCCGCGGAGCGTGGGTGGAGCAAGAGGCGCGCAGTATTGGAGTGG 120
DB 74 ProArgMetGluProArgAlaProTrpValGluGlnGlyProGluTyrTrpGluGlu 93
QY 121 ACCAGGGGTACGCCAAGCCCAACGACAGTACGAGTGGCGCCCTGAGGAACCTGCTC 180
DB 94 GluThrArgAsnThrLysAlaHisAlaGlnThrAspArgMetAsnLeuGlnThrLeuArg 113
QY 181 CCGCGCTCAACACGACGAGCGAGCGTGGTCTCACSCCTCCAGGAATCAATGGTGCAC 240
DB 114 GlyTyrTrpAsnGlnSerGluAlaSerSerHisThrLeuGlnTrpMetIleGlyCysAsp 133
QY 241 ATGGGCGCGACGCGCGCTCTCCGCGGTATACACGACGCGTACGACGCGCGAGGAT 300
DB 134 LeuGlySerAspGlyArgLeuLeuArgGlyTyrGluGlnTyrAlaTyrAspGlyLysAsp 153
QY 301 TACATCTCCTCAACGACGACCTGCGTCTCGACCGCGGCGACACCGTGGTCCAGATC 360
DB 154 TyrLeuAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle 173
QY 361 ACCACGCGCTTCTATGAGCGACAGGAATATGACAGGAGTTCAGGACCTACCTGAGGCG 420
DB 174 SerLysArgLysCysGluAlaAlaAsnValAlaGluGlnArgAlaTyrLeuGluGly 193
QY 421 GAGTGGCTGGAGTGTCTCCGAGATCTTGGAGATGGAGAGGACGCTACAGCGCGCA 480
DB 194 ThrCysValGlnTrpLeuHisArgTyrLeuGluAsnGlyLysGluMetLeuGlnArgAla 213
QY 481 GATCTCTCAAGGACACCTTGGCCACCACTCCATCCATGACCATGAGGACCCCTGAGG 540
DB 214 AspProProLysThrHisValThrHisHisProValPheAspTyrGluAlaThrLeuArg 233
QY 541 TGTGGCGCGCTGGCTTACCTCGGAGATCAGCTGACCTGCGAGCGGATGGGAG 600
DB 234 CysTrpAlaLeuGlyPheTyrProAlaGluIleLeuThrTrpGlnArgAspGlyGlu 253
QY 601 GAACAGCCAGGACACGAGCTGTGGAGACCGAGCGCTGCGAGG 645
DB 254 AspGlnThrGlnAspValGluLeuValGluThrArgProAlaGly 268

```

RESULT 8

```

US-10-210-172-160
; Sequence 160, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zernusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Perenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalt, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: Curaseq1 version 0.1
; SEQ ID NO 160
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-160

```

```

Alignment Scores:
Pred. No.: 2.12e-58 Length: 379
Score: 851.50 Matches: 160
Percent Similarity: 81.65% Conservative: 18
Best Local Similarity: 73.39% Mismatches: 37
Query Match: 71.98% Indels: 3
DB: 12 Gaps: 1

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US-09-819-371-3 (1-645) x US-10-210-172-160 (1-379)


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QY 121 ACCACGGGTACGCCAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGTGTC 180
Db 87 GluThrArgAsnThrLysAlaHisAlaGlnThrAspArgMetAsnLeuGlnThrLeuArg 106
QY 181 CGCCGCTACAAACAGAGCCAGGCT-----GGTCTCACSCCCTCCAGGAATGAAT 231
Db 107 GlyTyrTyrAsnGlnSerGluGlyValGlyProGlySerHisThrLeuGlnTrpMetile 126
QY 232 GGTGCGACATGGGCGCCGACGAGACGCTCTCCGCGGGTATCACACAGACGCGTACGAC 291
Db 127 GlyCysAspLeuGlySerAspGlyArgLeuLeuArgGlyTyrGluGlnTyrAlaTyrAsp 146
QY 292 GGCAGGATATCATCTCCCTGACAGGACCTCGCTCTGACCGCCGCGCGGACACCGGTG 351
Db 147 GlyLysAspTyrLeuAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAla 166
QY 352 GGTACATCACCCAGCGCTCTTATGACGAGGAGGAATATGCAGAGAGTTCACGACCTAC 411
Db 167 AlaGlnIleSerLysArgLysCysGluAlaAlaAsnValAlaGluGlnArgAlaTyr 186
QY 412 CTGAGGGCGAGTGCCTGAGAGTTCCTCCGAGATCTTCCGAGAAATGGGAGAGAGGCTA 471
Db 187 LeuGluGlyThrCysValGluTrpLeuHisArgTyrLeuGluAsnGlyLysGluMetLeu 206
QY 472 CAGCGCGCAGATCTCCAAAGGCACACGCTTGCCACCCACCTCTCTGACCATGAGGCC 531
Db 207 GlnArgAlaAspProProlLysThrHisValThrHisHisProValPheAspTyrGluAla 226
QY 532 ACCTGAGGTGTCGGCCCTCGGCTTCTACCTCGCGGATACACGCTGACCTGGAGCGGG 591
Db 227 ThrLeuArgCysTrpAlaLeuGlyPheTyrProAlaGluIleLeuThrTrpGlnArg 246
QY 592 GATGGGGGGAACAGACCCAGGACACAGAGCTGTGAGACACGAGGCTCGAGG 645
Db 247 AspGlyGluAspGlnThrGlnAspValGluLeuValGluThrArgProAlaGly 264

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RESULT 10

```

US-10-093-463-80
; Sequence 80, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei-Luca
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Pena, Carol
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gorman, Linda
; APPLICANT: Spaderna, Steven
; APPLICANT: Voess, Edward
; APPLICANT: Malyankar, Uriel
; APPLICANT: Anderson, David
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypeptides
; TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.

```

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; FILE REFERENCE: 21402-290A (Cura 590AT)
; CURRENT APPLICATION NUMBER: US/10/093,463
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/283,675
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,101
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-80

Alignment Scores:
Pred. No.: 8,17e-58 Length: 364
Score: 844.00 Matches: 157
Percent Similarity: 83.26% Conservative: 22
Best Local Similarity: 73.02% Mismatches: 36
Query Match: 71.34% Indels: 0
DB: 15 Gaps: 0

US-09-819-371-3 (1-645) x US-10-093-463-80 (1-364)
QY 1 ATCGCGCTGGAGTACGTAGACGACACGCAATCTCTCGGTTCGACAGCGCCGCCGCAATT 60
Db 47 ileAlaValGlyTyrValAspAspThrGluPheValArgPheAspSerAspSerValser 66
QY 61 CCGAGGNTGGAGCCGCGGAGCGCGTGGGTGGAGCAAGAGCGCGCAGTATTGGGAGTGG 120
Db 67 ProArgMetGluArgArgAlaProTrpValGluGlnGluGlyLeuGlyTyrTrpAspGln 86
QY 121 ACCACGGGTACGCCAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGTGTC 180
Db 87 GluThrArgAsnThrLysAlaHisAlaGlnThrAspArgMetAsnLeuGlnThrLeuArg 106
QY 181 CGCCGCTACAAACAGAGCCAGGCT-----GGTCTCACSCCCTCCAGGAATGAAT 231
Db 107 GlyTyrTyrAsnGlnSerGluGlyValGlyProGlySerHisThrLeuGlnTrpMetile 126

```

QY 241 ATGGGGCCGACGAGCGCTCTCCGCGGTATACACGACGCGGTACGACGCGCAAGAT 300
Db 127 ValGlyProAspArgLeuLeuArgTyrGluGlnPheAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGACTGGCTCTCCGCGGTATACACGACGCGGTACGACGCGCAAGAT 360
Db 147 TyrIleAlaLeuAsnGluAspLeuHisSerTrpThrAlaAlaAsnThrAlaAlaGluLeu 166
QY 361 ACCACGCGCTTCTATGAGCGACAGGAATATGACGAGGAGTTCAGGACCTACCTGAGGCG 420
Db 167 SerGlnHisLysTrpGluAlaAspLysTyrSerGluGlnValArgAlaTyrLeuGluGly 186
QY 421 GAGTCGCTGAGTTCCTCCGCGGTATACACGACGCGGTATACACGACGCGGTATACACGCGCA 480
Db 187 LysCysMetGluTrpLeuArgHisLeuGluAsnGlyLysGluThrLeuGlnHisAla 206
QY 481 GATCTCTCCAAAGCGACACGCTTCCACACCGCCATCTCTGACCATGAGCGCCACCTGAGG 540
Db 207 AspProProLysAlaHisValThrGlnHisProlSerAspHisGluAlaThrLeuArg 226
QY 541 TGCTGGCGCTGGCTTCTCCGCGGTATACACGACGCGGTATACACGACGCGGTATACACGCGCA 600
Db 227 CysTrpAlaLeuGlyLeuTyrProAlaGluIleThrLeuThrTrpGlnGlnAspGlyGlu 246
QY 601 GAACAGACCCGACACGAGCTTGTGGAGACGAGCGCTGACGCGTGCAGGG 645
Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 11

US-10-138-888-23
Sequence 23, Application US/10138888
Publication No. US20030148972A1
GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/552,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..365
OTHER INFORMATION: /note= "Human Major Histocompatibility Class I (MHC) protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-138-888-23

Alignment Scores:
Pred. No.: 1,41e-57 Length: 365
Score: 841.00 Matches: 157
Percent Similarity: 80.47% Conservative: 42
Best Local Similarity: 73.02% Mismatches: 0
Query Match: 71.09% Indels: 0
DB: 14 Gaps: 0

US-09-819-371-3 (1-645) x US-10-138-888-23 (1-365)

QY 1 ATGCGCGTGGAGTACGTAGACGACGCAATCTCGGTTTCGACGCGCGCGGATT 60
Db 47 IleAlaValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
QY 61 CCGAGGATGAGCGCGGAGCGCGTGGTGGACAGAGCGCGCGGATTCGGAGTGG 120
Db 67 GlnArgMetGluProArgAlaProTrpIleGluGlnGlyProGluTyrTrpAspGly 86
QY 121 ACCACGCGTACGCGCAAGCGCAACGACGACGACGAGTGGCGCTGAGGAACTGCTC 180
Db 87 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuGlyThrLeuArg 106
QY 181 CGCGCTTACAAACGAGCGAGCGTGGTCTCACCSCCCTCCAGGGAATGATGCTCGGAC 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnMetMetPheGlyCysAsp 126
QY 241 ATGGGGCGCGACGCGCGCTCTCCGCGGTATACACGACGCGGTACGACGCGCAAGGAT 300
Db 127 ValGlySerAspTrpArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTCGGACGCGCGCGGACACCGTGGCTCAGATC 360
Db 147 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 166
QY 361 ACCACGCGTCTTATGAGCGACGAGGATATGACGAGGAGTTCAGGACCTACCTGAGGCG 420
Db 167 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
QY 421 GAGTGGCTGAGTTCCTCCGCGGTATACACGACGCGGTATACACGACGCGGTATACACGCGCA 480
Db 187 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgThr 206
QY 481 GATCTCTCCAAAGCGACACGCTTGTGGAGACGAGCGCTGACGCGTGCAGGG 540
Db 207 AspAlaProLysThrHisMetThrHisAlaValSerAspHisGluAlaThrLeuArg 226
QY 541 TGCTGGCGCTGGCTTCTCCGCGGTATACACGACGCGGTATACACGACGCGGTATACACGCGCA 600
Db 227 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
QY 601 GAACAGACCCGACACGAGCTTGTGGAGACGAGCGCTGACGCGTGCAGGG 645
Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 12
US-10-073-300-6
; Sequence 6, Application US/10073300

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; Publication No. US20030003535A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-073-300-6

Alignment Scores:
Pred. No.: 1.63e-57 Length: 280
Score: 840.00 Matches: 156
Percent Similarity: 80.47% Conservative: 17
Best Local Similarity: 72.56% Mismatches: 42
Query Match: 71.01% Indels: 0
DB: 14 Gaps: 0

US-09-819-371-3 (1-645) x US-10-073-300-6 (1-280)
QY 1 ATCGCGGTGAGTACGTAGACACGCAATTCCTCGGTTTCGACAGCGCGCGCGGATT 60
DB 23 IleaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAser 42
QY 61 CCGAGATGAGCCCGCGGAGCGGTGGTGAGCAAGAGGGCCCGCAGTATGGAGTGG 120
DB 43 GlnArgMetGluProArgAlaProTrrIleGluGlnGluGlyProGluTyrTrpAspGly 62
QY 121 ACCACGGGTACGCCAAGCCACACAGACTGACCGAGTGGCCCTCAGGAACCTGCTC 180
DB 63 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuGlyThrLeuArg 82
QY 181 CGCGCGTACACACAGCGAGCGTGGTCTCACSCCTCCAGGGAATGAATGGCTGCAC 240
DB 83 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetTyrGlyCysasp 102
QY 241 ATGGGGCCCGAGCGCGCTCTCCCGGGTATCACCAGCAGCGGTACGAGCGCAAGGAT 300
DB 103 ValGlySerAspTrpArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysasp 122
QY 301 TACATCTCCCTGAACAGACCTCGGCTCTCGAGCCGCGGACACCGTGGCTCAGATC 360
DB 123 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 142
QY 361 ACCACGCGTCTTATGAGCAGAGGAATATGACAGAGGTTTCAGGACCTACCTGGAGGC 420
DB 143 ThrLysHisLysTrpGluAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 162
QY 421 GAGTGCTGAGTTGCTCCGAGATACCTTGGAGAATGGGAAGAGACGCTACAGCGCGCA 480
DB 163 ThrCysValGluTrpLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgThr 182
QY 481 GATCTCCAAAGCACACGTTGCCACCCACCTCTGACCATGAGGCCACCTCAGG 540
DB 183 AspAlaProLysThrHisMetThrHisAlaValSerAspHisGluAlaThrLeuArg 202
QY 541 TCGTGGCCCTGGCTTCTACCTGCGGAGATCACGCTGACCTGGCAGCGGATGGGAG 600
DB 203 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 222
QY 601 GAACAGACCCAGCACAGAGCTTGTGGAGACCAGCGCTGCAGGG 645
DB 223 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 237

RESULT 13
US-10-073-257-6
; Sequence 5, Application US/10073300
; Publication No. US20030003535A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23338
; CURRENT APPLICATION NUMBER: US/10/075,257
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-075-257-6

Alignment Scores:
Pred. No.: 1.63e-57 Length: 280
Score: 840.00 Matches: 156
Percent Similarity: 80.47% Conservative: 17
Best Local Similarity: 72.56% Mismatches: 42
Query Match: 71.01% Indels: 0
DB: 16 Gaps: 0

US-09-819-371-3 (1-645) x US-10-075-257-6 (1-280)
QY 1 ATCGCGGTGAGTACGTAGACACGCAATTCCTCGGTTTCGACAGCGCGCGCGGATT 60
DB 23 IleaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAser 42
QY 61 CCGAGATGAGCCCGCGGAGCGGTGGTGAGCAAGAGGGCCCGCAGTATGGAGTGG 120
DB 43 GlnArgMetGluProArgAlaProTrrIleGluGlnGluGlyProGluTyrTrpAspGly 62
QY 121 ACCACGGGTACGCCAAGCCACACAGACTGACCGAGTGGCCCTCAGGAACCTGCTC 180
DB 63 GluThrArgLysValLysAlaHisSerGlnThrHisArgValAspLeuGlyThrLeuArg 82
QY 181 CGCGCGTACACACAGCGAGCGTGGTCTCACSCCTCCAGGGAATGAATGGCTGCAC 240
DB 83 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetTyrGlyCysasp 102
QY 241 ATGGGGCCCGAGCGCGCTCTCCCGGGTATCACCAGCAGCGGTACGAGCGCAAGGAT 300
DB 103 ValGlySerAspTrpArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysasp 122
QY 301 TACATCTCCCTGAACAGAGCCTCGGCTCTCGAGCCGCGGACACCGTGGCTCAGATC 360
DB 123 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaAlaGlnThr 142
QY 361 ACCACGCGTCTTATGAGCAGAGGAATATGACAGAGGTTTCAGGACCTACCTGGAGGC 420
DB 143 ThrLysHisLysTrpGluAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 162
QY 421 GAGTGCTGAGTTGCTCCGAGATACCTTGGAGAATGGGAAGAGACGCTACAGCGCGCA 480
DB 163 ThrCysValGluTrpLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgThr 182
QY 481 GATCTCCAAAGCACACGTTGCCACCCACCTCTGACCATGAGGCCACCTCAGG 540
DB 183 AspAlaProLysThrHisMetThrHisAlaValSerAspHisGluAlaThrLeuArg 202
QY 541 TCGTGGCCCTGGCTTCTACCTGCGGAGATCACGCTGACCTGGCAGCGGATGGGAG 600
DB 203 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 222
QY 601 GAACAGACCCAGCACAGAGCTTGTGGAGACCAGCGCTGCAGGG 645
DB 223 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 237

RESULT 14
US-10-073-300-5
; Sequence 5, Application US/10073300
; Publication No. US20030003535A1
```

; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent version 3.0
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human beta2 microglobulin linked to MHC class I heavy chain
US-10-073-300-5

Alignment Scores:
Pred. No.: 1,71e-57 Length: 415
Score: 840.00 Matches: 156
Percent Similarity: 80.47% Conservative: 17
Best Local Similarity: 72.56% Mismatches: 42
Query Match: 71.01% Indels: 0
DB: 14 Gaps: 0

US-09-819-371-3 (1-645) x US-10-073-300-5 (1-415)

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QY 1 ATCCGCGTGGAGTACGACACGCAATTCCTGCGGTTTCGACAGCGCGCGCGATT 60
Db 138 ILeAlaValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaLaser 157
QY 61 CCGAGGATGAGCCGCGGAGCGCTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 120
Db 158 GlnArgMetGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAspGly 177
QY 121 ACCAGGGTACGCAAGCCACGACAGCTGACCGAGTGGCGCTGAGGAACCTGCTC 180
Db 178 GluThrArgLysValIleHisSerGlnThrHisArgValAspGluGlyThrLeuArg 197
QY 181 CGCCGCTACACAGAGCGAGCTGCTCACSCCTCCAGGGAAATGAATGGCTCGAC 240
Db 198 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetTyrGlyCysAsp 217
QY 241 ATGGGGCCGCGAGCGCTCTCCGCGGTATCACCAGCGCGCTAGCGGCAAGGAT 300
Db 218 ValGlySerAspTrpArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 237
QY 301 TACATCTCCCTGAACAGAGGACCTCGCTCCGCGGTATCACCAGCGCGCTAGATC 360
Db 238 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaGlnThr 257
QY 361 ACCAGCGCTTCTATGAGGAGAGGAATATGACAGAGGATTCAGGACCTACCTGGAGGC 420
Db 258 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 277
QY 421 GAGTGCCTGAGTTGCTCCGAGATACTTGGAGATGGGAAGGAGAGCGCTACAGCGCGCA 480
Db 278 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgThr 297
QY 481 GATCCTCCAAAGGACACAGTTCGCCACCCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 298 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 317
QY 541 TGTGGGCGCTGGCTTCTACCTCGGAGATCAGCTGACCTGCGAGCGGGATGGGAG 600
Db 318 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 337
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGCGCTGCAGGG 645
Db 338 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 352
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RESULT 15
US-10-075-257-5
; Sequence 5, Application US/10075257

; Publication No. US20040086960A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
; FILE REFERENCE: 02/23338
; CURRENT APPLICATION NUMBER: US/10/075,257
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent version 3.2
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human beta2 microglobulin linked to MHC class I heavy chain
US-10-075-257-5

Alignment Scores:
Pred. No.: 1,71e-57 Length: 415
Score: 840.00 Matches: 156
Percent Similarity: 80.47% Conservative: 17
Best Local Similarity: 72.56% Mismatches: 42
Query Match: 71.01% Indels: 0
DB: 16 Gaps: 0

US-09-819-371-3 (1-645) x US-10-075-257-5 (1-415)

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QY 1 ATCCGCGTGGAGTACGACACGCAATTCCTGCGGTTTCGACAGCGCGCGCGATT 60
Db 138 ILeAlaValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaLaser 157
QY 61 CCGAGGATGAGCCGCGGAGCGCTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 120
Db 158 GlnArgMetGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAspGly 177
QY 121 ACCAGGGTACGCAAGCCACGACAGCTGACCGAGTGGCGCTGAGGAACCTGCTC 180
Db 178 GluThrArgLysValIleHisSerGlnThrHisArgValAspGluGlyThrLeuArg 197
QY 181 CGCCGCTACACAGAGCGAGCTGCTCACSCCTCCAGGGAAATGAATGGCTCGAC 240
Db 198 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrValGlnArgMetTyrGlyCysAsp 217
QY 241 ATGGGGCCGCGAGCGCTCTCCGCGGTATCACCAGCGCGCTAGCGGCAAGGAT 300
Db 218 ValGlySerAspTrpArgPheLeuArgGlyTyrHisGlnTyrAlaTyrAspGlyLysAsp 237
QY 301 TACATCTCCCTGAACAGAGGACCTCGCTCCGCGGTATCACCAGCGCGCTAGATC 360
Db 238 TyrIleAlaLeuLysGluAspLeuArgSerTrpThrAlaAlaAspMetAlaGlnThr 257
QY 361 ACCAGCGCTTCTATGAGGAGAGGAATATGACAGAGGATTCAGGACCTACCTGGAGGC 420
Db 258 ThrLysHisLysTrpGluAlaAlaHisValAlaGluGlnLeuArgAlaTyrLeuGluGly 277
QY 421 GAGTGCCTGAGTTGCTCCGAGATACTTGGAGATGGGAAGGAGAGCGCTACAGCGCGCA 480
Db 278 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgThr 297
QY 481 GATCCTCCAAAGGACACAGTTCGCCACCCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 298 AspAlaProLysThrHisMetThrHisHisAlaValSerAspHisGluAlaThrLeuArg 317
QY 541 TGTGGGCGCTGGCTTCTACCTCGGAGATCAGCTGACCTGCGAGCGGGATGGGAG 600
Db 318 CysTrpAlaLeuSerPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 337
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGCGCTGCAGGG 645
Db 338 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 352
```

Search completed: June 18, 2004, 07:54:25
Job time : 204 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 02:51:36 ; Search time 3002 Seconds
(without alignments)
9312.544 Million cell updates/sec

US-09-819-371-3
 Title: 645
 Perfect score: 645
 Sequence: 1 atcgccgtggagtagctaga.....tggagaccaggcctgcagg 645

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_lm.*
5: gb_ov.*
6: gb_pl.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	640.2	99.3	645	6	E63815	E63815	Cancer cell
2	640.2	99.3	645	6	AX522557	AX522557	Sequence
3	640.2	99.3	645	6	BD187423	BD187423	Cancer pr
4	640.2	99.3	822	6	E63814	E63814	Cancer cell
5	640.2	99.3	822	6	AX522556	AX522556	Sequence
6	640.2	99.3	822	6	BD187422	BD187422	Cancer pr
7	640.2	99.3	972	9	AY216582	AY216582	Homo sapi
8	640.2	99.3	1041	9	AY253369	AY253369	Homo sapi
9	640.2	99.3	1041	9	AY2533270	AY2533270	Homo sapi
10	640.2	99.3	1089	6	E63813	E63813	Cancer cell
11	640.2	99.3	1089	6	AX522555	AX522555	Sequence
12	640.2	99.3	1089	6	BD187421	BD187421	Cancer pr
13	640.2	99.3	1167	9	BC062991	BC062991	Homo sapi
14	640.2	99.3	1523	9	BC009360	BC009360	Homo sapi
15	640.2	99.3	298	9	AK096962	AK096962	Homo sapi
16	638.6	99.0	1372	9	AY221102	AY221102	Homo sapi
17	627.4	97.3	1158	9	CHMPHCBD	CHMPHCBD	Pan trogl
18	593.8	92.1	1056	9	MMELAPHOM	MMELAPHOM	M.mullatta H
19	526.6	81.6	1029	9	SORSMHSO3	SORSMHSO3	S.oedipus M
20	504.8	78.3	1052	9	AY204736	AY204736	Macaca ne
21	501.6	77.8	822	9	HSAA40716	HSAA40716	Homo sapi
22	500.6	77.6	1358	9	MMU41833	MMU41833	Macaca mula
23	500	77.5	1101	9	HSHLACW07	HSHLACW07	H.sapiens m
24	500	77.5	1468	9	AK024836	AK024836	Homo sapi
25	500	77.5	1570	9	BC033293	BC033293	Homo sapi
26	499	77.4	1065	9	AF243178	AF243178	Macaca mul
27	498.4	77.3	1065	9	HLU50091	HLU50091	Hylobates l
28	498.4	77.3	1100	9	MMU41832	MMU41832	Macaca mula
29	497.4	77.1	1098	9	AY282761	AY282761	Saimiri s
30	496.8	77.0	1064	9	AF157397	AF157397	Macaca mul
31	496.8	77.0	1088	9	AF118891	AF118891	Pongo pyg
32	496.8	77.0	1089	9	AF165363	AF165363	Pan trogl
33	496.6	77.0	1089	9	AF179648	AF179648	Pan trogl
34	496.6	77.0	1101	9	D38526	D38526	Human mR
35	496.8	77.0	1101	9	D49819	D49819	Human mR
36	496.8	77.0	1272	9	HSHLAB27X	HSHLAB27X	H.sapiens m
37	496.8	77.0	1413	9	HUNHJACFO	HUNHJACFO	H.sapiens m
38	496.8	77.0	1534	9	BC007814	BC007814	Human MHC c
39	495.8	76.9	999	9	AY204737	AY204737	Macaca ne
40	495.2	76.8	822	9	HUNHMB2	HUNHMB2	Human MHC c
41	495.2	76.8	1017	9	HUNHMC	HUNHMC	Human MHC c
42	495.2	76.8	1065	9	PPU50068	PPU50068	Pongo pygma
43	495.2	76.8	1084	9	HUNHMH2N1A	HUNHMH2N1A	Human MHC c
44	495.2	76.8	1089	9	AF026218	AF026218	Homo sapi
45	495.2	76.8	1325	9	MMU41825	MMU41825	Macaca mula

ALIGNMENTS

RESULT 1	
E63815	
LOCUS	645 bp DNA linear PAT 27-AUG-2002
DEFINITION	Cancer cell-specific HLA-F antigen and method for diagnosing cancer using the same.
ACCESSION	E63815
VERSION	E63815.1 GI:22553653
KEYWORDS	JP 2001095584-A/3.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 645)
AUTHORS	EGAWA, K.
TITLE	Cancer cell-specific HLA-F antigen and method for diagnosing cancer

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using the same
Patent: JP 2001095584-A 3 10-APR-2001;
KOJI EGAWA, KK MEDINET, KEIJI KIMURA
OS Homo sapiens (human)
PN JP 2001095584-A/3
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279566
PI KOJI EGAWA
PC
C12N15/09, C07K14/82, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/PC
02,
G01N33/53, G01N33/574, G01N33/68// (C12N1/21, C12R1:19), (C12P21/02, PC
C12R1:19);
PC C12N15/00, C12N5/00
CC
FH Key Location/Qualifiers.
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DB 1 ATGCGCGTGGAGTACCTAGACGACGCAATTCCTCGGTTTCGACGAGCCGCCGCGATT 60
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RESULT 2
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LOCUS
DEFINITION
Sequence 3 from Patent EP1245675.
ACCESSION
AX552557
VERSION
AX552557.1 GI:25896577
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
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Egawa, K.
Cancer cell-specific hla-f antigen and a diagnostic method of
Cancer by using thereof
Patent: EP 1245675-A 3 02-OCT-2002;
Egawa, Kohji (JP); Medinet Co., Ltd. (JP); Kimura, Yoshiji (JP)
JOURNAL
Location/Qualifiers
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    Best Local Similarity 99.5%; Pred. No. 1.9e-109;
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DB 421 GAGTGCCTGGAGTTGCTCCGAGATACCTGGAGATGGAGAGCGCTACAGCGCGCA 480
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DB 481 GATCTCTCAAAGGACACGTTGCCACCAACCCCATCTCTGACCATGAGGCCACCTGAGG 540
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DB 541 TGTGGGCCCTTGGGCTTCTACCTTGGGAGATCACGCTGACCTGGCAGCGGATGGGGAG 600
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DB 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGGCTTGCAGGG 645
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RESULT 3
BD187423
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS human
PN JP 2003012544-A/3
PD 15-JAN-2003
PF 27-MAR-2002 JP 2002088991
PI Koji egawa
CC
FH Key Location/Qualifiers.
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ORIGIN
Query Match 99.3%; Score 640.2; DB 6; Length 645;
Best Local Similarity 99.5%; Pred. No. 1.9e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATCCCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTTCACAGCGCGCGCGATT 60
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Db 361 ACCCAGCGCTCTATGAGGACAGGAATATGACAGAGGATTCAGGACCTACCTGGAGGC 420
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Db 601 GAACAGACCCAGGACACAGAGCTTGTGGACACAGGCGCTGCAGGG 645
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RESULT 4

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E63814
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2001095584-A/2
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279566
PI KOJI EGAWA
PC
C12N15/09, C07K14/82, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/ PC
02,
PC
G01N33/53, G01N33/574, G01N33/68// (C12N1/21, C12R1:19), (C12P21/02, PC
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PC C12N15/00, C12N5/00
CC
FH Key Location/Qualifiers.
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Best Local Similarity 99.5%; Pred. No. 1.8e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 61 CCGAGGATGAGCGCGGAGCGGTCGTGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGG 120
Db 127 CCGAGGATGAGCGCGGAGCGGTCGTGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGG 186
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Db 187 ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 246
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Qy 241 ATGGGGGCCGACGACGCGCTCTCCGCGGGTATCCACAGACGCGTACGACGCGCAAGGAT 300
Db 307 ATGGGGGCCGACGACGCGCTCTCCGCGGGTATCCACAGACGCGTACGACGCGCAAGGAT 366
Qy 301 TACATCTCCCTGACAGGACCTCGCTCTCGGAGATCACTGCTACCTGGGACCGGGATCGATC 360
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DB 667 GAACAGACCCAGGACACAGAGTTTGGAGACCCAGGCTTGAGGG 711

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DEFINITION Sequence 2 from Patent EP1245675.
ACCESSION AX552556
VERSION AX552556.1 GI:25896576
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Egawa,K.
TITLE Cancer cell-specific bla-f antigen and a diagnostic method of
JOURNAL Cancer by using thereof
Egawa, Kohji (JP) ; Medinet Co., Ltd. (JP) ; Kimura, Yoshiji (JP)
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Best Local Similarity 99.5%; Pred. No. 1.8e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 CCGAGGATGGAGCCGCGGAGCCGTGGTGAGCAAGAGGGCCGCGAGTATTGGAGTGG 120
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LOCUS BD187422 822 bp DNA linear PAT 17-JUL-2003
DEFINITION Cancer prophylactic/treatment agent.
ACCESSION BD187422
VERSION BD187422.1 GI:32997161
KEYWORDS JP 2003012544-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 822)
AUTHORS Egawa,K.
TITLE Cancer prophylactic/treatment agent
JOURNAL Patent: JP 2003012544-A 2 15-JAN-2003;
Egawa, K.
COMMENT OS human
PN JP 2003012544-A/2
PD 15-JAN-2003
PF 27-MAR-2002 JP 2002088991
PI koji egawa
CC
FH Key Location/Qualifiers.
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Best Local Similarity 99.5%; Pred. No. 1.8e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCGCGGTGAGTACGTAGACACAGCGCAATTCCTGCGGTTTCGACAGCGCCGCGGATT 60
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QY 61 CCGAGGATGGAGCCGCGGAGCCGTGGTGAGCAAGAGGGCCGCGAGTATTGGAGTGG 120
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Db 667 GAACAGACCCAGGACAGAGCTTGGGAGACCGGCTGACGG 711

RESULT 7
LOCUS AY216682 972 bp mRNA linear PRI 10-FEB-2003
DEFINITION Homo sapiens nonclassical MHC class I antigen (HLA-F) mRNA,
HLA-F*0101 variant allele, partial cds.

ACCESSION AY216682
VERSION
KEYWORDS
SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 972)
AUTHORS He, X., Xu, L., Liu, Y., and Zeng, Y.
TITLE Nonclassical MHC class I HLA-F
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 972)
AUTHORS He, X., Xu, L., Liu, Y., and Zeng, Y.
TITLE Direct Submission
JOURNAL Submitted (10-JAN-2003) Key Laboratory of Ministry of Education for
Tissue Transplantation and Immunology, Jinan University, Shipai,
Guangzhou, Guangdong 510632, China

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ORIGIN
Query Match 99.3%; Score 640.2; DB 9; Length 972;
Best local Similarity 99.5%; Pred. No. 1.8e-109;

Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 178 CCGAGGATGAGACGCGCGGAGCCGCTGGTGGAGCAAGAGGCGCGCAGTAGTATTGGAGTGG 237
QY 121 ACCACGCTGAGTACGCAAGGCGCAACGACACAGCTGACCGAGTGGCCCTGAGGACCTGCTC 180
Db 238 ACCACGCTGAGTACGCAAGGCGCAACGACACAGCTGACCGAGTGGCCCTGAGGACCTGCTC 297
QY 181 CCGCGCTACCAACAGAGCGAGGCTGGGTCTCAGSCCCTCCAGGGAATGAATGGTGGCGAC 240
Db 298 CCGCGCTACCAACAGAGCGAGGCTGGGTCTCAGACCCCTCCAGGGAATGAATGGTGGCGAC 357
QY 241 ATGGGCGCGGACGCGACCGCTCTCCGCGGGTATCACAGCACGGTACGACGCGCAAGGAT 300
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QY 301 TACATCTCCCTGAAACGAGGACCTCGCTCTCTGGAACGCGGCGGACACCGTGGCTCAGATC 360
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QY 361 ACCACGCTTCTATGAGGACAGGAATATGAGAGAGTTCAGGACCTTACCTGGAGGGC 420
Db 478 ACCACGCTTCTATGAGGACAGGAATATGAGAGAGTTCAGGACCTTACCTGGAGGGC 537
QY 421 GAGTGCTGGAGTGTCTCCGCGATACTTGGAGATGGGAAGACGCTACACGCGCA 480
Db 538 GAGTGCTGGAGTGTCTCCGCGATACTTGGAGATGGGAAGACGCTACACGCGCA 597
QY 481 GATCTCCAAAGCACAGCTTGGCCACACCCATCTCTGACCATGAGGCCACCTGAGG 540
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Db 718 GAACAGACCCAGGACAGAGCTTGGGAGACCGGCTGACGG 762

RESULT 8
LOCUS AY253269 1041 bp mRNA linear PRI 09-APR-2003
DEFINITION Homo sapiens MHC class Ib antigen (HLA-F) mRNA, HLA-F*0101 variant
1 allele, complete cds.

ACCESSION AY253269
VERSION AY253269.1 GI:29650890
KEYWORDS
SOURCE

ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1041)
AUTHORS He, X., Liu, Y., Xu, L., and Zeng, Y.
TITLE Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1041)
AUTHORS He, X., Liu, Y., Xu, L., and Zeng, Y.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-2003) Key Laboratory of Ministry of Education for
Tissue Transplantation and Immunology, Jinan University, Shipai,
Guangzhou, Guangdong 510632, China

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Best Local Similarity 99.5%; Pred. No. 1.7e-109;
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DB 250 ACCACAGGTACGCCAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 309
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DEFINITION Homo sapiens MHC class Ib antigen (HLA-F) mRNA, HLA-F*0101 variant
2 allele, complete cds.
ACCESSION AY253270
VERSION AY253270.1 GI:29650892
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1041)
AUTHORS He, X., Xu, L., Liu, Y. and Zeng, Y.
TITLE Cloning of full-length HLA-F*0101 variant 2 cDNA from Han Chinese
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1041)
AUTHORS He, X., Xu, L., Liu, Y. and Zeng, Y.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-2003) Key Laboratory of Ministry of Education for
Tissue Transplantation and Immunology, Jinan University, Shipai,
Guangzhou, Guangdong 510632, China
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ORIGIN
Query Match 99.3%; Score 640.2; DB 9; Length 1041;
Best Local Similarity 99.5%; Pred. No. 1.7e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTGACAGCGCCCGCGGATT 60
DB 130 ATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTGACAGCGCCCGCGGATT 189
QY 61 CCAGAGTGGAGCCCGGAGCCGTTGGTGGAGCAGAGGCGCGCAGTATGGAGTGG 120
DB 190 CCAGAGTGGAGCCCGGAGCCGTTGGTGGAGCAGAGGCGCGCAGTATGGAGTGG 249
QY 121 ACCACGGGTACGCCAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
DB 250 ACCACAGGTACGCCAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 309
QY 181 CGCCGCTCAACACGAGCGAGCTGGGTCTCACCCCTCCAGGGGAATGAATGGCTGCAC 240
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RESULT 10
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DEFINITION
E63813
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
PI
KOJI EGAWA
PC
C12N15/09, C07K14/82, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/ PC
Q2,
PC
G01N33/53, G01N33/574, G01N33/68// (C12N1/21, C12R1:19), (C12P21/02, PC
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Query Match 99.3%; Score 640.2; DB 6; Length 1089;
Best Local Similarity 99.5%; Pred. No. 1.7e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATCGCGGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTTCGACAGCGCGCGCGGATT 60

DB 130 ATCGCGGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTTCGACAGCGCGCGGATT 189
QY 61 CCGAGGATGAGCGCGGAGCGCGTGGTGGACAGAGAGGGCGGAGTATTGGGAGTGG 120
DB 190 CCGAGGATGAGCGCGGAGCGCGTGGTGGACAGAGAGGGCGGAGTATTGGGAGTGG 249
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DB 310 CGCGCTTACAAACGAGCGAGGCTGGTCTTCAAGCCCTCCAGGGATGAGTGGCTGGGAC 369
QY 241 ATGGGGCCGACGGAGCGCTCTCTCCGGGGTATCACCAGCAGCGCTACGACGGCAGGAT 300
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LOCUS
DEFINITION
Sequence 1 from Patent EP1245675.
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REFERENCE
AUTHORS
TITLE
JOURNAL
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Best Local Similarity 99.5%; Pred. No. 1.7e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATCGCGGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTTCGACAGCGCGCGCGGATT 60

Db	130	ATCGCGCTGGAGTACGTAGACACGCAATCTCTGGGTTTCAGACGACGCGCGGATT	189
Qy	61	CGAGGATGAGCGCGGGAGCGCTGGGTGGAGCAAGAGGGCCCGCAGTATTGGGAGTGG	120
Db	190	CGAGGATGAGCGCGGGAGCGCTGGGTGGAGCAAGAGGGCCCGCAGTATTGGGAGTGG	249
Qy	121	ACCAGGGGTACGCCAAGGCCAACACAGATGACGAGTGGCGCTGAGGAACTGGCTC	180
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DEFINITION
BD187421
VERSION
BD187421.1 GI:32997160
KEYWORDS
JP 2003012544-A/1.
SOURCE
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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Egawa, K.
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TITLE
JP 2003012544-A 1 15-JAN-2003;
JOURNAL
K EGAWA et al
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PN JP 2003012544-A/1
PD 15-JAN-2003
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CC
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Db	250	ACCACAGGGTACGCCAAGGCCAACACAGATGACGAGTGGCGCTGAGGAACTGGCTC	309	
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Qy	361	ACCAGCGCTTCTATGAGGCGAGGATATGAGAGGAGTTCAGGACCTTACCTGAGGCGC	420	
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Qy	421	GAGTCTCCAAAGGACACAGCTGGCGGACACCGCCATCTGACCATGAGGCGCACCCTGAGG	480	
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Qy	601	GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGGCTTGCAGGG	645	
Db	730	GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGGCTTGCAGGG	774	

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ACCESSION
BC062991
VERSION
BC062991.1 GI:38649062
KEYWORDS
MGC.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1167)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahney, J., Helton, E., Kettenan, M., Madan, A., Young, A.C., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalish, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 1167)
Strausberg, R.
Direct Submission
Submitted (01-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapps-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>
Series: IRAK Plate: 135 Row: O Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9665231.
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misc_feature

ORIGIN
Query Match 99.3%; Score 640.2; DB 9; Length 1167;
Best Local Similarity 99.5%; Pred. No. 1.7e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATCCCGTGGAGTACGTAGACGACACGCAATTCCTCGGTTTCACAGCGCGCGGCGATT 60
Db 134 ATCCCGTGGAGTACGTAGACGACACGCAATTCCTCGGTTTCACAGCGCGCGGCGATT 133
QY 61 CCGAGGATGAGCGCGGAGCGCTGGTGGAGCAAGAGGCGCGGCGAGTATTGGAGTGG 120
Db 194 CCGAGGATGAGCGCGGAGCGCTGGTGGAGCAAGAGGCGCGGCGAGTATTGGAGTGG 253
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QY 181 CGCGCTTACAAACACGAGCGAGGCTGGGTCTCACSCCCTCCAGGGAATGAATGGCTCGAC 240
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Db 674 TGCTGGGCGCTGGCTTCTACCTCGGAGATACGCTGACCTGGCGAGCGGATGGGGAG 733
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGCGCTGCAGG 645
Db 734 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGCGCTGCAGG 778

RESULT 14
BC009260
LOCUS
DEFINITION
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(CDNA clone IMAGE:4039990), partial cds.
ACCESSION
BC009260
VERSION
BC009260.2 GI:39644655
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1523)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raja, S.S., Iqbal, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahay, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1523)

Strausberg, R.

Direct Submission

Submitted (08-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

On Dec 9, 2003 this sequence version replaced gi:14349361.

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: DCTP/DTP/Gazdar

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

Contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 25 Row: n Column: 10

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9665231.

Location/Qualifiers

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/note="MHC_I; Region: Class I Histocompatibility antigen,

domains alpha 1 and 2"

/db_xref="CDD:pfam00129"

/gene="HLA-F"

/note="IGC; Region: Immunoglobulin domain constant region subfamily"

/db_xref="CDD:cd00098"

ORIGIN

Query Match 99.3%; Score 640.2; DB 9; Length 1523;

Best Local Similarity 99.5%; Pred. No. 1.6e-109;

Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCGCTGAGTACGTAGACGACGCAATTCCTCGGTTTCACAGCGCGCGCGAATT 60

Db 186 ATGCGCTGAGTACGTAGACGACGCAATTCCTCGGTTTCACAGCGCGCGCGAATT 245

QY 61 CCGAGGATGAGCGCGGAGCGCTGGTGGAGCAAGAGGGCGCGAGTATTGGGAGTGG 120

Db 246 CCGAGGATGAGCGCGGAGCGCTGGTGGAGCAAGAGGGCGCGAGTATTGGGAGTGG 305

QY 121 ACCACGGGTACCCCAAGGCCAACGACACGACGACGAGTGGCCCTGAGGAACCTGCTC 180

Db 306 ACCACGGGTACCCCAAGGCCAACGACACGACGACGAGTGGCCCTGAGGAACCTGCTC 365

QY 181 CGCGCTTACCAACAGAGCGAGGCTGGTCTTCACSCCCTCCAGGGAATGAATGCTGCGAC 240

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QY 241 ATGGGGCCCGACGAGCGCTTCCTCCGCGGTATCACACGACGCGCTACGACGCGCAAGGAT 300

Db 426 ATGGGGCCCGACGAGCGCTTCCTCCGCGGTATCACACGACGCGCTACGACGCGCAAGGAT 485

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Db 506 GAGTGCCTGAGTTCCTCCGAGATACCTTGGAGAAATGGGAAGGAGAGCGCTACAGCGCGCA 665

QY 481 GATCCTCAAGGACACAGTTCGCCACACCCCATCTCTGACCATGAGGACACCGCTGAGG 540

Db 666 GATCCTCAAGGACACAGTTCGCCACACCCCATCTCTGACCATGAGGACACCGCTGAGG 725

QY 541 TGCTGGGCGCTTCTACCTTGGCGAGATCACGCTGACCTGGCAGCGGATGGGAG 600

Db 726 TGCTGGGCGCTTCTACCTTGGCGAGATCACGCTGACCTGGCAGCGGATGGGAG 785

QY 601 GAACAGACCCAGGACACAGAGCTTTGTGGAGACCAAGGCGCTGCGAGG 645

Db 786 GAACAGACCCAGGACACAGAGCTTTGTGGAGACCAAGGCGCTGCGAGG 830

RESULT 15

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LOCUS

AK096962 2598 bp mRNA linear PRI 15-JUL-2002

DEFINITION Homo sapiens CDNA FLJ139643 fis, clone SMINT2004023, highly similar to HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F PRECURSOR.

ACCESSION AK096962

VERSION AK096962.1 GI:21756582

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,

misc_feature

Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Magatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2598)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
Location/Qualifiers
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/clone="SMINT2004023"
/tissue_type="small intestine"
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/note="cloning vector: pME18SFL3"

FEATURES
source

ORIGIN

Query Match 99.3%; Score 640.2; DB 9; Length 2598;
Best Local Similarity 99.5%; Pred. No. 1.5e-109;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCGCTGGAGTACGTAGACGACGCAATTCCTCGGTTTCACAGCGCGCGCGGATT 60
DB 160 ATGCGCTGGAGTACGTAGACGACGCAATTCCTCGGTTTCACAGCGCGCGCGGATT 219

QY 61 CCGAGGATGAGCGCGGAGCGCTGGTGGTGGAGAGGGGCGCGAGTATTGGGAGTGG 120
DB 220 CCGAGGATGAGCGCGGAGCGCGTGGTGGTGGAGAGGGGCGCGAGTATTGGGAGTGG 279

QY 121 ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
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QY 181 CGCGCTTACACACGAGGAGGCTGGTCTCAGCCCTCCAGGGGATGATGGCTCGAC 240
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QY 361 ACCCAGCGCTTCTATGAGGAGAGGAATATGACAGGAGTTTACAGGACCTACCTGGAGGGC 420
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QY 481 GATCCTCCAAAGGCACAGTTGCCACACCCCATCTCTGACCATGAGGCCACCTCAGG 540
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QY 601 GAAACAGACCCAGGACACAGAGCTTTGTGGAGACACAGGCGCTGACAGGG 645
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Job time : 3015 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 02:45:16 ; Search time 373 Seconds
(without alignments)
7345.080 Million cell updates/sec

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Perfect score: 645
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	640.2	99.3	645	4	Aah45557 Human can
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3	640.2	99.3	822	4	Aah45556 Human can
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7	510.8	79.2	1414	5	Aas93415 DNA encod
8	493.6	76.5	1026	1	Aan70935 Sequence
9	492	76.3	1221	6	Abz11440 Human pol
10	490.4	76.0	1571	7	Abx63576 Human cdn
11	487.2	75.5	1600	4	Aah98419 Human EST
12	487.2	75.5	4059	2	AAQ75974 pHLA-B7 e
13	486.6	75.4	1175	6	Abv99366 Human NOV
14	485.6	75.3	1101	2	Aaql2116 HLA-C exo
15	485.6	75.3	1271	6	AbL69369 Prostate
16	485.6	75.3	1377	7	Abx63563 Human cdn
17	485.6	75.3	4965	2	AaQ75973 pHLA-B7/b
18	483.4	74.9	1523	6	Abx83649 Human cdn
19	482.6	74.8	1073	5	Aah42223 Nucleotid
20	482.4	74.8	1089	2	AAQ12115 HLA-B35 e
21	480.8	74.5	1089	2	AAQ12114 HLA-Bw53
22	479.2	74.3	1101	2	AAQ12117 HLA-C exo
23	479.2	74.3	2225	6	Abz11436 Human pol

24	477.6	74.0	952	5	AAH42222
25	476	73.8	1086	2	AAQ01822
26	474.6	73.6	1554	4	AAI93004
27	474.4	73.6	1089	2	AAQ05693
28	474.4	73.6	1089	2	AAQ05701
29	473.8	73.5	1567	4	AAH98676
30	472.8	73.3	1086	2	AAQ01834
31	470.6	73.0	1080	6	ABK64554
32	470.6	73.0	1082	6	ABL70010
33	469	72.7	1170	7	AAAD54522
34	469	72.7	1530	7	AAAD54524
35	467.4	72.5	1098	5	AAQ07697
36	467.4	72.5	1098	7	ABZ57846
37	467.4	72.5	1284	2	AAV30457
38	467.4	72.5	1466	7	ABX63564
39	467.4	72.5	1526	7	ABX63561
40	465.8	72.2	1642	9	ADE07070
41	463.6	71.9	2225	6	ABZ11436
42	461	71.5	1063	5	AAH42221
43	460.6	71.4	1495	6	ABZ11434
44	454.8	70.5	1210	6	ABV99365
45	454.8	70.5	1210	9	ADE40253

ALIGNMENTS

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ID AAH45557 standard; DNA; 645 BP.
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AC AAH45557;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human cancer cell specific HLA-F antigen encoding DNA SEQ ID 3.
XX
KW HLA-F antigen; cancer cell specific; human; ds.
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OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..645
FT /tag= a
FT /partial
FT /product= "Cancer cell specific HLA-F antigen"
XX
PN JP2001095584-A.
XX
PD 10-APR-2001.
XX
PF 30-SEP-1999; 99JP-00279566.
XX
PR 30-SEP-1999; 99JP-00279566.
XX
PA (EGAW/) EGAWA K.
PA (MEDI-) MEDINET KK.
PA (KIMU/) KIMURA K.
XX
DR WPI; 2001-360493/38.
DR P-PSDB; AA646419.
XX
PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX
PS Claim 3; Page 9; 12pp; Japanese.
XX
CC This invention relates to a cancer cell specific HLA-F antigen. The
CC invention includes DNA encoding the antigen and a method for the
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC used in a method to diagnose cancer, in which the protein is used to
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC sequence represents DNA encoding the cancer cell-specific HLA-F antigen
CC of the invention

XX SQ Sequence 645 BP; 143 A; 194 C; 215 G; 93 T; 0 U; 0 Other;

Query Match 99.3%; Score 640.2; DB 4; Length 645;
 Best Local Similarity 99.5%; Pred. No. 3.2e-129; Indels 0; Gaps 0;
 Matches 642; Conservative 0; Mismatches 3;

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QY 361 ACCGAGCGCTTATGAGGCGAGAGGATATGACAGAGGTTACAGGACCTACCTGGAGGCG 420
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QY 421 GAGTGGCTGGAGTGTCTCCGACATCTTGGAGAATGGAGAGAGCGTACAGCGCGCA 480
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QY 481 GATCTCTCAAGGACACAGTGGCCACACCCCATCTCTGACCATGAGCGCCACCTGAGG 540
 Db 481 GATCTCTCAAGGACACAGTGGCCACACCCCATCTCTGACCATGAGCGCCACCTGAGG 540

QY 541 TGTGGCGCTGGGCTTCTACCTGGGAGATCACGCTGACCTGGCGAGCGGATGGGGAG 600
 Db 541 TGTGGCGCTGGGCTTCTACCTGGGAGATCACGCTGACCTGGCGAGCGGATGGGGAG 600

QY 601 GAACAGACCCAGGACACAGAGTGTGGAGACAGGCGCTGCAGG 645
 Db 601 GAACAGACCCAGGACACAGAGTGTGGAGACAGGCGCTGCAGG 645

RESULT 2
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 ID AAC78195 standard; cDNA; 816 BP.
 XX AC AAC78195;
 XX DT 08-FEB-2001 (first entry)
 XX DE Human cancer associated gene sequence SEQ ID NO:589.

XX Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;
 KW antidiabetic; antihypertensive; antihypertensive; antihypertensive;
 KW antiinflammatory; antihypertensive; antihypertensive; antihypertensive;
 KW dermatological; neuroprotective; thrombolytic; coagulant; neurotropic;
 KW vasotrophic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening; ss.

OS Homo sapiens.
 XX WO200005350-A1.
 XX 21-SEP-2000.
 PD 08-MAR-2000; 2000WO-US005882.
 PF 12-MAR-1999; 99US-0124270P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 XX WPI; 2000-587533/55.
 XX P-PSDB; AAB43986.
 DR Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer.
 PT Claim 1; Page 1111-1112; 2352pp; English.
 PS AAC77607 to AAC78448 encode the human cancer associated proteins given in
 CC AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnary; immunomodulator;
 CC antidiabetic; antihypertensive; antihypertensive; antihypertensive;
 CC antiinflammatory; antihypertensive; antihypertensive; antihypertensive;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC neotrophic; vasotrophic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention

SQ Sequence 816 BP; 165 A; 258 C; 268 G; 125 T; 0 U; 0 Other;

Query Match 99.3%; Score 640.2; DB 3; Length 816;
 Best Local Similarity 99.5%; Pred. No. 3.3e-129; Indels 0; Gaps 0;
 Matches 642; Conservative 0; Mismatches 3;

QY 1 ATGCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTTCGACAGCGCCCGCGATT 60
 Db 149 ATGCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTTCGACAGCGCCCGCGATT 208

QY 61 CCGAGATGAGCGCGCGGAGCGTGGTGGAGCAGAGAGGCGCGAGTATTGGAGTGG 120
 Db 209 CCGAGATGAGCGCGCGGAGCGTGGTGGAGCAGAGAGGCGCGAGTATTGGAGTGG 268

QY 121 ACCACGGGTACGCCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTCGAGGAACCTGCTC 328
 Db 269 ACCACGGGTACGCCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTCGAGGAACCTGCTC 328

QY 181 CGCGCGTACACACAGAGCGAGGCTGGTCTCAGSCCTTCAGGGAATGAATGGCTGCGAC 240
 Db 329 CGCGCGTACACACAGAGCGAGGCTGGTCTCAGSCCTTCAGGGAATGAATGGCTGCGAC 388

QY 241 ATGGGCGCGACGAGCGCTCTCCCGGGTATCACAGCAGCGGTACAGCGGCAAGGAT 300
 Db 389 ATGGGCGCGACGAGCGCTCTCCCGGGTATCACAGCAGCGGTACAGCGGCAAGGAT 448

QY 301 TACATCTCCGTAAACGAGGACCTGGCTCTTGAGACCGCGCGGACACCGTGGCTCAGATC 360
 Db 449 TACATCTCCGTAAACGAGGACCTGGCTCTTGAGACCGCGCGGACACCGTGGCTCAGATC 508

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QY	421	GAGTCCTCGAGTTGCTCCGCGAGATCTTGGAGATGGGAGAGAGCGCTACAGCGCGCA	480		
DB	569	GAGTCCTCGAGTTGCTCCGCGAGATCTTGGAGATGGGAGAGAGCGCTACAGCGCGCA	628		
QY	481	GATCCTCCAAAGGCACACGTTGTCGCCACACACCCCATCTCTGACCATGAGGCCACCTGAGG	540		
DB	629	GATCCTCCAAAGGCACACGTTGTCGCCACACACCCCATCTCTGACCATGAGGCCACCTGAGG	688		
QY	541	TGCTGGCCCTGGGCTTACCTCGCGAGATCACGCTGACCTGCGAGCGGGATGGGGAG	600		
DB	689	TGCTGGCCCTGGGCTTACCTCGCGAGATCACGCTGACCTGCGAGCGGGATGGGGAG	748		
QY	601	GAACAGACCCAGGACACAGAGTTTGTGAGACCCAGGCGCTGCAGGG	645		
DB	749	GAACAGACCCAGGACACAGAGTTTGTGAGACCCAGGCGCTGCAGGG	793		
RESULT 3					
AAH45556					
ID	AAH45556 standard; DNA; 822 BP.				
AC	AAH45556;				
CC					
DT	12-SEP-2001 (first entry)				
XX					
DE	Human cancer cell specific HLA-F antigen encoding DNA SEQ ID 2.				
XX					
KW	HLA-F antigen; cancer cell specific; human; ds.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
CDS		1..822			
FT		/*tag= a			
FT		/partial			
FT		/product= "Cancer cell specific HLA-F antigen"			
XX					
PN	JP2001095584-A.				
XX					
PD	10-APR-2001.				
XX					
PF	30-SEP-1999; 99JP-00279566.				
XX					
PR	30-SEP-1999; 99JP-00279566.				
XX					
PA	(EGAW/) EGAWA K.				
PA	(MEDI-) MEDINET KK.				
PA	(KIMU/) KIMURA K.				
XX					
WPI	2001-360493/38.				
DR	P-PSDB; AAG64618.				
XX					
PT	Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.				
XX					
PS	Claim 3; Page 9; 12pp; Japanese.				
XX					
CC	This invention relates to a cancer cell specific HLA-F antigen. The				
CC	invention includes DNA encoding the antigen, and a method for the				
CC	preparation of the cancer cell specific HLA-F antigen. The antigen may				
CC	be used in a method to diagnose cancer, in which the protein is used to				
CC	detect anti-HLA-F antibodies in bodily fluids of the patient. The present				
CC	sequence represents DNA encoding the cancer cell-specific HLA-F antigen				
XX					
SQ	Sequence 822 BP; 174 A; 250 C; 273 G; 125 T; 0 U; 0 Other;				

Query Match 99.3%; Score 640.2; DB 4; Length 822;
Best Local Similarity 99.5%; Pred. No. 3.3e-129;

[illegible]

30-SEP-1999; 99JP-00279566.
30-SEP-1999; 99JP-00279566.
(EGAW/) EGAWA K.
(MEDI-) MEDINET KK.
(KIMU/) KIMURA K.
WPI; 2001-360493/38.
P-PSDB; AAG64618.
Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer
Claim 3; Page 9; 12pp; Japanese.

XX This invention relates to a cancer cell specific HLA-F antigen. The
CC invention includes DNA encoding the antigen, and a method for the
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC used in a method to diagnose cancer, in which the protein is used to
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC sequence represents DNA encoding the cancer cell-specific HLA-F antigen
CC of the invention

Sequence 822 BP; 174 A; 250 C; 273 G; 125 T; 0 U; 0 Other;

Query Match	99.3%;	Score 640.2;	DB 4;	Length 822;
Best Local Similarity	99.5%;	Pred. No. 3.3e-129;		

Db 1177 ACCACAGGATACCCAAAGCCAAACGACAGATGACCGAGTGGCCCTGAGGAACCTGTC 1236
QY 181 CCGCGCTACAACACAGACGAGGCTGGTCTACSCCCTCCAGGGAATGAATGGCTGCGAC 240
Db 1237 CCGCGCTACAACACAGACGAGGCTGGTCTACACCCCTCCAGGGAATGAATGGCTGCGAC 1296
QY 241 ATGGGGCCGACGAGGAGCTCTCCCGGGTATCACCAGACGCTACGACGGCAAGAT 300
Db 1297 ATGGGGCCGACGAGGAGCTCTCCCGGGTATCACCAGACGCTACGACGGCAAGAT 1356
QY 301 TACATCTCCTGAACGAGGACCTGCGCTCTGAGACCGCGCGGACACCGTGGCTCAGATC 360
Db 1357 TACATCTCCTGAACGAGGACCTGCGCTCTGAGACCGCGCGGACACCGTGGCTCAGATC 1416
QY 361 ACCAGCGCTTATAGGACGAGGAATATGAGAGGAGTTCAGGACCTACCTGAGGGC 420
Db 1417 ACCAGCGCTTATAGGACGAGGAATATGAGAGGAGTTCAGGACCTACCTGAGGGC 1476
QY 421 GAGTGCCTGGAGTTGCTCCGAGATCTTGGAGATGGGAAGGAGACGCTACAGCGCGCA 480
Db 1477 GAGTGCCTGGAGTTGCTCCGAGATCTTGGAGATGGGAAGGAGACGCTACAGCGCGCA 1536
QY 481 GATCTCCAAAGGACACAGTTGCGCCACACCCCATCTTGACATGAGGCCACCTGAGG 540
Db 1537 GATCTCCAAAGGACACAGTTGCGCCACACCCCATCTTGACATGAGGCCACCTGAGG 1596
QY 541 TCGTGGCCCTGGCTTCTACCTGGGAGATCAGCTGACCTGGCAGCGGATGGGGAG 600
Db 1597 TCGTGGCCCTGGCTTCTACCTGGGAGATCAGCTGACCTGGCAGCGGATGGGGAG 1656
QY 601 GAAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCGCTGCAGGG 645
Db 1657 GAAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCGCTGCAGGG 1701

RESULT 6

AA590740
ID AA590740 standard; cDNA; 2037 BP.
XX
AC AA590740;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #26544.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDE; ABG26553.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics; forensics; gene mapping; identification of mutations
PT responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
PS Claim 1; SEQ ID NO 26544; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food imaging
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polynucleotide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA594564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2037 BP; 547 A; 511 C; 629 G; 350 T; 0 U; 0 Other;

Query Match 99.3%; Score 640.2; DB 5; Length 2037;

Best Local Similarity 99.5%; Pred. No. 3.6e-129;

Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCGCGCTGAGTACCTAGACGACACCAATCTCTGCGGTTCGACGCGCGCGCGGATT 60
Db 1060 ATCGCGCTGAGTACCTAGACGACACCAATCTCTGCGGTTCGACGCGCGCGGATT 1119
QY 61 CCGAGGATGAGCGCGCGGAGCCGCTGGGTGAGCAAGAGGGCGCGCGAGTATGGAGTGG 120
Db 1120 CCGAGGATGAGCGCGCGGAGCCGCTGGGTGAGCAAGAGGGCGCGCGAGTATGGAGTGG 1179
QY 121 ACCACGGGTACGCGCAAGCCCAACGACAGCTACCGAGTGGCGCTGAGGAACCTGCTC 180
Db 1180 ACCACGGGTACGCGCAAGCCCAACGACAGCTACCGAGTGGCGCTGAGGAACCTGCTC 1239
QY 181 CGCGCTACAACACAGAGCGAGGCTGGGTCTCACGCCCTCCAGGGAATGAATGGCTGGAC 240
Db 1240 CGCGCTACAACACAGAGCGAGGCTGGGTCTCACGCCCTCCAGGGAATGAATGGCTGGAC 1299
QY 241 ATGGGGCCGACGAGCGCTCTCCCGGGTATCACCAGACGCGGTACGACGGCAAGAT 300
Db 1300 ATGGGGCCGACGAGCGCTCTCCCGGGTATCACCAGACGCGGTACGACGGCAAGAT 1359
QY 301 TACATCTCCTGAACGAGGACCTGCGCTCTGAGACCGCGCGGACACCGTGGCTCAGATC 360
Db 1360 TACATCTCCTGAACGAGGACCTGCGCTCTGAGACCGCGCGGACACCGTGGCTCAGATC 1419
QY 361 ACCACGCGCTTCTATGAGGACAGGAATATGACAGGAGTTCAGGACCTACCTGGAGGGC 420
Db 1420 ACCACGCGCTTCTATGAGGACAGGAATATGACAGGAGTTCAGGACCTACCTGGAGGGC 1479
QY 421 GAGTGCCTGAGTTCCTCCGAGATACCTTGGAGATGGGAAGGAGACGCTACAGCGCGCA 480
Db 1480 GAGTGCCTGAGTTCCTCCGAGATACCTTGGAGATGGGAAGGAGACGCTACAGCGCGCA 1539
QY 481 GATCTCCAAAGGACACAGTTTGGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 1540 GATCTCCAAAGGACACAGTTTGGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 1599
QY 541 TCGTGGCCCTGGGCTTCTACCTGGGAGATCAGCTGACCTGGCAGCGGATGGGGAG 600
Db 1600 TCGTGGCCCTGGGCTTCTACCTGGGAGATCAGCTGACCTGGCAGCGGATGGGGAG 1659
QY 601 GAAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCGCTGCAGGG 645
Db 1660 GAAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCGCTGCAGGG 1704

RESULT 7
 ID AAS93415/c
 XX AAS93415 standard; cDNA; 1414 BP.
 AC AAS93415;
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #29219.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG29228.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 29219; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1414 BP; 232 A; 469 C; 359 G; 354 T; 0 U; 0 Other;
 Query Match 79.2%; Score 510.8; DB 5; Length 1414;
 Best Local Similarity 87.9%; Pred. No. 3.4e-101;
 Matches 568; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
 QY 1 ATGCGCTGGAGTACGTAGACGACGCAATTCCTGGGTTCCAGACGCGCGCGGAT 60
 DB 914 ATGCGCTGGAGTACGTAGACGACGCAATTCCTGGGTTCCAGACGCGCGGAT 855
 QY 61 CGAGGATGAGCGCGCGGAGCCGTGGGTGGAGACAGAGCGCGCGGATTTGGAGTGG 120

DB 854 CCAGGATGGAGCGCGGGAGCCGTGGGTGGAGACAGAGCGGCGCCAGATTATGGGAGTGG 795
 QY 121 ACCACGGGTACCCCAAGGCCAAGCAGACAGACTGACCGAGTGGCCCTGAGAGACCTGCTC 180
 DB 794 ACCACAGGGTACGCCAAGGCCCGCGGGTGGGCGGGAGGGGGCGGCTAGCTGCTC 735
 QY 181 CGCGCTTACAAACAGAGCGAGGCT-GGGTCTCACSCCTCCAGGGAATGAATGGCTGCGA 239
 DB 734 CGCGCTGACTGGGGGACCGGCTAGGGTCTCACCTCCAGGGAATGAATGGCTGCGA 675
 QY 240 CATGGGCGCGACGCGCTCTCTCCGCGGTATACACGACGCGTACGACGGCAAGGA 299
 DB 674 CATGGGCGCGACGCGCTCTCTCCGCGGTATACACGACGCGTACGACGGCAAGGA 615
 QY 300 TTACATCTCCCTGAACGAGGACCTGCGCTCTCGACCGCGGGGACACCGTGGCTCAGAT 359
 DB 614 TTACATCTCCCTGAACGAGGACCTGCGCTCTCGACCGCGGGGACACCGTGGCTCAGAT 555
 QY 360 CACCCAGCGCTTCTATGAGGACAGGAATATGAGAGGAGTTGAGACCTTACCTGAGGG 419
 DB 554 CACCCAGCGCTTCTATGAGGACAGGAATATGAGAGGAGTTGAGACCTTACCTGAGGA 495
 QY 420 CGAGTGCCTGGAGTGTCTCCGACAGACTTGGAGAGTGGAGAGACGCTACAGCGCG 479
 DB 494 TGGGTGCTGCTGGGTTTCCATGAGAGTGCAGAGTGCCTGAATTTCTGACTCTTCTC 435
 QY 480 AGATCTCTCCAAAGGCACACGTTGCCACCAACCCCATCTCTGACCATGAGGCCACCTGAG 539
 DB 434 AGATCTCTCCAAAGGCACACGTTGCCACCAACCCCATCTCTGACCATGAGGCCACCTGAG 375
 QY 540 GTGCTGGCGCTGGGCTTCTACCTGCGGAGATCAAGCTGACCTGGCAGCGGATGGGA 599
 DB 374 GTGCTGGCGCTGGGCTTCTACCTGCGGAGATCAAGCTGACCTGGCAGCGGATGGGA 315
 QY 600 GGAACAGACCCAGGACACAGAGCTTGTGGAGACGAGGCTGACAGG 645
 DB 314 GGAACAGACCCAGGACACAGAGCTTGTGGAGACGAGGCTGACAGG 269

RESULT 8
 AAN70935
 ID AAN70935 standard; DNA; 1026 BP.
 XX AAN70935;
 AC AAN70935;
 DT 10-APR-1991 (first entry)
 XX
 DE Sequence encoding the human histocompatibility antigen HLA B27.
 XX
 KW Rheumatic disorder; genetic screening; diagnosis; ankylosing spondylitis;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1026
 XX
 FN DE3542024-A.
 XX
 PD 04-JUN-1987.
 XX
 PF 28-NOV-1985; 85DE-03542024.
 XX
 PR 21-DEC-1985; 85DE-03545576.
 XX
 PA (BEHW) BEHRINGERWERKE AG.
 XX
 PI Riethmülle G, Moe T, Weiss E, Szots H;
 XX
 DR WPI; 1987-157893/23.
 DR P-PSDB; AAP70590.
 XX
 PT DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA,

PT antigen or antibody.
 XX Claim 2; Page 4; 5pp; German.
 CC The DNA may be used as a hybridisation probe for detecting the HLA B27
 CC gene, e.g. for assessing susceptibility to rheumatic disorders such as
 CC ankylosis spondylitis, or may be used to transform cells for prodn. of
 CC HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human
 CC serum, or to produce mono- or polyclonal HLA B27 antibodies for use in
 CC immunoassay
 XX
 SQ Sequence 1026 BP; 213 A; 307 C; 344 G; 162 T; 0 U; 0 Other;
 Query Match 76.5%; Score 493.6; DB 1; Length 1026;
 Best Local Similarity 85.4%; Pred. No. 1.7e-97;
 Matches 550; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
 QY 1 ATCGCGGTGAGTACGTAGACGACGCAATTCCTCGGTTGACAGCGCCCGCGGATT 60
 Db 67 ATCACCGTGGCTACGTGACGACGCGCTGTTGTTGAGGTTGACAGCGACCGCGGATT 126
 QY 61 CCGAGGATGAGCGCGGGAGCGTGGTGGAGCAAGAGGGCGGAGATTGGGAGTGG 120
 Db 127 CCGAGAGAGGAGCGCGGGCGCGTGGTAGACAGAGGGCGGAGATTGGGAGCGG 186
 QY 121 ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
 Db 187 GAGACACAGATCTTCAAGGCCAAGGCACAGACTGACCGAGAGACCTGGGACCTGCTC 246
 QY 181 CGCGGCTAACACAGAGCGGCTGGTCTACSCCCTCCAGGAGTGAATGGCTCGAC 240
 Db 247 CGCTACTACCAACAGAGCGAGGCGGGTCTCACACCTTCAGAAATATGATGGCTCGAC 306
 QY 241 ATGGGGCCGACGAGCGCTCTCCGCGGTATCACGACGCGTACGACGCGCAAGGAT 300
 Db 307 GTGGGCGGACGCGGCGCTCTCCGCGGTATCACGACGCGTACGACGCGCAAGGAT 366
 QY 301 TACATCTCCCTGAACGAGGACCTGGCTCTCGGACCGCGCGGACACCGTGGCTCAGATC 360
 Db 367 TACATCGCCCTGAACGAGGACCTGGCTCTCGGACCGCGCGGACACCGGCGGCTCAGATC 426
 QY 361 ACCAGCGCTTCTATGAGGAGAGGAATATGACAGAGGTTTCAGGACCTACCTGGAGGGC 420
 Db 427 ACCAGCGCAAGTGGAGGCGGCGCGTGTGGAGCAGCTGAGAGCTTACCTGGAGGGC 486
 QY 421 GAGTGTGAGTGTCTCCGAGATCTTGGAGAAATGGGAGGAGACGCTTACAGCGCGCA 480
 Db 487 GAGTGTGAGTGTCTCCGAGATCTTGGAGAAATGGGAGGAGACGCTTACAGCGCGTG 546
 QY 481 GATCCTCAAGGACACGCTTGGCCACCCATCTCTGACCATGAGCCACCTGAGG 540
 Db 547 GACCCCGCAAGACACACGCTGACCCACCCATCTCTGACCATGAGGCGCCCTGAGG 606
 QY 541 TGCTGGCCCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGGCAGCGGATGGGGAG 600
 Db 607 TGCTGGCCCTGGGCTTCTACCTGCGGAGATCACATGACCTGGCAGCGGATGGCGAG 666
 QY 601 GAACAGACCCAGGACACAGAGCTTGGAGAACACGAGCGCTGAGG 644
 Db 667 GACCAAACTCAGGACACTGAGCTTGTGGAGACCAAGACCAAGCAGG 710
 RESULT 9
 ABZ11440
 ID ABZ11440 standard; cDNA; 1221 BP.
 XX
 AC ABZ11440;
 XX
 DT 20-JAN-2003 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 322.
 XX
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;

KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
 XX antiarthritic; gene; ss.
 OS Homo sapiens.
 XX
 PN WO200270539-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 05-MAR-2002; 2002WO-US005095.
 XX
 PR 05-MAR-2001; 2001US-00799451.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 DR WPI; 2002-759812/82.
 DR P-PSDB; ABP69223.
 XX
 PT New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX
 PS Claim 1; SEQ ID NO 322; 1012pp + Sequence Listing; English.
 CC
 CC The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12056) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burn, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ffp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1221 BP; 242 A; 373 C; 419 G; 187 T; 0 U; 0 Other;
 Query Match 76.3%; Score 492; DB 6; Length 1221;
 Best Local Similarity 85.2%; Pred. No. 3.9e-97;
 Matches 549; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
 QY 1 ATCGCGGTGAGTACGTAGACGACGCAATTCCTCGGTTGACAGCGCCCGCGGATT 60
 Db 267 ATCTCAGTGGGCTACGTGACGCGCACCCAGTTCGTGAGTTTCGACAGCAGCCCGGAGT 326
 QY 61 CCGAGGATGAGCGCGCGGAGCCGTTGGTGGAGCAAGAGGGCGCGAGTATTGGAGTGG 120
 Db 327 CCGAGGACGAGCGCGCGCGCGCTGGATAGAGCAAGAGGGCGCGAGTATTGGAGCGG 386
 QY 121 ACCAGSGGTAGCCAGGCGCAACCGACAGACTACCGAGTGGCCCTGAGGAACCTGCTC 180
 Db 387 AACACACAGATCTCCAGACCAACACACAGACTTACCGAGAGGACCTCGGACCCCTGCTC 446
 QY 181 CGCCGCTACACAGAGCGAGGCTGGGTCTCACSCCTCCAGGGGAATGAATGGCTGCGAC 240
 Db 447 CGCTACTACACAGAGCGAGGCGGGTCTCACACCATCCAGAGGATGCTGGCTGCGAC 506

241	ATGGGGCCCGACGGACGGCTCTCTCGCGGGTATCACACAGACACGGGTACAGACGGCAGGAT	300
Qy		
507	GTGGGGCCCGACGGCGCGCTCTCTCGCGGGTATTAACCAAGTTCCGCTACGACGGCAAGGAT	566
Db		
301	TACATCTCCCTCAACAGAGGACCTGCGCTCTCTGGACCGCGCGACACCGTGGCTCAGATC	360
Qy		
567	TACATGCCCCGAAACAGAGGACCTGAGCTCTCTGGACCGCGCGGAGACACCGCGGCTCAGATC	626
Db		
361	ACCACGCGCTTCTATGAGCGACAGAGAAATATGACAGAGGAGTTCAGGACCTACCTGGAGGCG	420
Qy		
627	ACCCAGCGCAAGTGGGAGGCGGCCCGTGTGCGGAGCAGGACAGAGCTACTCTGGAGGCG	686
Db		
421	GAGTGCCTGGAGTTGCTCGGCAGATACTTGGAGAAATGGGAGAGAGACGCTTACAGCGCGCA	480
Qy		
687	ACGTGCGTGGAGTGGCTCCGACAGTACCTGGAGAACGGGAGGAGACGCTGTACAGCGCG	746
Db		
481	GATCTCTCAAAAGGACACAGTTTGCCACCAACCCCATCTCTGACCATGAGGCCACCTCTGAGG	540
Qy		
747	GACCCCCCAAGACACATGTGACCAACACCCCATCTCTGACCATGAGGCCACCTCTGAGG	806
Db		
541	TGCTGGGGCCCTGGGCTTCTACCTCGCGGAGATCACTGCTACCTGGCAGCGGAGTGGGGAG	600
Qy		
807	TGCTGGGGCCCTGGGCTTCTACCTCGCGGAGATCACCTGACCTGGCAGCGGAGTGGCGAG	866
Db		
601	GAAACAGCCGAGACACAGAGCTTGTGAGACCAAGCGGCTGGCAGG	644
Qy		
867	GACCAAACTTCAGGACACCGAGGTTTGTGAGACCAAGCCAGCAGG	910
Db		

RESULT 10	
ABX63576	
ID	ABX63576 standard; cDNA; 1571 BP.
XX	
XX	AC
XX	ABX63576;
XX	
XX	26-FEB-2003 (first entry)
DT	
XX	
DE	Human cDNA #576 differentially expressed in activated vascular tissue.
XX	
XX	Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
KW	hypertensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;
KW	gene therapy; vascular disease; cancer; coronary; artery disease;
KW	hypertension; diabetes; pre-eclampsia; restenosis;
KW	ischaemia-reperfusion injury; stroke.
XX	
XX	
OS	Homo sapiens.
XX	
XX	US2002137081-A1.
PN	
XX	
PD	26-SEP-2002.
XX	
XX	08-JAN-2002; 2002US-00044090.
PF	
XX	
XX	28-JUL-2000; 2000US-0222469P.
PR	
XX	08-JAN-2001; 2001US-0260483P.
XX	
XX	
PA	(BAND/) BANDMAN O.
XX	
XX	Bandman O;
PI	
XX	
DR	WPI; 2003-110597/10.
XX	
XX	Combination for diagnosing, staging, treating, or monitoring the
PT	progression of treatment of a vascular disease, e.g. atherosclerosis,
PT	comprises several cDNAs that are differentially expressed in activated
PT	vascular tissue.
XX	
XX	
PS	Claim 1; Page; 18pp; English.
XX	
XX	This invention relates to a combination comprising several cDNAs that are
CC	differentially expressed in activated vascular tissue. The invention also
CC	discloses a high throughput method for detecting differentially expressed
CC	cDNAs in a sample. The cDNAs of the invention may have

CC antiarteriosclerotic, cytostatic; cardiant; hypotensive; antidiabetic;
CC gynaecological, vasotropic and cerebroprotective activities and may be
CC used in gene therapy. The cDNAs of the invention may be used in a high-
CC throughput methods for detecting differential expression of one or more
CC cDNAs in a sample, or screening several molecules or compounds to
CC identify a molecule or compound that specifically binds a cDNA of the
CC invention. A protein encoded by the cDNA may be used to screen several
CC molecules or compounds to identify a ligand that specifically binds to
CC the protein, or to produce or purify an antibody to the protein that can
CC be used to detect a protein in a sample or purify a natural or
CC recombinant protein from a sample. The nucleotides may be useful for
CC diagnosing, staging, treating, or monitoring the progression of treatment
CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery
CC disease, hypertension, diabetes, pre-eclampsia, ischaemia- reperfusion
CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale
CC genetic or gene expression analysis of several new nucleic acid
CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for
CC diagnosing pre-pathologic disorders, and chronic or acute diseases
CC associated with abnormalities in the expression, amount or distribution
CC of the protein. The present sequence represents a cDNA of the invention
CC that is differentially expressed in activated vascular tissue. Note: The
CC sequence data for this patent did not form part of the specification, but
CC was obtained in electronic format directly from USPTO at
CC <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>
XX
SQ Sequence 1571 BP: 345 A; 450 C; 470 G; 305 T; 0 U; 1 Other;

Db 778 GACCAAACTCAGACACTGAGCTTGTGGAGACCAGACGAGG 821

RESULT 11

AAH98419
ID AAH98419 standard; cDNA; 1600 BP.

XX AC
XX AAH98419;

DT 12-OCT-2001 (first entry)

DE Human EST-derived coding sequence SEQ ID NO: 276.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

KW gene therapy; nutrition; ss.

XX Homo sapiens.

OS

XX WO200154477-A2.

PN

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002687.

XX 25-JAN-2000; 2000US-00491404.

PR 17-JUL-2000; 2000US-00617746.

PR 03-AUG-2000; 2000US-00631451.

PR 15-SEP-2000; 2000US-00663870.

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI: 2001-476164/51.

DR F-PDDB; AAH23760.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use.

PT Claim 1; Page 391; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)

CC from the organism of interest. They can be used in diagnostics,

CC forensics, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a cDNA

CC of the invention

XX

SQ Sequence 1600 BP; 348 A; 456 C; 480 G; 316 T; 0 U; 0 Other;

XX

Query Match 75.5%; Score 487.2; DB 4; Length 1600;

Best Local Similarity 84.8%; Pred. No. 4.3e-96;

Matches 546; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

XX

QY 1 ATCGCGGTGAGTACGACGACGCAATTCCTGGTTTCGACAGCGCCCGCGATT 60

Db 144 ATCTCAGTGGGTACCTGGTACGACACCCAGTTCGTGAGTTCGACAGCGCCCGGAGT 203

QY 61 CCAGGATGAGCGCGGGGCGGTGGTGGAGAGGCGCGCGAGTATTGGAGTGG 120

Db 204 CCAGAGAGAGCGCGGGCGCGGTGGTGGAGAGGCGCGCGAGTATTGGAGCGG 263

QY 121 ACCACGGGTACGCCAAGGCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180

Db 264 AACACACAGACTTACAAAGGCCCGGACAGACTGACCGAGAGCGCTCGGAACCTGGC 323

QY 181 CGCCGCTACACACAGAGCGGCTGGTCTCAGCCCTCAGGGAATGAATGGCTGCGAC 240

Db 324 GGCTACTACAACAGAGCGAGCGGGTCTCACACCTCCAGAGCATGTACGGCTGCGAC 383

QY 241 ATGGGGCCGACGAGCGCTCTCCGGGGTATCACAGACCGGTACGACGCAAGGAT 300

Db 384 GTGGGGCCGACGAGCGGGCGCTCTCCGGGGCATGACCACTACCGCTACGACGCAAGGAT 443

QY 301 TACATCTCCCTGAACGAGGACCTCGCGCTCTCGGACCGCGCGGACACCGCGCTCAGATC 360

Db 444 TACATCGCCCTGAACGAGGACCTCGCGCTCTCGGACCGCGCGGACACCGCGCTCAGATC 503

QY 361 ACCAGCGCTTCTATGAGCGAGGAGATATGACAGAGGATTCAGGACCTTACCTGGAGGGC 420

Db 504 ACCAGCGCAAGTGGGAGCGCGCGGTGAGCGGAGCGGAGCGCTTACCTTGGAGGGC 563

QY 421 GAGTGCCTGAGTGTCTCCGACAGATCTTGGAGATGGGAAGGAGAGCGCTTACAGCGCGCA 480

Db 564 GAGTGCCTGAGTGTCTCCGACAGATCTTGGAGACGGAAGGAGCAAGCTGGAGCGCGCT 623

QY 481 GATCTCCAAAGGACACAGTTCGCCACCCACCCATCTTGACCATGAGGACACCTTGAGG 540

Db 624 GACCCCAAGACACACGTCGACCCACCCATCTTGACCATGAGGACACCTTGAGG 683

QY 541 TGCTGGGCGCTTCTTACCTGCGGAGATCACGCTGACCTGCGGAGCGGATGCGGAG 600

Db 684 TGCTGGGCGCTTCTTACCTGCGGAGATCACACTGACCTGCGGAGCGGATGCGGAG 743

QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGCGCTGCGAG 644

Db 744 GACCAAACTCAGGACACTGAGCTTGTGGAGACCCAGCAGG 787

RESULT 12

AAQ75974/c

ID AAQ75974 standard; cDNA; 4059 BP.

XX AC AAQ75974;

XX 25-MAR-2003 (revised)

DT 23-AUG-1995 (first entry)

XX pHLA-B7 expression vector.

XX expression vector; pHLA-B7; heavy human HLA-B*7; bicistronic mRNA;

KW light beta-2 microglobulin; class I major histocompatibility complex;

KW MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.

XX Synthetic.

PH Key Location/Qualifiers

FT misc_feature 1..354

FT /note= "pBR322 backbone contg. bacterial origin of

FT replication"

FT /tag= a

FT /tag= b

FT /note= "kanamycin resistance gene open reading frame; the

FT gene is taken from the transposable element Tn903"

FT complement(1410..1177)

FT /tag= c

FT /note= "SV40 polyA signal sequence"

FT complement(1412..1560)

FT /tag= d

FT /note= "SV40 small t intron"

FT complement(1561..1794)

FT /tag= e

FT /note= "3' untranslated region of HLA-B*7 heavy chain

FT mRNA"

FT complement(1795..2880)

FT /tag= f

FT /note= "HLA-B*7 open reading frame"

FT complement(2886..3415)

FT /tag= g

FT /note= "Rous sarcoma virus 3' LTR promoter region"

FT

misc_feature 3416..4059
/*tag= h
/note= "pBR322 backbone"

W09429469-A2.
22-DEC-1994.
27-MAY-1994; 94WO-US006069.
07-JUN-1993; 93US-00074344.
(VICA-) VICAL INC.
(UNMI) UNIV MICHIGAN.
Nabel GJ, Nabel EG, Lew D, Marquet M;
WPI; 1995-036494/05.
New vectors for gene therapy, partic for tumours - comprising genetic material encoding one or more cistron(s) which express immunogenic or therapeutic peptide(s).
Claim 9; Page 42-43; 50pp; English.
This HLA-B7 antigen encoding plasmid was developed to incorporate many advantageous features, eg. the kanamycin resistance gene. The eradication of two open reading frames encoding portions of SV40 viral proteins lowers the risk of tumorigenicity. The vector may also operate as a cassette into which cistrons may be inserted and removed at will for the transcription and subsequent translation of peptides of interest. The vector is used partic. for the treatment of neoplastic disease, eg. melanoma, and provides enhanced gene delivery and expression in vivo.
(Updated on 25-MAR-2003 to correct PN field.)

Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T; 0 U; 0 Other;
Query Match 75.5%; Score 487.2; DB 2; Length 4059;
Best Local Similarity 84.8%; Pred. No. 4.7e-96;
Matches 546; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATCCGCGTGGAGTACGTAGACACGCAATTCCTGCGGTTCCGACGCGCGCGCGGATT 60
DB 2745 ATCTCAGTGGGTACGTGGACGACACCCAGTTCGTGAGTTGACGACGCGCGGAGT 2686
QY 61 CCGAGATGGACCGCGGAGCGGTGGTGGAGCAGAGAGGCGCGCGAGTATGGAGTGG 120
DB 2685 CCGAGAGAGGAGCGCGCGCGCGGTGGATAGACGAGGAGGCGCGAGTATGGAGCGG 2626
QY 121 ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCGCTGAGGAACCTGCTC 180
DB 2625 AACACACAGATCTACAGGCCACGACAGACTGACCGAGAGGCTCGGNACTTGGC 2566
QY 181 CGCGGTACACACGAGCGAGGCGTGGTCTACSCCTCCAGGGAATGATGGCTGGAC 240
DB 2565 GGCTACTACAAACGAGCGAGGCGCGGTCTCACCCCTCCAGAGCATGTACGGTGGCAG 2506
QY 241 ATGGGCGCGAGCGAGCGCTCTCCGGGGTATCACACGACGCGGTACGACGCGAGAT 300
DB 2505 GTGGGCGCGAGCGGCGCGCTCTCCGGGGCATGACAGTACGCTTACGACGCGAGAT 2446
QY 301 TACATCTCCCTGAACGAGGACCTTCCGCTCTCTGACCGCGCGGACACCGTGGCTCAGATC 360
DB 2445 TACATCGCTTGAACGAGGACCTTCCGCTCTCTGACCGCGGACACCGCGCTCAGATC 2386
QY 361 ACCAGCGCTTATAGGCGAGGAGGATATGACGAGAGTTCAGGACCTTACCTGGAGGCG 420
DB 2385 ACCAGCGCAAGTGGGAGGCGCGCGCTTGGAGCGGAGCAGCGGAGCGCTTACCTGGAGGCG 2326
QY 421 GAGTGGCTGAGTGTGCTCCGAGATCTTGGAGAAATGGGAAGGAGAGCTACAGCGCGCA 480
DB 2325 GAGTGGCTGAGTGTGCTCCGAGATCTTGGAGAAATGGGAAGGAGAGCTGAGCGCGCT 2265

QY 481 GATCTCTCAAAGGACACAGTTCGCCACCAACCCCATCTCTGACCATGAGGCGACCTGAGG 540
DB 2265 GACCCGCCAAAGACACAGTGGACCAACCCCATCTCTGACCATGAGGCGACCTGAGG 2206
QY 541 TGCTGGCGCTGGGCTTCTACCTGGGAGATCAGCTGACCTGGCAGCGGATGGGAG 600
DB 2205 TGCTGGCGCTGGGCTTCTACCTGGGAGATCAGCTGACCTGGCAGCGGATGGGAG 2146
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGACG 644
DB 2145 GACCAAACTCAGGACACTGAGCTTGTGGAGACAGACAGCAGCAGG 2102

RESULT 13
ABV99366
ID ABV99366 standard; DNA; 1175 BP.
XX AC ABV99366;
XX DT 27-JAN-2003 (first entry)
XX DE Human NOV16a coding sequence.
XX KW Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS;
KW antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic;
KW neotropic; immunosuppressive; osteopathic; antiparkinsonian; cancer;
KW antiinfectivity; cerebroprotective; gene therapy; NOVX; NOV; fertility;
KW metabolic disorder; diabetes; obesity; infectious disease; anorexia;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; cardiovascular disorder;
KW bronchial asthma; dyslipidemia; metabolic disorder; neurogenesis;
KW metabolic syndrome X; wasting disorder; cell differentiation; gene;
KW cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
XX OS Homo sapiens.
XX PN WO200272771-A2.
XX PD 19-SEP-2002.
XX PF 08-MAR-2002; 2002WO-US007288.
XX PR 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-027676P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 20-MAR-2001; 2001US-0277338P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.

PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 08-MAR-2002; 2002US-00093463.
XX (CURA-) CURAGEN CORP.
XX
XX Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ;
PI Boldog Fu, Li L, Zehausen BD, Tchernev VT, Gangolli EA, Vernet CAM;
PI Pena CE, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK;
PI Voss EZ, Malvankar UM, Anderson DW, Patturajan M, Miller CE;
PI Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY, Pochart PF;
PI Zhong M;
XX
XX WPI; 2002-732824/79.
DR DR
DR P-PSDB; ABP70088.
XX
XX New NOVX polypeptides and polynucleotides, useful for preventing,
PT diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer,
PT Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
PT disorders, and asthma.
XX
XX Claim 16; Page 153; 619pp; English.
XX
XX The present invention relates to new isolated proteins (NOVX) and their
CC coding sequences (ABV9327-ABV9395 and ABP70049-ABP70149), where X is
CC any number from 1 to 48. The NOVX proteins and coding sequences are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The NOVX coding sequences and proteins are useful for treating,
CC preventing or diagnosing diseases such as metabolic disorders, diabetes,
CC obesity, infectious diseases, anorexia, cancer-associated cachexia,
CC cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's
CC disease, immune disorders, hematopoietic disorders, cardiovascular
CC disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic
CC disturbances associated with obesity, metabolic syndrome X or wasting
CC disorders associated with chronic diseases or various cancers. The NOVX
CC coding sequences and proteins may also be used as targets for the
CC identification of small molecules that modulate or inhibit e.g.
CC neurogenesis, cell differentiation, cell proliferation, hematopoiesis,
CC wound healing and angiogenesis, in gene therapy, in generation of
CC antibodies that bind immunospecifically to NOVX substances for use in
CC therapeutic or diagnostic methods
XX
XX Sequence 1175 BP; 247 A; 344 C; 376 G; 208 T; 0 U; 0 Other;

Query Match 75.4%; Score 486.6; DB 6; Length 1175;
Best Local Similarity 84.7%; Pred. No. 5.7e-96;
Matches 546; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 1 ATCGCGGTGGAGTACGTAGACGACACGCAATTCCTGGGTTTCGACAGCGCGCGGATT 60
DB 159 ATCGCGGTGGGCTACGTGGACGACACAGAGTTCTGTGGGTTTCGACAGCGATCCGTTGAGT 218
QY 61 CCGAGGATGGAGCGCGCGGCGCGGCTGGGTGGAGCAAGAGGCGCGCGAGTATTGGGAGTGG 120
DB 219 CCGAGGATGGAGCGCGCGCGCGGCTGGGTGGAGCAGGAGGCGCTGGAGTATTGGGACGAG 278
QY 121 ACCACGGGTACGCGCGGCGCGGCGCGGCTGGGTGGAGCAAGAGTGGCCCTGAGAGAACTGCTC 180
DB 279 GAGACACGGAACGCGCGGCGCGGCGCGGCTGGGTGGAGCAAGAGTGGCCCTGAGAGAACTGCTC 338
QY 181 CGCGCTACAAACGAGAGCGAGGCTGGGCTCTCACCCCTCCAGGGAATGAATGGTGGCGAC 240
DB 339 CGCTATTACACGAGCGAGGAGTGGTTCACACCATCCAGAGGAGCATGGCTGGCGAC 398
QY 241 ATGGGGCCCGAGCGGAGCGGCTCTCCGCGGGGTATCACAGCACCGGTAGCAGCGCAAGGAT 300
DB 399 GTGGGCGCGGACAGCGCGGCTCTCCGCGAGGTATGAACAGTTTCGCTACGATGGCAAGGAT 458
QY 301 TACATCTCCCTGAACGAGGAGCTCGGCTCTCGGACCGCGCGGCGGACACCGTGGCTCAGATC 360
DB 459 TACATCGCCCTGAACGAGGAGCTCGACTCTCGGACCGCGCGGCGGACACAGCGGCTCAGATC 518
QY 361 ACCCAGCGCTTCTATGAGGCGAGAGGAATATGACAGAGGAGTTTCAAGACCTACCTGAGAGGC 420
DB 519 TCCACGACAAAGTGGGAGGCGACAAATACCTCAGACGAGGTCAAGGCGCTACCTGAGGCGC 578
QY 421 GAGTCCCTGGAGTTGCTCCGCGAGATACCTTGAGAGATGGGAGGAGACCTACAGCGCGCA 480
DB 579 AAGTGCATGGAGTGGCTCCGCGAGACACCTTGAGAACGGGAGGAGACCTGCGAGCAGCGC 638
QY 481 GATCTCTCAAAGGCGACAGTTGGCCACACACCCCATCTCTGACCATGAGGCCACCCCTGAGG 540
DB 639 GATCCCCCAAGGCGACATGTGACCCAGCACCCCATCTCTGACCATGAGGCCACCCCTGAGG 698
QY 541 TGCTGGGCGCTGGGCTTCTACCTTCGCGGAGATCAGCTGACCTGCGACCGGGATGGGAG 600
DB 699 TGCTGGGCGCTGGGCTTCTACCTTCGCGGAGATCAGCTGACCTGCGACGAGGATGGGAG 758
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGGCTGCGAGG 645
DB 759 GACCAAGCCAGGACACGAGCTTGTGGAGACCGAGGCTGCGAGACCGAGGATGGGAG 803
RESULT 14
AAQ12116
ID AAQ12116 standard; DNA; 1101 BP.
XX
AC AAQ12116;
XX
DT 25-MAR-2003 (revised)
DT 29-AUG-1991 (first entry)
XX
DE HLA-C exon Cb-1.
XX
XX Human leukocyte antigen; probe; major histocompatibility complex; MHC;
KW class I; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 1..1101
FT /*tag= a
XX
XX JP03112485-A.
XX
XX 14-MAY-1991.
PD

XX 22-SEP-1989; 89UP-00247695.
 XX 22-SEP-1989; 89UP-00247695.
 XX (OLYU) OLYMPUS OPTICAL CO LTD.
 XX WPI; 1991-182989/25.
 XX P-PSDB; ARL12465.
 XX HLA-C gene, DNA probe and transformant cells - for immunisation of
 XX animals and monoclonal antibody development.
 XX Claim 1; Page 1; 13pp; Japanese.
 XX Probes comprising part of the sequence can be used to identify Class I
 XX genes. The DNA can be expressed for immunisation of animals and prodn. of
 XX monoclonal antibodies specific for the HLA-C antigen. See also AAQ12117
 XX (same patent) and J03112486 and J03112487. (Updated on 25-MAR-2003 to
 XX correct PA field.)
 XX Sequence 1101 BP; 211 A; 337 C; 377 G; 176 T; 0 U; 0 Other;
 Query Match 75.3%; Score 485.6; DB 2; Length 1101;
 Best Local Similarity 84.6%; Pred. No. 9.3e-96;
 Matches 545; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
 QY 1 ATCCGCGTGGAGTACGTAGACACACGCAATTCCTCGGTTCCGACAGCGCGCGCGGATT 60
 Db 139 ATCCGAGTGGGTACGTGACACACGCAATTCCTCGGTTCCGACAGCGCGCGGATT 198
 QY 61 CCGAGATCGACCGCGGAGCGGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 Db 199 CCGAGAGGCGAGCGCGGCGCGGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258
 QY 121 ACCAGGGTACGCCAGGCGCAACACACAGCTGACCGGCGCTGAGGAACCTGCTC 180
 Db 259 GAGACACAGAGTACAGCGCGCGAGCGCAATTCCTCGGTTCCGACAGCGCGCGGATT 318
 QY 181 CCGCGCTACACACAGAGCGAGTGGTCTACSCCCTCCAGGGATGAATGGCTGCGAC 240
 Db 319 GCGTACTACACACAGAGCGAGCGGCTCTCACCCCTCCAGTGGATTTGGCTGCGAC 378
 QY 241 ATGGGCGCGCGAGCGCTCTCCGCGGTATCCAGCAGCGCGTACGAGCGGAAGAT 300
 Db 379 CTGGGCGCGAGCGGCGCTCTCCGCGGTATCCAGCAGCGCGTACGAGCGGAAGAT 438
 QY 301 TACATCTCCCTGAACAGAGACCTGGGCTCTCTGGACCGCGGCGACACCGTGGCTCAGATC 360
 Db 439 TACATCGCTTGAACAGAGATCTGGCTCTCTGGACCGCGGCGACACCGGCTCAGATC 498
 QY 361 ACCAGCGCTTCTATGAGCAGAGGATATGAGAGAGTTCAGGACCTTACCTGAGGCGC 420
 Db 499 ACCAGCGAAGTGGAGCGCGCGGTGGAGCGGAGCAGCGGAGCGCTTACCTGAGGCGC 558
 QY 421 GAGTGGCTGGAGTGGCTCCGAGATATCTGGAGATGGAGAGGAGACGCTACAGCGCGCA 480
 Db 559 ACCTGGTGGAGTGGCTCCGAGATATCTGGAGATGGAGAGGAGACGCTTACAGCGCGC 618
 QY 481 GATCTCCAAAGGACACAGCTGGCGGACACCCCATCTTGAACATGAGGCGCACTCTGAGG 540
 Db 619 GAACACCCAAAGACACAGCTGGCGGACACCCCATCTTGAACATGAGGCGCACTCTGAGG 678
 QY 541 TGGTGGCGCTGGGCTTCTACCTGGGAGATCAGCTGACCTGGGAGCGGATGGGAG 600
 Db 679 TGGTGGCGCTGGGCTTCTACCTGGGAGATCAGCTGACCTGGGAGCGGATGGGAG 738
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTGCGAGG 644
 Db 739 GACCAAACTCAGGACACCGAGCTTGTGGAGACCGGCTGCGAGG 782

RESULT 15

ABL69369
 ID ABL69369 standard; DNA; 1271 BP.
 XX ABL69369;
 AC ABL69369;
 XX 15-MAY-2002 (first entry)
 XX Prostate cancer related gene sequence SEQ ID NO:7706.
 XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 XX cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 XX gene; ds.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200194629-A2.
 XX 13-DEC-2001.
 XX 30-MAY-2001; 2001WO-US010838.
 XX 05-JUN-2000; 2000US-0209473P.
 XX 05-JUN-2000; 2000US-0209531P.
 XX 18-SEP-2000; 2000US-0233133P.
 XX 18-SEP-2000; 2000US-0233617P.
 XX 20-SEP-2000; 2000US-0234009P.
 XX 20-SEP-2000; 2000US-0234034P.
 XX 20-SEP-2000; 2000US-0234052P.
 XX 22-SEP-2000; 2000US-0234509P.
 XX 22-SEP-2000; 2000US-0234567P.
 XX 23-SEP-2000; 2000US-0234923P.
 XX 25-SEP-2000; 2000US-0234924P.
 XX 25-SEP-2000; 2000US-0235077P.
 XX 25-SEP-2000; 2000US-0235082P.
 XX 25-SEP-2000; 2000US-0235134P.
 XX 26-SEP-2000; 2000US-0235280P.
 XX 26-SEP-2000; 2000US-0235637P.
 XX 26-SEP-2000; 2000US-0235838P.
 XX 27-SEP-2000; 2000US-0235711P.
 XX 27-SEP-2000; 2000US-0235720P.
 XX 27-SEP-2000; 2000US-0235840P.
 XX 27-SEP-2000; 2000US-0235863P.
 XX 28-SEP-2000; 2000US-0236028P.
 XX 28-SEP-2000; 2000US-0236032P.
 XX 28-SEP-2000; 2000US-0236033P.
 XX 28-SEP-2000; 2000US-0236034P.
 XX 28-SEP-2000; 2000US-0236109P.
 XX 28-SEP-2000; 2000US-0236111P.
 XX 29-SEP-2000; 2000US-0236842P.
 XX 29-SEP-2000; 2000US-0236891P.
 XX 02-OCT-2000; 2000US-0237172P.
 XX 02-OCT-2000; 2000US-0237173P.
 XX 02-OCT-2000; 2000US-0237278P.
 XX 02-OCT-2000; 2000US-0237294P.
 XX 02-OCT-2000; 2000US-0237295P.
 XX 02-OCT-2000; 2000US-0237316P.
 XX 03-OCT-2000; 2000US-0237425P.
 XX 03-OCT-2000; 2000US-0237598P.
 XX 03-OCT-2000; 2000US-0237604P.
 XX 03-OCT-2000; 2000US-0237606P.
 XX 03-OCT-2000; 2000US-0237608P.
 XX 01-NOV-2000; 2000US-0244867P.
 XX 01-NOV-2000; 2000US-0245084P.
 XX (AVAL-) AVALON PHARM.
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 XX Soppet DR, Weaver Z;
 XX WPI; 2002-188264/24.
 XX Screening for anti-neoplastic agent involves exposing cells to a chemical

Search completed: June 18, 2004, 04:29:42
Job time : 375 secs

agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
Claim 1; SEQ ID NO 7706; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABU61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour

XX Sequence 1271 BP; 258 A; 396 C; 405 G; 212 T; 0 U; 0 Other;

Query Match 75.3%; Score 485.6; DB 6; Length 1271;

Best Local Similarity 84.6%; Pred. No. 9.4e-96;

Matches 545; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 ATCCGCGTGGAGTACGTACGACACGCAATTCCTGCGTTCGACAGCGCCGCCCGGATT 60
DB 139 ATCCGAGTGGGTACGTGACACACCCAGTTCGTGAGTTCGACAGCGACGCCCGGAGT 198
QY 61 CCGAGGATGAGCGCGGAGCGGTGGTGGAGCAAGAGGGCCCGCAGTATTGGAGTGG 120
DB 199 CCGAGGATGGCGCCCGCGCCCATGATAGACAGAGGGCGCGAGTATTGGACCGG 258
QY 121 ACCAGSGGTACGCCAAGCCACACGACAGACTGCGAGTGGCCCTGAGGAACTGCTC 180
DB 259 GAGACACAGATCTCCAAGACCACACACAGACTTACCGAGAGGCTCGGAACTGGCG 318
QY 181 CGCGGTACAAACAGAGCGAGGTGGTCTCACGCCCTCCAGGGAATGAATGGCTGCCAC 240
DB 319 GGCTACTACAAACAGAGCGAGCGCGGTCTCACGCCCTCCAGAGGATGTAGGCTGCCAC 378
QY 241 ATGGGCGCCGACGAGCGCTCTCCCGCGGTATCACCAGCAGCGGTACGACCGCAGGAT 300
DB 379 GTGGGCGCGAGCGGGCGCTCTCCCGCGGCATGACCACTCCGCTACGACGGCAAGGAT 438
QY 301 TACATCTCCTGAACGAGGACCTGCGCTCTGGACCGCGCGGACACACCGTGGCTCAGATC 360
DB 439 TACATCGCCTGACACAGGACCTGAGCTCTGGACCGCGCGGACACACCGCGCTCAGATC 498
QY 361 ACCAGCGCTTCTATGAGGACAGGAATATGACAGAGGTTGAGGACCTTACCTGGAGGGC 420
DB 499 ACCAGCGCAAGTGGGAGCGCGCCCGTGGAGCGGAGCAGTGGAGAGCTTACCTGGAGGGC 558
QY 421 GAGTGTCTGAGTGTCTCCGACATCTTGGGAATGGGAAGGAGACGCTACAGCGCGCA 480
DB 559 CTGTGGGTGAGTGGTCTCCGACATACCTGAGACGCGGAGGAGAGCGCTGAGCGCGG 618
QY 481 GATCTCCAAAGGACACAGCTGTGCGCACACCCCATCTCTGACCATGAGGCCACCTGAGG 540
DB 619 GACCCCGCAAGACACATGTGACCCACCCCATCTCTGACCATGAGGCCACCTGAGG 678
QY 541 TGTGTGGGCTTGGGCTTACCTTGGGAGATCACGCTGACCTGGCAGCGGGATGGGAG 600
DB 679 TGTGTGGGCTTGGGCTTACCTTGGGAGATCACACTGACCTGGCAGCGGGATGGCGAG 738
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCGCTGCAGG 644
DB 739 GACCAAACTCAGGACACCGAGCTTGTGGAGACCCAGACACGACGAGG 782

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 03:33:22 ; Search time 78 seconds
(without alignments)
4589.017 Million cell updates/sec

Title: US-09-819-371-3

Perfect score: 645

Sequence: 1 atcgccgtggagtacgtaga.....tggagaccaggcctgcagg 645

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/prodata/2/ina/5A COMB.seq:*
 - 2: /cgn2_6/prodata/2/ina/5B COMB.seq:*
 - 3: /cgn2_6/prodata/2/ina/6A COMB.seq:*
 - 4: /cgn2_6/prodata/2/ina/6B COMB.seq:*
 - 5: /cgn2_6/prodata/2/ina/PCUS COMB.seq:*
 - 6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490.4	76.0	1521	4	Sequence 130, App
2	487.2	75.5	4059	2	Sequence 2, Appl
3	487.2	75.5	4059	5	Sequence 2, Appl
4	485.6	75.3	4965	2	Sequence 1, Appl
5	485.6	75.3	4965	5	Sequence 1, Appl
6	451.6	69.9	1086	4	Sequence 2, Appl
7	448.6	69.5	1095	4	Sequence 36, Appl
8	445.4	69.1	1086	4	Sequence 35, Appl
9	443.4	68.7	1086	4	Sequence 3, Appl
10	441.4	68.4	1086	4	Sequence 1, Appl
11	439.8	68.2	1086	4	Sequence 1, Appl
12	438.6	68.0	1095	4	Sequence 5, Appl
13	436	67.6	1095	4	Sequence 5, Appl
14	409.8	63.5	1183	3	Sequence 4, Appl
15	409.8	63.5	1183	4	Sequence 11, Appl
16	244.8	38.0	468	4	Sequence 11, Appl
17	212.5	33.0	6593	1	Sequence 133, App
18	210.4	32.6	276	1	Sequence 1, Appl
19	210.4	32.6	276	3	Sequence 134, App
20	208.6	32.3	3520	4	Sequence 40, Appl
21	207.2	32.1	276	4	Sequence 84, Appl
22	207.2	32.1	276	4	Sequence 23, Appl
23	204	31.6	276	4	Sequence 673-809-73
24	202.4	31.4	276	1	Sequence 128, App
25	200.8	31.1	276	1	Sequence 116, App
26	200.8	31.1	276	1	Sequence 112, App
27	200.8	31.1	276	1	Sequence 113, App
28	200.8	31.1	276	1	Sequence 117, App

28	200.8	31.1	276	1	US-08-127-954-118	Sequence 118, App
29	200.8	31.1	276	1	US-08-127-954-123	Sequence 123, App
30	200.8	31.1	276	1	US-08-127-954-126	Sequence 126, App
31	200.8	31.1	276	1	US-08-127-954-127	Sequence 127, App
32	199.2	30.9	276	1	US-08-127-954-121	Sequence 121, App
33	199.2	30.9	276	1	US-08-127-954-124	Sequence 124, App
34	199.2	30.9	276	1	US-08-127-954-133	Sequence 133, App
35	197.6	30.6	276	1	US-08-127-954-104	Sequence 104, App
36	196	30.4	276	1	US-08-127-954-119	Sequence 119, App
37	196	30.4	276	1	US-08-127-954-120	Sequence 120, App
38	196	30.4	276	4	US-09-673-809-75	Sequence 75, Appl
39	194.4	30.1	276	1	US-08-127-954-106	Sequence 106, App
40	194.4	30.1	276	1	US-08-127-954-107	Sequence 107, App
41	194.4	30.1	276	1	US-08-127-954-108	Sequence 108, App
42	194.4	30.1	276	1	US-08-127-954-111	Sequence 111, App
43	194.4	30.1	276	1	US-08-127-954-115	Sequence 115, App
44	194.4	30.1	276	1	US-08-127-954-122	Sequence 122, App
45	194.4	30.1	276	1	US-08-127-954-131	Sequence 131, App

ALIGNMENTS

RESULT 1

US-09-566-921-130
; Sequence 130, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 1040429.6
US-09-566-921-130

Query Match		76.0%	Score 490.4; DB 4;	Length 1521;
Best Local Similarity		85.1%	Pred. No. 2.8e-108;	
Matches 548;		Conservative 0;	Mismatches 96;	Indels 0; Gaps 0;
QY	1	ATCGCGTGGAGTACGTAGACGACGCAATTCTCGGTTTCGACAGCGCGCGCGGATT	60	
Db	143	ATCTAGTGGGCTAGTGGACGACGCGGTTCTGAGTTTCGACGCGCGCGGATT	202	
QY	61	CCGAGGATGGAGCGCGGAGCGGCGGTTGGGTTGGAGCAAGAGGCGCGCGGATTGGGAGTGG	120	
Db	203	CCGAGAGAGGAGCGCGGCGCGGCGGTTGGATAGACGAGAGGCGCGGAGTATTGGGACCGG	262	
QY	121	ACCACGGGTACGCCAGGCGCAACGACAGACTACCGAGTGGCGCTGAGGAACCTGCTC	180	
Db	263	AACACACAGATCTTCAAGACCAACACAGACTACCGAGAGAGGCTTCGGAACTTGGCC	322	
QY	181	CGCGCTTCAACACAGAGCGGCTGGGTCTCACGCGCTTCCAGGGAATGAATGGCTGGCAC	240	
Db	323	GGCTACTACACAGAGCGGCGGCTCTCACACCTCCAGAGGATGTACGGCTGGCAC	382	
QY	241	ATGGGCGCGGAGCGGCTCTCTCGCGGGTATCACAGACGCGGTACGAGCGGAGAT	300	
Db	383	GTGGGCGCGGAGCGGCGGCTCTCTCGCGGGGATACACAGTACGCTACGAGCGGAGAT	442	
QY	301	TACATCTCCCTGAACGAGGACCTGGGCTCTCTGGACCGCGGCGGACACCGTGGCTCAGATC	360	
Db	443	TACATCGGCTTGAACGAGGACCTGGGCTCTCTGGACCGCGGCGGACACCGGCTCAGATC	502	


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SOFTWARE: FastSeq Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033VPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4059 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN: HLA-B7
PCT-US94-06069-2

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Query Match 75.5%; Score 487.2; DB 5; Length 4059;
Best Local Similarity 84.8%; Pred. No. 2e-107;
Matches 546; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTTCGACAGCGCCCGCGGATT 60
DB 2745 ATCTCAGTGGCTACGTGGACGACACCCAGTTCGTGAGGTTTCGACAGCGCCCGCGGATT 2686

QY 61 CCAGGATGAGCGCGGCGGCGGCGTGGTGGAGCAGAGGCGCGCGAGTATTGGGAGTGG 120
DB 2685 CCAGGAGAGCGCGGCGGCGGCGTGGTGGAGCAGAGGCGCGCGAGTATTGGGAGTGG 2626

QY 121 ACCACGGGTACGCCAAGGCCAACGACACAGACTGACCGAGTGCGCCCTGAGGAACCTGCTC 180
DB 2625 AACACACAGACTTACAAAGGCCAGGACACAGACTGACCGAGAGCGCTGCGGAACCTGCGC 2566

QY 181 CGCGGTACAAACAGAGCGGCGTGGTCTCAGCCCTCCAGGATGAATGCTGCGGAC 240
DB 2565 GGCTACTTAAACAGAGCGGCGGCGGCTTCCACCCCTCCAGAGCATGTACGGCTGCGGAC 2506

QY 241 ATGGGCGCGGACGAGCGCTCTCTCCGCGGATATCACAGCAGCGCTACGACGCGCAAGGAT 300
DB 2505 GTGGGCGCGGACGCGGCGCTCTCTCCGCGGATATCACAGCAGCGCTACGACGCGCAAGGAT 2446

QY 301 TACATCTCCCTGAACAGAGACCTGCGCTCTGACCGCGCGGACACCGTGGCTCAGATC 360
DB 2445 TACATCGCCCTGAACAGAGACCTGCGCTCTGACCGCGCGGACACCGTGGCTCAGATC 2386

QY 361 ACCACGCGCTTCTATAGGCGAGAGGAATATGACAGAGGATTCAGGACCTTACCTGAGGCGC 420
DB 2385 ACCACGCGCAAGTGGAGCGGCGGCGGCGTGGCGGAGCAGCGGAGACCTTACCTGAGGCGC 2326

QY 421 GAGTGGCTGAGTGTTCGCGAGATATGAGAGATGGGAGAGGAGACGCTACAGCGCGCA 480
DB 2325 GAGTGGCTGAGTGTTCGCGAGATATGAGAGATGGGAGAGGAGACGCTTACAGCGCGCT 2266

QY 481 GATCTCCRAAGGACACAGCTGTCACCCACCCATCTCTGACCATGAGCGCCACCTGAGG 540
DB 2265 GACCCCCAAGACACACAGTGAACCCACCCATCTCTGACCATGAGCGCCACCTGAGG 2206

QY 541 TGCTGGGCGCTGGGCTTCTACCTTGGGAGATCACGCTGACCTGGCAGCGGGATGGGGAG 600
DB 2205 TGCTGGGCGCTGGGCTTCTACCTTGGGAGATCACGCTGACCTGGCAGCGGGATGGGGAG 2146

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QY 601 GAACAGACCCAGACACAGAGCTTGTGGAGACCGACCGCTGCAGG 644
DB 2145 GACCAACTCAGACACTGAGCTTGTGGAGACCGACCGACGAGG 2102

RESULT 4
US-08-564-313-1
; Sequence 1, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7 and Beta-2
; US-08-564-313-1

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Query Match 75.3%; Score 485.6; DB 2; Length 4965;
Best Local Similarity 84.6%; Pred. No. 5.1e-107;
Matches 545; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTTCGACAGCGCCCGCGGATT 60
DB 673 ATCTCAGTGGGCTACGTGGAGCAGCACCCAGTTCGTGAGTTTCGACAGCGACCGCGGAGT 732

QY 61 CCAGGATGAGCGCGGCGGAGCCGCTGGTGGAGCAAGAGGCGCGCGAGTATTGGGAGTGG 120
DB 733 CCAGGAGGAGGCGCGCGCGCGCTGGATAGAGCAGGAGGCGCGGAGTATTGGGACCGG 792

QY 121 ACCACGGGTAGCGCAAGGCCAACGACAGACTACCGAGTGGCCCTGAGGAACCTGCTC 180
DB 793 AACACAGATCTTCAAGGGCCCGGACAGACTACCGAGAGAGCGCTCGGGAACCTGCGC 852

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181 CGCGCTACAAACAGAGAGGCTGGGTCTCACCCCTCCAGGAATGAATGGCTGGAC 240
Db G3CTACTACAAACAGAGAGGCTGGGTCTCACCCCTCCAGGATGTACGGTGGAC 912
Qy 241-ATGGGGCCGAGAGAGGCTCTCGGGGTATCACAGACGGGTAGGAGGCAAGAT 300
Db 913 GTGGGGCCGAGAGAGGCTCTCGGGGTATCACAGACGGGTAGGAGGCAAGAT 972
Qy 301 TACATCTCCCTGAACAGAGAGCTGGCTCTCGGGGTATCACAGACGGGTAGGAGGCA 360
Db 973 TACATCGCCCTGAACAGAGAGCTGGCTCTCGGGGTATCACAGACGGGTAGGAGGCA 1032
Qy 361 ACCAGAGCCCTGATAGAGAGAGATATGAGAGAGGTTTACAGGCTTACAGGAGGCA 420
Db 1033 ACCAGAGCCCTGATAGAGAGAGATATGAGAGAGGTTTACAGGCTTACAGGAGGCA 1092
Qy 421 GAGTGCCCTGGAGTTGCTCCGAGATATTTGAGAGATGGGAGGAGAGCTACAGCGGCA 480
Db 1093 GAGTGCCCTGGAGTTGCTCCGAGATATTTGAGAGATGGGAGGAGAGCTACAGCGGCT 1152
Qy 481 GATCCTCAAAAGGAGAGCTGGTCCGAGATATTTGAGAGATGGGAGGAGAGCTTACAGG 540
Db 1153 GATCCTCAAAAGGAGAGCTGGTCCGAGATATTTGAGAGATGGGAGGAGAGCTTACAGG 1212
Qy 541 TGCTGGGCTGGAGTTGCTCCGAGATATTTGAGAGATGGGAGGAGAGCTTACAGGAG 600
Db 1213 TGCTGGGCTGGAGTTGCTCCGAGATATTTGAGAGATGGGAGGAGAGCTTACAGGAG 1272
Qy 601 GAACAGAGCCCTGATAGAGAGAGATATGAGAGAGGTTTACAGGCTTACAGGAGGCA 644
Db 1273 GAACAGAGCCCTGATAGAGAGAGATATGAGAGAGGTTTACAGGCTTACAGGAGGCA 1316

RESULT 5

PCT-US94-06069-1

Sequence 1, Application PC/TUS9406069

GENERAL INFORMATION:

APPLICANT: Vical Incorporated
APPLICANT: Regents of the University of Michigan

APPLICANT: Nabel, Elizabeth

APPLICANT: Nabel, Gary

APPLICANT: Lew, Denise

APPLICANT: Marquet, Magda

TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06069

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/074,344

FILING DATE: 07-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Israelsen, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: VICAL-033VPC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4965 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

SPRAIN, HLA-B7 and Beta-2

PCT-US94-06069-1

Query Match

Best Local Similarity 75.3%; Score 485.6; DB 5; Length 4965;

Matches 545; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 1 ATCCGCTGGAGTACGTAGACGACGCAATTCCTCGGTTTCGACAGCGCCCGCGAT 60
Db 673 ATCTCAGTGGGTACGTGGACGACACCCAGTTCGTGAGTTTCGACAGCGACCCCGGAGT 732
Qy 61 CCGAGGATGGAGCCGCGGAGCCGTGGGTGGAGCAAGAGGGGCGCCGAGTATTGGAGTGG 120
Db 733 CCGAGAGAGAGCCGCGGCGCGGTGGATAGAGAGGAGGGCGCGAGTATTGGACCGG 792
Qy 121 ACCAGGGGTACGCCAAGCCCAAGCAGACAGACTGACCGAGTGGCCCTGAGGAACTGCTC 180
Db 793 AACACACAGATCTAACAGGCCCGAGCAGACAGACTGACCGAGAGAGCTTGGGAACTGGCG 852
Qy 181 CGCGCTACAAACAGAGAGGAGGCTGGTCTCACSCCTCCAGGGAATGAATGGCTGCGAC 240
Db 853 GGCTACTACAAACAGAGAGGAGGCGGGTCTCACACCTCCAGAGCATGTACGGCTGCGAC 912
Qy 241 ATGGGGCCCGAGCGAGCGCTCTCCGCGGTTATCCAGGACGCGTACGAGCGCAAGGAT 300
Db 913 GTGGGGCCCGAGCGGCGCTCTCCGCGGCGCATGACCACTACGCTACGACGCGCAAGGAT 972
Qy 301 TACATCTCCCTGAACAGAGAGCTGGCTCTCGACCGGGCGGACACCGTGGCTCAGATC 360
Db 973 TACATCGCCCTGAACAGAGAGCTGGCTCTCGACCGGGCGGACACCGCGGCTCAGATC 1032
Qy 361 ACCAGCGCTTCTATGAGCAGAGGAATATGAGAGGAGTTTACAGGACTTACCTGAGGGC 420
Db 1033 ACCAGCGCAAGTGGGAGGCGCGCGCTGAGGCGGAGCAGCGAGAGCTTACCTGAGGGC 1092
Qy 421 GAGTGCTGGAGTTGCTCGGAGATACCTGGAGATGGGAGATGGGAGAGAGCGCTACAGCGCA 480
Db 1093 GAGTGCTGGAGTTGCTCGGAGATACCTGGAGATGGGAGATGGGAGAGAGCGCTTACAGCG 1152
Qy 481 GATCTCTCAAAGGAGCAGCGTTGCGCCACCAACCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 1153 GACCGCCCAAGACACACGTCGACCCACCCATCTCTGACCATGAGGCCACCTGAGG 1212
Qy 541 TCGTGGCCCTGGGCTTCTACCCCTGGGAGATACGCTGAGTACCTGGAGCGGAGTGGGAG 600
Db 1213 TCGTGGCCCTGGGTTTCTACCCCTGGGAGATACCTGGGAGAGCGGAGAGCAAGCTGAGCGCG 1272
Qy 601 GAACAGAGCCCGAGCAGAGAGCTTGTGGAGAGCAGCGCTGCGAGG 644
Db 1273 GACCAAACTCAGGACACTGAGCTTGTGGAGAGCAGCAGGAGG 1316

RESULT 6

US-08-914-372C-2

Sequence 2, Application US/08914372C

Patent No. 6521448

GENERAL INFORMATION:

APPLICANT: Edge, Albert S.B.

APPLICANT: Oettinger, Henry F.

TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF

FILE REFERENCE: 05742/009001

CURRENT APPLICATION NUMBER: US/08/914,372C

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; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; TYPE: DNA
; LENGTH: 1086
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1083)
US-08-914-372C-2

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Query Match 69.9%; Score 451; DB 4; Length 1086;
Best Local Similarity 81.1%; Pred. No. 6.7e-99;
Matches 523; Conservative 1; Mismatches 121; Indels 0; Gaps 0;

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QY 1 ATCCGCGTGGAGTACGTAGACACGCAATTCCTGCGGTTTCGACAGCGCGCGCGATT 60
DB 130 ATCTCCGTGCGTACGTGGACGACAGCGAGTTCGTGCGGTTTCGACAGCGCGCGCGCAAT 189
QY 61 CCGAGGATGGAGCCCGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGCAGTATTGGGAGTGG 120
DB 190 CCGCGGATGGAGCCCGCGGCGCGTGGATACAGCAGGAGGGGCGAGAAGTATTGGGATGAG 249
QY 121 ACCACGCGGTACGCCAAGGCCMACCGACAGACTGACCGAGTGGCGCTGAGGAACCTGCTC 180
DB 250 GAGACGCGCAACGCCATGGGCGCGCACAGACTTTCCGAGTGAACCTGAAGAACCTGCGC 309
QY 181 CCGCGCTACCAACAGACGAGCGTGGTCTACSCCCTCCAGGGAAATGAATGGCTGCGAC 240
DB 310 GGCTACTACCAACAGACGAGCGCGGTCTACACCTCCAGAGCATGATCGGCTGCGAC 369
QY 241 ATGGGCGCGGACGCGACGCTCTCCCGCGGTATACACAGCAGCGGTACGAGCGCAAGGAT 300
DB 370 GTGGGACAGACGCGGTCTCTCCCGCGGTACCATCAGACGCGCTACGAGCGCGCGCAT 429
QY 301 TACATCTCCCTGAAAGAGACCTGCGTCTGGAGCGCGGCGGACACCGTGGCTCAGATC 360
DB 430 TACATCTCCCTGAAAGAGACCTGCGTCTGGAGCGCGGCGGACACCGTGGCTCAGATC 489
QY 361 ACCACGCGTCTTATGAGCAGAGGAATATGAGAGGAGTTCAGGACCTACCTGAGGCGC 420
DB 490 GCCAGCGCAAGTGGAGCGCGCGGTATGCGTGGAGTGGAGGAGTACCTGGAGGCGC 549
QY 421 GAGTGGCTGGAGTGTCTCCGCGAGATCTTGGAGAGATGGAGAGGAGACCGTACAGCGCGCA 480
DB 550 GCGTGTGTGGAGTGTCTCCGAGAAATACCTGGAGATGGGAAATACACGCTGCGAGCGCGCA 609
QY 481 GATCTCTCCAAAGCAGACGCTTGCACACCGCCATCTGTACCATGAGGCGCACCTGAGG 540
DB 610 GAGCTTCCAAAGACATGTGACCCCGCACCCCGCTGACCTGGGGGTACCTTGAGG 669
QY 541 TGTGGGCGCTGGGCTTACCTCGGAGATACAGCTGACCTGGAGCGGAGTGGGAG 600
DB 670 TGTGGGCGCTGGGCTTACCTCGGAGATACAGCTGACCTGGAGCGGAGTGGGAG 729
QY 601 GAACAGCCAGACACAGCTTGTGGAGACGAGCGCTGCGAGG 645
DB 730 GACCAGAGCCAGACATGAGTGTGGAGACGAGCGCGCTCAGG 774

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RESULT 7

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US-08-914-372C-36
; Sequence 36, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: consensus sequence
; NAME/KEY: misc feature
; LOCATION: (271)....(271)
; OTHER INFORMATION: n = A,C or G
; NAME/KEY: misc feature
; LOCATION: (272)....(272)
; OTHER INFORMATION: n = G,A or C
; NAME/KEY: misc feature
; LOCATION: (275)....(275)
; OTHER INFORMATION: n = A,G or T
; NAME/KEY: misc feature
; LOCATION: (527)....(527)
; OTHER INFORMATION: n = T,C or A
; NAME/KEY: misc feature
; LOCATION: (560)....(560)
; OTHER INFORMATION: n = T,G or C
US-08-914-372C-36

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Query Match 69.5%; Score 448; DB 4; Length 1095;
Best Local Similarity 80.8%; Pred. No. 3.5e-98;
Matches 520; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

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QY 1 ATCCGCGTGGAGTACGTAGACACGCAATTCCTGCGGTTTCGACAGCGCGCGCGATT 60

DB 139 ATCCGCGTGGAGTACGTAGACACGCAATTCCTGCGGTTTCGACAGCGCGCGCGCAAT 198

QY 61 CCGAGGATGGAGCCCGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGCAGTATTGGGAGTGG 120

DB 199 CCGCGGATGGAGCCCGCGGCGCGTGGATACAGCAGGAGGGGCGAGGATATTGGATCGG 258

QY 121 ACCACGCGGTACGCCAAGGCCAACCGACAGACTGACCGAGTGGCGCTTGGAGAACTGCTC 180

DB 259 GAGACACAGATCNCANGGACACCGACAGCTTACCGAGTGGACCTGAACCTCGCGC 318

QY 181 CCGCGCTACAAACAGAGCGAGGCTGGTCTCASCCTCCAGGAGTGAATGGCTGCGAC 240

DB 319 GCGTACTACAAACAGAGCGAGGCGGCTCTCACACCTCCAGAGCATGTACGCTGCGAC 378

QY 241 ATGGGCGCGGACGAGCGCTCTCCCGGGGTATCACAGCAGCGTACGACGCGCAAGGAT 300

DB 379 GTGGGACAGAGCGGCTCTCTCCCGGGGTACAGTCACTGCTGCGCTACGAGCGCGCGAT 438

QY 301 TACATCTCCCTGAAACGAGGACCTGCGCTCTTGGACCGCGCGGACACCGTGGCTCAGATC 360

DB 439 TACCTCGCTGAAACGAGGACCTGCGCTCTTGGACCGCGCGGACACCGGCGCTCAGATC 498

QY 361 ACCAGCGCTTCTATGAGGACAGGAGATATGACAGAGGATTCAGGACCTACCTGGAGGGC 420

DB 499 TCCAAGCGCAAGTGGAGGGCGGCGCAATGNGCGGAGCAGGAGAGGAGTACCTCAGGGC 558

QY 421 GAGTGGCTGGAGTGTCTCCGCGAGATCTTGGAGAAATGGGAGAGAGCGCTACAGCGCGCA 480

DB 559 CNGTGTGGAGTGGCTCTCCGCGAGATCTTGGAGATGGGAGAGACACGCTGACGCGCGCA 618

QY 481 GATCTCTCCAAAGCAGCAGTGTGCGCACACCCCAATCTCTGACCATGAGGCGCACCTGAGG 540

DB 619 GAGCTTCCAAAGACACATGTGACCCCGCACCCCAAGCTCTGACCTGGGGGTACCTTGAGG 678

QY 541 TGTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGAGCTGGCAGCGGAGTGGGAG 600

DB 679 TGTGGGCGCTGGGCTTCTACCTTAAGAGATCTCTCTGACCTGAGCGGAGGCGGCGAG 738

QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGGCTGCGAGG 645

DB 739 GACCAGAGCCAGGACATGAGTGTGGAGACCGAGGCGCTCAGG 783

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RESULT 8
US-08-914-372C-35
; Sequence 35, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; APPLICANT: Oettinger, Henry F.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: consensus sequence
; LOCATION: (126)...(126)
; OTHER INFORMATION: n = G,T or C
; NAME/KEY: misc feature
; LOCATION: (261)...(261)
; OTHER INFORMATION: n = A,C or T
; NAME/KEY: misc feature
; LOCATION: (272)...(272)
; OTHER INFORMATION: n = A,G or C
; NAME/KEY: misc feature
; LOCATION: (490)...(490)
; OTHER INFORMATION: n = T,G or A
; NAME/KEY: misc feature
; LOCATION: (551)...(551)
; OTHER INFORMATION: n = G,C or T
; NAME/KEY: misc feature
; LOCATION: (939)...(939)
; OTHER INFORMATION: n = T,C or G
; OTHER INFORMATION: n = T,C or G
US-08-914-372C-35

Query Match      69.1%; Score 445.4; DB 4; Length 1086;
Best Local Similarity 80.3%; Pred. No. 1.5e-97;
Matches 518; Conservative 1; Mismatches 126; Indels 0; Gaps 0;

QY 1 ATCCGCTGAGTACGTAGACACGCAATTCCTCGGTTTCGACAGCGCGCGCGATT 60
DB 130 ATCCGCTGCGCTACGTGGACACGCGAGTTCGTGCGTTTCGACACTAGCCCCGAT 189
QY 61 CCGAGATGGAGCCGCGGAGCCCTGCGTGGATACAGAGAGGGCGCGCAGTAGTGG 120
DB 190 CCGGATGGAGCCTCGGTCGCGTGGATACAGAGAGGGCGCGCAGTAGTGGATGG 249
QY 121 ACCAGGGTACGCCAAGCCAAACGACAGACTGACCGAGTGGCGCCCTCAGGAACCTGTC 180
DB 250 GAGACGCGGAATGTCAAGGAAACCGCACAGACTTACGGAGTGGCGCTGAACACCTCGCG 309
QY 181 CGCGCTACAAACAGAGCGAGCTGGTCTCACSCCTCCAGGGAATGAATGGCTGCGAC 240
DB 310 GGCTACTACACAGAGCGAGCGCGGTCTCACACCTCCAGAGCATGTACGGCTGTAC 369
QY 241 ATGGGGCCGAGCGAGCGCTCTCCCGGGTATCAACAGACGCGTACGACGGCAAGGAT 300
DB 370 TTGGACACAGCGGGCTCTCTCCACGGGTACAGACAGGACGCGCTACGACGGCGCGAT 429
QY 301 TACATCTCCCTAAACAGAGACCTGCGCTCTGGACCGCGCGGACACCGTGGCTCAGATC 360
DB 430 TACATCGCCCTGAACAGAGACCTGCGCTCTGGACCGCGCGGACACATGGCGGCTCAGATC 489
QY 361 ACCAGCGCTTCTATGAGCGAGGAAATATGACAGAGAGTTCAGGACCTACCTGGAGGC 420
DB 490 ACCAAGCGCAAGTGGAGGGCGCGCGATGAGGCGGAGCGTAGGAGGAGCTACCTGACGGA 549
QY 421 GAGTGCCTGAGTGTCTCGCAGATACCTTGGAGAAATGGGAAGAGAGCGCTACAGCGGCA 480
DB 550 CTGTGTGTGAGTGTCTCGCAGATACCTTGGAGATGGGAAGAGACACGCTGACGCGCA 609
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RESULT 9
US-08-914-372C-3
; Sequence 3, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; APPLICANT: Oettinger, Henry F.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1083)
US-08-914-372C-3

Query Match      68.7%; Score 443; DB 4; Length 1086;
Best Local Similarity 80.3%; Pred. No. 5.5e-97;
Matches 518; Conservative 1; Mismatches 126; Indels 0; Gaps 0;

QY 1 ATCCGCTGAGTACGTAGACACGCAATTCCTCGGTTTCGACAGCGCGCGCGATT 60
DB 130 ATCCGCTGCGCTACGTGGACACGCGAGTTCGTGCGTTTCGACAACTACCGCCCGGAT 189
QY 61 CCGAGATGGAGCCGCGGAGCCGTGGTGGACCAAGAGGGCGCGCAGTAGTGGAGTGG 120
DB 190 CCGGATGGAGCCTCGGTCGCGTGGATACAGAGAGGGCGCGCAGTAGTGGATGG 249
QY 121 ACCAGGGTACGCCAAGCCAAACGACAGACTGACCGAGTGGCGCCCTGAGGAACCTGTC 180
DB 250 GAGACGCGGAATGTCAAGGAAACCGCACAGACTTACGGAGTGGCGCTGAACACCTCGCG 309
QY 181 CGCGCTACAAACAGAGCGAGCTGGTCTCACSCCTCCAGGGAATGAATGGCTGCGAC 240
DB 310 GGCTACTACACAGAGCGAGCGCGGTCTCACACCTCCAGAGCATGTACGGCTGTAC 369
QY 241 ATGGGGCCGAGCGAGCGCTCTCCCGGGTATCAACAGACGCGTACGACGGCAAGGAT 300
DB 370 TTGGACACAGCGGGCTCTCTCCACGGGTACAGACAGGACGCGCTACGACGGCGCGAT 429
QY 301 TACATCTCCCTAAACAGAGACCTGCGCTCTGGACCGCGCGGACACCGTGGCTCAGATC 360
DB 430 TACATCGCCCTGAACAGAGACCTGCGCTCTGGACCGCGCGGACACATGGCGGCTCAGATC 489
QY 361 ACCAGCGCTTCTATGAGCGAGGAAATATGACAGAGAGTTCAGGACCTACCTGGAGGC 420
DB 490 NCCAAGCGCAAGTGGAGGCGCGCGATGAGGCGGAGCGGAGGAGGAGTACCTGCGAGGC 549
QY 421 GAGTGCCTGAGTGTCTCGCAGATACCTTGGAGAAATGGGAAGAGACGCTACAGCGCA 480
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QY 481 GATCTCCAAAGGACACGTTGGCCACACCCCTCTCTGACCATGAGGCCACCTTGAGG 540
Db 610 GAGCTTCCAAAGACACATGTGACCCGACCCAGCTCTGACCTCGGGGTCACTTGAGG 669
QY 541 TGTGGGCGCTGGGCTTCTACCTGCGGAGATCACTGCTGCGAGCGGATGAGGAG 600
Db 670 TGTGGGCGCTGGGCTTCTACCTTAAGGAGATCTCCCTGACCTGCGAGCGGAGGCCAG 729
QY 601 GAACAGACCCAGGACACAGACTTGTGGAGACCCAGGCTGAGAG 645
Db 730 GACCAGACCCAGGACATGTGTGTGGAGACCCAGGCTCAGGG 774

RESULT 10

US-08-914-372C-1
; Sequence 1, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; APPLICANT: Oettinger, Henry F.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1083)
US-08-914-372C-1

Query Match 68.4%; Score 441.4; DB 4; Length 1086;
Best Local Similarity 80.2%; Pred. No. 1.3e-96;
Matches 517; Conservative 1; Mismatches 127; Indels 0; Gaps 0;

QY 1 ATCGCGGTGGAGTAGTAGACACGCAATTCCTGCGGTTTCGACAGCGCCGCCCGATT 60
Db 130 ATCGCGGTGGAGTAGTAGACACGCAATTCCTGCGGTTTCGACAGCGCCGCCCGATT 189
QY 61 CCGAGATGGAGCCCGGGAGCCGTGGTGGAGCAAGAGGGGCCCGACGATTGGAGTGG 120
Db 190 CCGCGGATGGAGCCCTCGGTTGCGGTGATACAGCAGGAGGGGCGACGACTATGGGATAG 249
QY 121 ACCAGGGGTACGCCAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 250 GAGACGCGAAAGTCAAGACACGACAGACTCTCCGAGTGGGCTTGAACACCTTGCGC 309
QY 181 CGCGGCTACAAACAGAGGAGGCTGGTCTACSCCCTCCAGGGAAATGAATGGCTGCGAC 240
Db 310 GGCTACTACAAACAGAGGAGGCTGGTCTACACCCCTCCAGAGCATGTTGGCTGTAC 369
QY 241 ATGGGCGCGAGCGGACCTCTCCGCGGATACACGACGCGCTACGAGCGCAAGAT 300
Db 370 TTGGGACCAAGAGCGGCTCTCTCTCCAGGGTACAGACAGGACCTTACGAGCGCCGAT 429
QY 301 TACATCTCCCTGAACAGGACCTGCGCTCTCGACCGCGCGGACACCGTGGCTCAGATC 360
Db 430 TACATCGCCTGAACAGGACCTGCGCTCTCGACCGCGCGGACATGCGGCTCAGATC 489
QY 361 ACCAGCGCTTCTATGAGGACAGGATATGACAGGAGTTGAGGACCTTACCTGAGGGC 420
Db 490 TCCAAAGCGAAGTGGGAGCGCGGATGAGGCGGAGCGGATGAGGAGCTTACCTGAGGGC 549
QY 421 GAGTGGCTGAGTGTCTCCGCGAGATCTTGGAGAAATGGGAAGGAGACGCTACAGCGCGCA 480
Db 550 CGGTGTGTGGAGGGGCTCCGAGATACCTGCGAGTGGGGAAGGACACGCTGAGCGCGCA 609
QY 481 GATCTCCAAAGGACACGTTGGTGGCCACACCCCATCTCTGACATGAGGCCACCTTGAGG 540

Db 610 GACCTTCCAAAGACACATGTGACCCGACCCAGCTCTGACCTGGGGGTCACTTGAGG 669
QY 541 TGTGGGCGCTGGGCTTCTACCTGCGGAGATCACTGCTGACCTGCGAGCGGATGAGGAG 600
Db 670 TGTGGGCGCTGGGCTTCTACCTTAAGGAGATCTCCCTGACCTGCGAGCGGAGGCCAG 729
QY 601 GAACAGACCCAGGACACAGACTTGTGGAGACCCAGGCTGAGAG 645
Db 730 GACCAGACCCAGGACATGTGTGTGGAGACCCAGGCTCAGGG 774

RESULT 11

US-08-914-372C-6
; Sequence 6, Application US/08914372C
; Patent No. 6521448
; GENERAL INFORMATION:
; APPLICANT: Edge, Albert S.B.
; APPLICANT: Oettinger, Henry F.
; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
; FILE REFERENCE: 05742/009001
; CURRENT APPLICATION NUMBER: US/08/914,372C
; CURRENT FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1092)
US-08-914-372C-6

Query Match 68.2%; Score 439.8; DB 4; Length 1095;
Best Local Similarity 80.0%; Pred. No. 3.2e-96;
Matches 516; Conservative 1; Mismatches 128; Indels 0; Gaps 0;

QY 1 ATCGCGGTGGAGTAGTAGACACGCAATTCCTGCGGTTTCGACAGCGCCGCCCGATT 60
Db 139 ATCGAAGTCGGTACGTGGAGCAACGACGCTTCGTGGGTTTCGACAGCGCGCCCGAAT 198
QY 61 CCGAGGATGGAGCCCGGGAGCCGTGGTGGAGCAAGAGGGGCCCGAGTATGGAGTGG 120
Db 199 CCGCGGATGGAGCTCGGGCGCGTGATACAGCAGAGGGGCGAGGATATGGGATAGG 258
QY 121 ACCAGGGGTACGCCAAGCCCAACGACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 259 AACACGCGGAACGCCCATGGGCAACGACAGATTTACCGAGGGAACCTTGCACAGCTCTC 318
QY 181 CGCGCTTACAAACAGAGCGAGGCTGGGTCTTACSCCCTCCAGGGAAATGAATGGCTGCGAC 240
Db 319 GGCTACTTACAAACAGAGCGAGGCGGGTCTTACACCATCCAGATCATGTACGGCTGCGAC 378
QY 241 ATGGGCGCGAGCGGACCGCTCTCCGCGGATATCACAGCAGCGGTCAGCGGCAAGAT 300
Db 379 GTGGGACACAGACGGGCTCTCTCTCCGCGGATACAGTACAGACGCTTACGAGCGGCGCAT 438
QY 301 TACATCTCCCTGAACAGGACCTGCGCTCTCGACCGCGCGGACACCGTGGCTCAGATC 360
Db 439 TACATCGCCTTGAACAGGACCTTCCGCTCTTGSACCGCGCGGACACCGGCTCAGATC 498
QY 361 ACCAGCGCTTCTATGAGGACAGGAAATGACAGAGAGTTTACGAGCCTTACCTGAGGGC 420
Db 499 ACCAAGCGCAAGTGGGAGGCGCGGATGAGGCGGAGCGGTAGGAGGAGCTACCTGCAAGGC 558
QY 421 GAGTGGCTGAGTGTCTCCGAGATCTTGGAGAAATGGGAAGGAGAGCGCTACAGCGCGCA 480
Db 559 ACGTGTGTGAGTGGCTTCCAGAAATACCTGAGATGGGGAAGGACACGCTTGCAGCGCGCA 618
QY 481 GATCTCCAAAGGACACGTTGGTGGCCACACCCCATCTCTGACATGAGGCCACCTTGAGG 540
Db 619 GAGCTTCCAAAGACACATGTGTGACCCGCCACCCCGAGCTCTGACCTCGGGGTCACTTGAGG 678

QY 541 TGCTGGGCGCTTCTACCTCGGAGATCACGCTACCTGGCAGCGGATGGGAG 600
 Db 679 TGCTGGGCGCTTCTACCTCGGAGATCACGCTACCTGGCAGCGGATGGGAG 738
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGCCCTGCAGGG 645
 Db 739 GACCAGAGCCAGGACATGGAGCTGTGGAGACCAAGCCCTGCAGGG 783

RESULT 12
 US-08-914-372C-5
 ; Sequence 5, Application US/08914372C
 ; Patent No. 6521448
 ; GENERAL INFORMATION:
 ; APPLICANT: Edge, Albert S.B.
 ; APPLICANT: Oettinger, Henry F.
 ; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
 ; FILE REFERENCE: 05742/009001
 ; CURRENT APPLICATION NUMBER: US/08/914,372C
 ; CURRENT FILING DATE: 1997-08-19
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 1095
 ; TYPE: DNA
 ; ORGANISM: Sus scrofa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1092)
 US-08-914-372C-5

Query Match 68.0%; Score 438.6; DB 4; Length 1095;
 Best Local Similarity 80.0%; Pred. No. 6.1e-96;
 Matches 516; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
 QY 1 ATCCGCGTGGAGTACGTAGACACACCAATTCCTCGGTTGACAGCGCGCGGAT 60
 Db 139 ATCCGCGTGGAGTACGTAGACACACCAATTCCTCGGTTGACAGCGCGCGGAT 198
 QY 61 CCGAGATGGAGCCCGGAGCCGCTGGTGGAGCAAGAGGGCGCAGTATTGGAGTGG 120
 Db 199 CCGAGATGGAGCCCGGAGCCGCTGGTGGAGCAAGAGGGCGCAGTATTGGAGTGG 258
 QY 121 ACCAGCGGTACGCCAAGGCCAAGCAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
 Db 259 GAGACACAGATACAAAGGACACCTCAGACTTACCGAGTGGACCTGAAGACCTGCGC 318
 QY 181 CGCGCTACACAGAGCGAGCTGGGTCTCAGCCCTCAGGGAGTGAATGGCTGGAC 240
 Db 319 GCGTACTACAAACAGAGCGAGCGGGTCTCAGCCCTCAGAGCATGTACGGCTGCTAC 378
 QY 241 ATGGGGCCGAGCGAGCGCTCTCTCGCGGTATCAGCAGCAGCGGTACGAGCGCAAGGAT 300
 Db 379 TTGGAGCCAGAGCGGCTCTCTCTCGCGGTATCAGCAGCAGCGGTACGAGCGCGGAT 438
 QY 301 TACATCTCCCTGAACAGAGCACTCGCTTCTGGACCGCGCGGACACCGTGGCTCAGATC 360
 Db 439 TACCTCGGCTGAACAGAGCACTCGCTTCTGGACCGCGCGGACACCGTGGCTCAGATC 498
 QY 361 ACCAGCGCTCTATGAGCGAGAGCAATATGACAGAGGATTCAGGACCTACTCGAGGGC 420
 Db 499 TCAGAGCGCAAGTGGAGCGCGCCAAATGCGCGGAGCAGAGAGAGTACTCTGAGGGC 558
 QY 421 GAGTGCCTGGAGTGTCTCGCAGATACCTTGGAGAAATGGGAAAGGAGACGCTACAGCGGCA 480
 Db 559 CGGTGTGGAGTGTCTCGCAGATACCTTGGAGAAATGGGAAAGGAGACGCTACAGCGGCA 618
 QY 481 GATCTCCAAAGGACACAGTGTCCCAACCCCACTCTGACCATGAGGCCACCTGAGG 540
 Db 619 GAGCTCCAAAGGACACAGTGTCCCAACCCCACTCTGACCATGAGGCCACCTGAGG 678
 QY 541 TGCTGGGCGCTTCTACCTCGGAGATCACGCTACCTGGCAGCGGATGGGAG 600

Db 679 TGCTGGGCGCTTCTACCTCGGAGATCACGCTACCTGGCAGCGGATGGGAG 738
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGCCCTGCAGGG 645
 Db 739 GACCAGAGCCAGGACATGGAGCTGTGGAGACCAAGCCCTGCAGGG 783

RESULT 13
 US-08-914-372C-4
 ; Sequence 4, Application US/08914372C
 ; Patent No. 6521448
 ; GENERAL INFORMATION:
 ; APPLICANT: Edge, Albert S.B.
 ; APPLICANT: Oettinger, Henry F.
 ; TITLE OF INVENTION: PORCINE MHC CLASS I GENES AND USES THEREOF
 ; FILE REFERENCE: 05742/009001
 ; CURRENT APPLICATION NUMBER: US/08/914,372C
 ; CURRENT FILING DATE: 1997-08-19
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 1095
 ; TYPE: DNA
 ; ORGANISM: Sus scrofa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1092)
 US-08-914-372C-4

Query Match 67.6%; Score 436; DB 4; Length 1095;
 Best Local Similarity 79.8%; Pred. No. 2.6e-95;
 Matches 514; Conservative 0; Mismatches 130; Indels 0; Gaps 0;
 QY 2 TCGCGTGGAGTACGTAGACACACCAATTCCTCGGTTGACAGCGCGCGGATTC 61
 Db 140 TCACCGTGGTACGTAGACACACCAATTCCTCGGTTGACAGCGCGCGGATTC 199
 QY 62 CAGAGATGGAGCCCGGAGCCGCTGGTGGAGCAAGAGGGCGCAGTATTGGAGTGA 121
 Db 200 CAGAGATGGAGCCCGGAGCCGCTGGTGGAGCAAGAGGGCGCAGTATTGGAGTGG 259
 QY 122 CCAGCGGTACGCCAAGGCCAAGCAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 181
 Db 260 AGACACAGATCAGAAAGGAAACCGCAGACTTACCGAGTGGACCTGAACACCTGCGCA 319
 QY 182 GCGCTTACAAACAGAGCGAGGTGGGTCTCAGCCCTCAGGGAGTGAATGGCTGGACA 241
 Db 320 GCTTACTACAAACAGAGCGAGCGGTCTCAGCCCTCAGAGCATGTACGGCTGCGAG 379
 QY 242 TGGGGCCCGAGCGACCGCTCTCGCGGTATCAGCAGCAGCGGTACGAGCAAGGAT 301
 Db 380 TGGGGCCCGAGCGAGGTCTTCTCTCGCGGTATCAGTCACTTGGCTACGAGCGCGGAT 439
 QY 302 ACATCTCCCTGAACAGAGCACTCGCTCTGGACCGCGCGGACACCGTGGCTCAGATCA 361
 Db 440 ACCTCGCTTGAACAGAGCACTCGCTCTGGACCGCGCGGACACCGTGGCTCAGATCT 499
 QY 362 CCAGCGCTTCTATGAGCGAGAGATATGACAGAGGATTCAGGACCTACCTGGAGCGG 421
 Db 500 CCAAGCGCAAGTGTATGACGCAATGTGGCGAGCAGAGAGGAGTACTCTGAGGGCC 559
 QY 422 AGTGCCTGGAGTGTCTCCGAGATATCTGGAGAAATGGGAAAGGAGACGCTACAGCGCGAG 481
 Db 560 TGTGTGTGGAGGGGCTCCGAGATACCTGGAGATGGGAAAGGACACGCTGACGCGGAG 619
 QY 482 ATCTCCAAAGGACACAGTGTGCCACACCCCACTCTGACCATGAGGCCACCTGAGGT 541
 Db 620 AGCTCCAAAGGACACATGTGTGACCCCGCAGCTCTGACCTGGGGGTCACTTGGGT 679
 QY 542 GCTGGGCGCTTCTACCTCGGAGATCACGCTACCTGGCAGCGGATGGGAGG 601
 Db 680 GCTGGGCGCTTCTACCTCGGAGATCACGCTACCTGGCAGCGGATGGGAGG 739

QY 602 AACAGACCCAGGACACAGAGCTTGTGAGACAGGCTGAGGG 645
DB 740 ACCAGAGCCAGGACATGGAGCTGTGGAGACCCAGGCTGAGG 783

RESULT 14
US-09-029-045-11
; Sequence 11, Application US/09029045
; Patent No. 6056952
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Amy Sonya
; TITLE OF INVENTION: Selective Elimination of T Cells That
; TITLE OF INVENTION: Recognize Specific Preselected Targets
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,045
; FILING DATE: 02-JUN-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,964
; FILING DATE: 30-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/13873
; FILING DATE: 29-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-236100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..1107
; OTHER INFORMATION: /product= "d-D MHC"
; OTHER INFORMATION: /note= "nucleic acid encoding d-D MHC"
US-09-029-045-11

Query Match 63.5%; Score 409.8; DB 3; Length 1183;
Best Local Similarity 77.2%; Pred. No. 4.7e-89;
Matches 498; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTTCAGACGCGCGCGGAT 60
DB 148 ATGGAAGTGGCTACGTGTGACACACGAGTTCGTCGCTTCGACGACGCGGAGAT 207

QY 61 CCGAGGATGAGCGCGCGGAGCGGTGGTGGAGCAAGAGGCGCGCAGTATTGGAGTGG 120
DB 208 CCGAGATATGAGCGCGCGCGCGGTGGATAGACGAGGCGCGGAGTATTGGAGCGG 267

QY 121 ACCACGGGTAGCCCAAGCCACGACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 180
DB 268 GAGACACGGAGAGCCCAAGGCGCAATGAGCAGAGTTCCGAGTGGACCTGAGGACCGCGCTG 327

QY 181 CGCGGCTACACACGAGAGGAGCTGGGTCTCAACSCCTCCAGGGAATGAATGGCTGGAC 240
DB 328 CGCTACTACACACGAGAGCGGGCGGCTCTCACACACTCCAGTGGATGGCTGGCTGTGAC 387

QY 241 ATGGGCGCGGAGCGGCGCTCTCCGCGGGTATCACACGCGCTAGACGCGCAAGGAT 300
DB 388 GTGGAGTCGGACGCGGCGCTCTCCGCGGGTACTGGCAGTTCGCCCTACGACGCGTCCGAT 447

QY 301 TACATCTCCCTGAACGAGGACCTGGGCTCTTGAGACGCGGCGGACACCGTGGCTCAGATC 360
DB 448 TACATCGCCCTGAACGAGACCTGAAAAGCTGAGCGGCGGACATGCGCGGCGCAGATC 507

QY 361 ACCAGCGCTTCTATGAGCAGAGGAATATGACAGAGGAGTTCAGACCTACCTGGAGGCG 420
DB 508 ACCCGACGCAAGTGGGAGCAGGCTGGTGTGACAGAGAGACCGGCGCTTACCTGGAGGCG 567

QY 421 GAGTGCCTGAGTGTCTCCGAGATACCTTGGAGATGGGAAGAGAGACGCTACAGCGCGCA 480
DB 568 GAGTGGCTGGAGTGGCTCCGAGATACCTGAGAGCGGGAATGCTACGCTGTCTGGCACA 627

QY 481 GATCCTCCAAAGGACACGTTGCCACACCCCATCTCTGACCATGAGGCCACCTTGAGG 540
DB 628 GATCCCGCAAGGCGCCATGTGACCCATCACCGCAGACCTGAAAGTGATGTCCACCTGAGG 687

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DB 688 TGCTGGCGCTGGGCTTCTACCTGTGACATCACCTGACCTGGCAGCTTGAATGGGAG 747

QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGACGG 645
DB 748 GAGCTGACCCAGGAATGGAGCTTGTGGAGACAGGCGCTGACGG 792

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; Sequence 11, Application US/09435321
; Patent No. 6491908
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Amy Sonya
; TITLE OF INVENTION: Selective Elimination of T Cells That
; TITLE OF INVENTION: Recognize Specific Preselected Targets
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/435,321
; FILING DATE: 04-No. 6491908-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,045
; FILING DATE: 02-JUN-1998
; APPLICATION NUMBER: US 60/002,964
; FILING DATE: 30-AUG-1995
; APPLICATION NUMBER: WO PCT/US96/13873
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-236100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..1107
; OTHER INFORMATION: /product= "d-D MHC"
; /note= "nucleic acid encoding d-D MHC"
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-435-321-11

Query Match      63.5%; Score 409.8; DB 4; Length 1183;
Best Local Similarity 77.2%; Pred. No. 4.7e-89;
Matches 498; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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Db      208 CCGAGATATGAGCGCGGGCGGTGGATAGACGAGGGCGCGGAGTATTGGGAGCGG 267

Qy      121 ACCACGGGTACCGCAGGCGCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
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Db      328 CGCTACTACAAACAGACGCGGGCGGCTCTCACACACTCCAGTGGATGGCTGGCTGTGAC 387

Qy      241 ATGGGGCCGACGAGCGCTCTCCCGGGGTATCAACGACCGGTACGACCGCAAGGAT 300
Db      388 GTGGAGTCGAGCGGGCGGCTCTCCCGGGGTATCGGCGAGTTCGCCCTACGACGCGCTCGGAT 447

Qy      301 TACATCTCCCTGAACGAGGACCTGCGCTCCTGGACCGCGCGGACACCCGTGGCTCAGATC 360
Db      448 TACATCGCCCTGAACGAGACCTGAACACGTTGGACGGCGCGGACATGGCGGCGCAGATC 507

Qy      361 ACCCAGCGCTTCTATAGGAGGAGGAATATGACAGGAGTTCAGGACCTTACCTGGAGGGC 420
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Qy      421 GAGTGCCTGGAGTTGCTCCGCGAGATACCTTGAGAAATGGGAAGGAGAGCGCTACAGCGCGCA 480
Db      568 GAGTGCCTGGAGTTGCTCCGCGAGATACCTGAGAACCGGGAATGCTAGCTGCTGGCGACA 627

Qy      481 GATCCTCCAAAGGCACACGTTGCCCCACACGCCATCTCTGACCAATGAGGCCACCCCTGAGG 540
Db      628 GATCCCCCAAAGGCCCATGTGACCCATCACCGCAGACTGAAGGTGATGTCAACCCTGAGG 687

Qy      541 TGCTGGGCCCTGGGCTTCTACCTCGGAGATCACGCTGACCTGGCAGCGGATGGGGAG 600
Db      688 TGCTGGGCCCTGGGCTTCTACCTGCTGACATCACCTGACCTGGCAGCTGGATGGGGAG 747

Qy      601 GAACAGACCCAGGACACAGAGCTTTGTGGAGACCAAGGCTTCAGGG 645
Db      748 GAGCTGACCCAGGAATGAGCTTTGTGGAGACCAAGGCTTCAGGG 792
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 05:20:24 ; Search time 1514 Seconds
(without alignments)
1951.653 Million cell updates/sec

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Perfect score: 645

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Gapop 10.0 , Gapext 1.0

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- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644.2	99.9	645	13	US-09-819-371-3
2	640.2	99.3	816	9	US-09-925-301-589
3	640.2	99.3	1089	13	US-09-819-371-1
4	640.2	99.3	1188	13	US-10-342-887-1806
5	640.2	99.3	1188	13	US-10-172-118-1806
6	637	98.8	822	13	US-09-819-371-2
7	492	76.3	1221	13	US-10-302-172-322
8	490.4	76.0	1089	13	US-10-342-887-1160
9	490.4	76.0	1089	13	US-10-172-118-1160
10	490.4	76.0	1571	14	US-10-044-090-576
11	485.6	75.4	1175	16	US-10-093-463-79
12	485.6	75.3	1271	9	US-09-969-708-235
13	485.6	75.3	1377	14	US-10-044-090-563
14	479.2	74.3	2225	13	US-10-302-172-318

15	477.8	74.1	1533	10	US-09-971-429B-11	Sequence 11, Appl
16	475.6	73.7	1083	13	US-10-398-308-6	Sequence 6, Appl1
17	475.4	73.7	1840	13	US-10-388-360-375	Sequence 375, App
18	470.6	73.0	1080	10	US-09-960-706-711	Sequence 711, App
19	470.6	73.0	1080	10	US-09-873-319-449	Sequence 449, App
20	470.6	73.0	1082	9	US-09-969-347-218	Sequence 218, App
21	469	72.7	1170	13	US-10-108-511-1	Sequence 1, Appl1
22	469	72.7	1530	13	US-10-108-511-4	Sequence 4, Appl1
23	468.4	72.6	1559	13	US-10-302-172-317	Sequence 317, App
24	467.6	72.5	1014	13	US-10-398-308-25	Sequence 25, Appl
25	467.6	72.5	1092	13	US-10-398-308-1	Sequence 1, Appl1
26	467.4	72.5	1098	15	US-10-173-138A-46	Sequence 46, Appl
27	467.4	72.5	1466	14	US-10-044-090-564	Sequence 564, App
28	467.4	72.5	1526	14	US-10-044-090-561	Sequence 561, App
29	465.4	72.2	1069	13	US-10-398-308-16	Sequence 16, Appl
30	464.4	72.0	1083	13	US-10-398-308-5	Sequence 5, Appl1
31	463.8	71.9	1086	13	US-10-398-308-15	Sequence 15, Appl
32	463.6	71.9	2225	13	US-10-302-172-318	Sequence 318, App
33	460.6	71.4	1495	13	US-10-302-172-316	Sequence 316, App
34	457.4	70.9	1077	13	US-10-398-308-10	Sequence 10, Appl
35	457.4	70.9	1077	13	US-10-398-308-12	Sequence 12, Appl
36	457.4	70.9	1083	13	US-10-398-308-7	Sequence 7, Appl1
37	454.8	70.5	1210	13	US-10-210-172-159	Sequence 159, App
38	454.8	70.5	1210	16	US-10-093-463-77	Sequence 77, Appl
39	454.2	70.4	1059	13	US-10-398-308-9	Sequence 9, Appl1
40	453	70.2	1077	13	US-10-398-308-17	Sequence 17, Appl
41	452.6	70.2	1546	13	US-10-302-172-323	Sequence 323, App
42	451.6	70.0	1069	13	US-10-398-308-3	Sequence 3, Appl1
43	451.6	70.0	1090	13	US-10-398-308-4	Sequence 4, Appl1
44	451	69.9	1086	13	US-10-398-308-13	Sequence 13, Appl
45	450.4	69.8	1491	13	US-10-302-172-324	Sequence 324, App

ALIGNMENTS

RESULT 1

US-09-819-371-3
; Sequence 3, Application US/09819371
; Publication No. US2004005344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Car
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-819-371-3

Query Match 99.9%; Score 644.2; DB 13; Length 645;
Best Local Similarity 100.0%; Pred. No. 6.5e-171;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATCGCGGTGAGTACGTAGACGACGCAATTCCTCGGTTGACAGCGCGCGCGGATT	60
Db	1	ATCGCGGTGAGTACGTAGACGACGCAATTCCTCGGTTGACAGCGCGCGCGGATT	60
Qy	61	CCGAGGATGAGCGCGGAGCGCGTGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG	120
Db	61	CCGAGGATGAGCGCGGAGCGCGTGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG	120
Qy	121	ACCACGGGTAGCCCAAGCCCAACGACAGCTAGCCGAGTGGCCCTGAGGACCTGCTC	180
Db	121	ACCACGGGTAGCCCAAGCCCAACGACAGCTAGCCGAGTGGCCCTGAGGACCTGCTC	180
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Db 181 CGCGCTACAAACAGAGCGAGGCTGGGTCTCAGSCCTCCAGGAATGAATGGCTGGAC 240
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Qy 301 TACATCTCCCTGAAACAGAGACCTGGCTCCTCGAGCGCGCGGACACCGCTGGCTCAGATC 360
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Qy 421 GAGTGCTGAGTTGCTCCGAGATATCTTGAGAGATGGAGAGAGAGCTACAGCGCGCA 480
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Qy 541 TGCTGGCCCTGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 600
Db 541 TGCTGGCCCTGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 600
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RESULT 2

US-09-925-301-589

; Sequence 589, Application US/09925301

; Patent No. US20020052308A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA106

; CURRENT APPLICATION NUMBER: US/09/925.301

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05882

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1694

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 589

; LENGTH: 816

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-301-589

Query Match 99.3%; Score 640.2; DB 9; Length 816;

Best Local Similarity 99.5%; Pred. No. 8.7e-170;

Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 61 CCGAGATGGAGCCGCGGAGCCGTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 120
Db 209 CCGAGATGGAGCCGCGGAGCCGTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 268
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Db 269 ACCAGCGGTACGCCAAGGCCAAGCAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 328
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Qy 361 ACCAGCGCTTCATAGGCGAGAGGAATATGCGAGAGGTTTACGAGCTTACCTGAGGGC 420
Db 509 ACCAGCGCTTCATAGGCGAGAGGAATATGCGAGAGGTTTACGAGCTTACCTGAGGGC 568
Qy 421 GAGTGCTGAGTTGCTCCGAGATATCTTGAGAGATGGAGAGAGAGCTACAGCGCGCA 480
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Db 629 GATCCTCAAAGGCACACGTTGGCCACCCCATCTGTGACCATGAGGCGACCTGTAGG 688
Qy 541 TGCTGGCCCTGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 600
Db 689 TGCTGGCCCTGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 748
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RESULT 3

US-09-819-371-1

; Sequence 1, Application US/09819371

; Publication No. US2004005344A1

; GENERAL INFORMATION:

; APPLICANT: Egawa, Kohji

; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca

; TITLE OF INVENTION: Using Thereof

; FILE REFERENCE: 30815

; CURRENT APPLICATION NUMBER: US/09/819,371

; CURRENT FILING DATE: 2002-03-15

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 1089

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-819-371-1

Query Match 99.3%; Score 640.2; DB 13; Length 1089;

Best Local Similarity 99.5%; Pred. No. 8.8e-170;

Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 61 CCGAGATGGAGCCGCGGAGCCGTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 120
Db 190 CCGAGATGGAGCCGCGGAGCCGTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 249
Qy 121 ACCAGCGGTACGCCAAGGCCAAGCAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 250 ACCAGCGGTACGCCAAGGCCAAGCAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 309
Qy 181 CGCGCTCAACACAGAGCGAGGCTGGGTCTCAGSCCTCCAGGGAATGAATGGCTGGAC 240
Db 310 CGCGCTCAACACAGAGCGAGGCTGGGTCTCAGSCCTCCAGGGAATGAATGGCTGGAC 369
Qy 241 ATGGGGCCGACGAGCGCTTCCTCCGCGGTATCACAGACGCTACAGCGCAAGGAT 300
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; Sequence 1806, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-03-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1806
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1806

Query Match 99.3%; Score 640.2; DB 13; Length 1188;
Best Local Similarity 99.5%; Pred. No. 8.8e-170;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 550 GAGTGCCTGAGATTGCTCCGAGATACCTTGGAGAAATGAGAGAGCGCTACAGCGGCA 609
Qy 481 GATCCTCCAAAGGACACAGCTTGCCACACACCCCATCTCTGACATGAGGCCACCTTGAGG 540
Db 610 GATCCTCCAAAGGACACAGCTTGCCACACACCCCATCTCTGACATGAGGCCACCTTGAGG 669
Qy 541 TGCTGGGCGCTTCTACCTGGGAGATACCGTGCAGCGGATGAGCGGATGAGGAG 600
Db 670 TGCTGGGCGCTTCTACCTGGGAGATACCGTGCAGCGGATGAGCGGATGAGGAG 729
Qy 601 GAAACAGCCAGGACACAGAGCTTGTGGAGACCAAGGCTGCGAGG 645
Db 730 GAAACAGCCAGGACACAGAGCTTGTGGAGACCAAGGCTGCGAGG 774

RESULT 5
US-10-172-118-1806
; Sequence 1806, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1806
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_018950
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1806

Query Match 99.3%; Score 640.2; DB 13; Length 1188;
Best Local Similarity 99.5%; Pred. No. 8.8e-170;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATCGCGCTGAGTACGTAGACACGCAATTCCTGCGGTTCCGACGCGCGCCCGCGATT 60
Db 130 ATCGCGCTGAGTACGTAGACACGCAATTCCTGCGGTTCCGACGCGCGCCCGCGATT 189
Qy 61 CCGAGGATGGAGCCGCGGAGCGGTGGTGGAGCAAGAGGGCCCGCAGTATTGGAGTGG 120
Db 190 CCGAGGATGGAGCCGCGGAGCGGTGGTGGAGCAAGAGGGCCCGCAGTATTGGAGTGG 249
Qy 121 ACCACGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGGAACCTGTC 180
```

Db 250 ACCACAGGTACGCCAAGCCACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 309
Qy 181 CGCGGCTACAAACAGAGCGAGGTGGTCTCAGCCCTCAGGGAATGAATGGCTGGAC 240
Db 310 CGCGGCTACAAACAGAGCGAGGTGGTCTCAGCCCTCAGGGAATGAATGGCTGGAC 369
Qy 241 ATGGGCGCGAGCGACGCTCTCCGCGGTATACACAGACGCGTACGACGCGCAAGAT 300
Db 370 ATGGGCGCGAGCGACGCTCTCCGCGGTATACACAGACGCGTACGACGCGCAAGAT 429
Qy 301 TACATCTCCCTGAAACAGAGACCTGCGCTCTCGAGCCGCGGAGACACCTGGCTCAGATC 360
Db 430 TACATCTCCCTGAAACAGAGACCTGCGCTCTCGAGCCGCGGAGACACCTGGCTCAGATC 489
Qy 361 ACCAGCGCTTCTATGAGGAGAGGAATATGAGAGAGTTCAGGACCTTACCTGGAGGCG 420
Db 490 ACCAGCGCTTCTATGAGGAGAGGAATATGAGAGAGTTCAGGACCTTACCTGGAGGCG 549
Qy 421 GAGTGGCTGAGTGTCTCCGAGATCTTGGAGAAATGGGAAGAGACGCTACAGCGCGCA 480
Db 550 GAGTGGCTGAGTGTCTCCGAGATCTTGGAGAAATGGGAAGAGACGCTACAGCGCGCA 609
Qy 481 GATCTCCAAAGGACACGTTGCGCACCCACCTCTGACCATGAGGCCACCTGAGG 540
Db 610 GATCTCCAAAGGACACGTTGCGCACCCACCTCTGACCATGAGGCCACCTGAGG 669
Qy 541 TGCTGGGCGCTGGGCTTCTACCTGGGAGATCACGCTGACCTGGCAGCGGATGGGAG 600
Db 670 TGCTGGGCGCTGGGCTTCTACCTGGGAGATCACGCTGACCTGGCAGCGGATGGGAG 729
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGGCTGCAGG 645
Db 730 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGGCTGCAGG 774

RESULT 6

US-09-819-371-2
; Sequence 2, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-819-371-2

Query Match 98.8%; Score 637; DB 13; Length 822;
Best Local Similarity 99.2%; Pred. No. 6.8e-169;
Matches 640; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATCCGCGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGCGCGCGCGATT 60
Db 67 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCGACAGCGCGCGCGATT 126
Qy 61 CCGAGGATGGAGCCGCGGAGCCGCTGGGTGAGCAAGAGGGGCGCAGTATGGAGTGG 120
Db 127 CCGAGGATGGAGCCGCGGAGCCGCTGGGTGAGCAAGAGGGGCGCAGTATGGAGTGG 186
Qy 121 ACCACGGGTACGCCAAGGCCAAACGACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 187 ACCACGGGTACGCCAAGGCCAAACGACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 246
Qy 181 CGCGGCTACAAACAGAGCGAGGTGGTCTCAGCCCTCAGGGAATGAATGGCTGGAC 240
Db 247 CGCGGCTACAAACAGAGCGAGGTGGTCTCAGCCCTCAGGGAATGAATGGCTGGAC 306

Qy 241 ATGGGCGCGAGCGACGCTCTCCGCGGTATCACACAGACGCGTACGACGCGCAAGAT 300
Db 307 ATGGGCGCGAGCGACGCTCTCCGCGGTATCACACAGACGCGTACGACGCGCAAGAT 366
Qy 301 TACATCTCCCTGAAACAGAGACCTGCGCTCTCGAGCCGCGGAGACACCTGGCTCAGATC 360
Db 367 TACATCTCCCTGAAACAGAGACCTGCGCTCTCGAGCCGCGGAGACACCTGGCTCAGATC 426
Qy 361 ACCAGCGCTTCTATGAGGAGAGGAATATGAGAGAGTTCAGGACCTTACCTGGAGGCG 420
Db 427 ACCAGCGCTTCTATGAGGAGAGGAATATGAGAGAGTTCAGGACCTTACCTGGAGGCG 486
Qy 421 GAGTGGCTGAGTGTCTCCGAGATCTTGGAGAAATGGGAAGAGACGCTACAGCGCGCA 480
Db 487 GAGTGGCTGAGTGTCTCCGAGATCTTGGAGAAATGGGAAGAGACGCTACAGCGCGCA 546
Qy 481 GATCTCCAAAGGACACGTTGCGCACCCACCTCTGACCATGAGGCCACCTGAGG 540
Db 547 GATCTCCAAAGGACACGTTGCGCACCCACCTCTGACCATGAGGCCACCTGAGG 606
Qy 541 TGCTGGGCGCTGGGCTTCTACCTGGGAGATCACGCTGACCTGGCAGCGGATGGGAG 600
Db 607 TGCTGGGCGCTGGGCTTCTACCTGGGAGATCACGCTGACCTGGCAGCGGATGGGAG 666
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGGCTGCAGG 645
Db 667 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGGCTGCAGG 711

RESULT 7

US-10-302-172-322
; Sequence 322, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids a
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803.1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 322
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(213)
US-10-302-172-322

Query Match 76.3%; Score 492; DB 13; Length 1221;
Best Local Similarity 85.2%; Pred. No. 3.2e-128;
Matches 549; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 1 ATCCGCGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGCGCGCGCGATT 60
Db 267 ATCTCAGTGGGCTACGTGAGCGGACCCAGTTCGTGAGGTTCCGACAGCGCGCGAGT 326
Qy 61 CCGAGGATGGAGCCGCGGAGCCGCTGGGTGAGCAAGAGGGGCGCAGTATGGAGTGG 120
Db 327 CCGAGGATGGAGCCGCGGAGCCGCTGGGTGAGCAAGAGGGGCGCAGTATGGAGTGG 386
Qy 121 ACCACGGGTACGCCAAGGCCAAACGACAGCTGACCGAGTGGCCCTGAGGAACCTGCTC 180

Db 387 AACACAGATCTCCAAAGACCAACACAGACATTCACGAGAGGACCTCGCGACCTTGCTC 446
Qy 181 CGCGGTACAAACAGAGCGAGGTGGTCTCASCCTTCAGGGAAATGAATGGCTCGCAC 240
Db 447 CGTACTACAAACAGAGCGAGGCGGGTCTCACACCATCCAGAGGATGTCTGGCTGCGAC 506
Qy 241 ATGGGGCCACAGGACGCTCTCCCGGGGTATCACCAGCACGCTACGACGGCAAGGAT 300
Db 507 GTGGGCGGACGGGCGCTCTCCCGGGGTATAACAGTTCCCTACGAGGCAAGGAT 566
Qy 301 TACATCTCCCTGAACGAGGACCTGGCTCTGGACCGGGCGGACACCGTGGCTCAGATC 360
Db 567 TACATCGCCCTGAACGAGGACCTGAGCTCTGGACCGGGCGGACACCGGGCTCAGATC 626
Qy 361 ACCAGCGCTTCTATGAGGAGAGGAATATGACAGAGGATTCAGGACCTACCTGGAGGGC 420
Db 627 ACCAGCGCAAGTGGAGGGCGGCGGTGGTGGCGGACGACAGAGCCTACCTGGAGGGC 586
Qy 421 GAGTGCCTGAGGTGTCTCCAGATACCTGGAGAAATGGGAAGAGAGCGCTACAGCGCGCA 480
Db 687 ACGTGCCTGAGTGGCTCCGAGATACCTGGAGAAACGGGAAGGAGAGCGCTGACAGCGCG 746
Qy 481 GATCCTCCAAAGGACACAGCTGTCACCCACCCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 747 GACCCCAAGACACATGTGACCCACCCCATCTCTGACCATGAGGCCACCTGAGG 806
Qy 541 TGCTGGGCGCTTCTACCTGGGAGATCACGCTGACCTGGGAGCGGGATGGGGAG 600
Db 807 TGCTGGGCGCTTCTACCTGGGAGATCACACTGACCTGGGAGCGGGATGGCGAG 866
Qy 601 GAACAGACCCAGGACACAGAGCTGTGGAGACCGAGGCTTCAGG 644
Db 867 GACCAACTCAGGACCGAGCTTGTGGAGACCGAGCAGG 910

RESULT 8

US-10-342-887-1160
; Sequence 1160, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1160
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1160

Query Match 76.0%; Score 490.4; DB 13; Length 1089;
Best Local Similarity 85.1%; Pred. No. 9e-128;
Matches 548; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy 1 ATCCGCGTGGAGTACGTAGACGACCGCAATTCCTGGGTTCGACAGCGCGCGCGATT 60
Db 139 ATCTCAGTGGGCTACGTGGAGACGACCGCAGTTCGTGAGGTTTCGACGAGCGCGCGGAT 198

Qy 61 CCGAGATGGAGCCGCGGAGCCGTGGGTGGAGCAAGAGGGGCGGCAGTATTGGAGTGG 120
Db 199 CCGAGAGAGAGCCGCGGGCGCGCTGGATAGAGCAGGAGGGGCGCGGAATATTGGACCGG 258
Qy 121 ACCACGGGGTACGCGAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGAACTGCTC 180
Db 259 AACACACAGATCTGCAAGACCAACACAGACTGACCGAGAGAGCCTTCGCGAACTTGGCG 318
Qy 181 CGCGCTACAAACAGAGCGAGGCTGGGTCTCACGCCCTCCAGGGAATGAATGGCTTCGAC 240
Db 319 GGCTACTACACAGAGCGAGGCGGGTCTCACACCTCCAGTGGATGATGATGGCTGCGAC 378
Qy 241 ATGGGGCCGACGAGCGCTCTCCCGGGGTATCACAGCAGCGGTACAGCGGCAAGGAT 300
Db 379 GTGGGGCGGACGCGGCGCTCTCCCGGGGTATAACCAAGTTCCGCTACGACGGCAAGGAT 438
Qy 301 TACATCTCCCTGAACGAGGACCTGGCTTCCTGGACCGGGCGGACACCGTGGCTCAGATC 360
Db 439 TACATCGCCCTGAACGAGGACCTGAGCTCTTGGACCGGGCGGACACCGCGGCTCAGATC 498
Qy 361 ACCAGCGCTTCTATGAGGCGAGAGGAATATCAGAGGAGTTTCAGGACCTACCTGGAGGGC 420
Db 499 ACCAGCGCAAGTGGGAGGCGCGCTGAGCGGAGCAGCTGAGAGCCTACCTGGAGGGC 558
Qy 421 GAGTGCCTGGAGTTGCTCGCAGATACCTGGAGATGGAGAGGAGACGCTACAGCGCGCA 480
Db 559 AGGTGCGTGGAGTGGCTCCGACAGACCTGGAGAACGGGAAGGAGACGCTTCGAGCGCGG 618
Qy 481 GATCCTCCAAAGGACACAGCTTGGCCACCCACCCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 619 GACCCCAAGACACATGTGACCCACCCCATCTCTGACCATGAGGCCACCTGAGG 678
Qy 541 TGCTGGGCGCTTGGCTTCTACCTGGGAGATCAGCTGACCTGGCAGGGATGGGAG 600
Db 679 TGCTGGGCGCTTGGCTTCTACCTGGGAGATCAGCTGACCTGGCAGGGATGGGAG 738
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGGCTTCGAGG 644
Db 739 GACCAACTCAGGACCGAGCTTGTGGAGACCGAGCAGG 782

RESULT 9

US-10-172-118-1160
; Sequence 1160, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1160
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 005514
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1160

Query Match 76.0%; Score 490.4; DB 13; Length 1089;
Best Local Similarity 85.1%; Pred. No. 9e-128;

Matches 548; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGCGTTTCGACAGCGCCGCGGAT 60
 Db 178 ATCACCCTGGGCTACGTGGAGACGACGCTGTTCTGAGGTTTCGACAGCGCCGCGAT 237

QY 61 CCAGGATGAGCGCGGAGCGGCTGGTGGAGCAAGAGGGGCGCGATTTGGAGTGG 120
 Db 238 CCAGGAGAGCGCGCGGCGCATGATAGACAGGAGGGCGCGGATTTGGAGCGG 297

QY 121 ACCACGGGTACGCCAAGGCCACGACAGATGACCGAGTGGCCCTGAGGAACTTGTCTC 180
 Db 298 GAGACACAGATCTCCAAAGACCAACACAGACTTACCGAGAGGCTTGGAACTTGGC 357

QY 181 CGCGCTTACAAACAGAGCGAGGCTGGTCTCACSCCTCCAGGAAATGATGCTGGAC 240
 Db 358 GGCTACTACAAACAGAGCGAGGCGGCTCTCACACCTCCAGAGGATGTTTGGCTGCGAC 417

QY 241 ATGGGGCCCGACGAGCGCTCTCCGGGGTATCACGACCGCGTACGACGCAAGGAT 300
 Db 418 GTGGGGCCCGACGAGCGGCTCTCCGGGGTATCACGAGGACGCTTACGACGCAAGGAT 477

QY 301 TACATCTCCCTGAACAGAGGACCTCGGCTCTCGAGAGCGCGCGGACACCTTGGTTCAGATC 360
 Db 478 TACATCGCTTGAACAGAGGACCTGAGCTCTCGAGCGCGCGGACACCTTGGTTCAGATC 537

QY 361 ACCAGCGCTTGTATGAGGAGGAGGATATGAGAGGATTCAGAGCTTACCTTGGAGGC 420
 Db 538 ACCAGCGCAAGTGGAGGCGGCGCTGTGGCGGAGCAGCTGAGAGCTTACCTTGGAGGC 597

QY 421 GAGTGCCTGGAGTGTCTCCGAGATATCTGGAGAGTGGAGAGAGCGCTTACAGCGCGCA 480
 Db 598 GAGTGCCTGGAGTGTCTCCGAGATATCTGGAGAGTGGAGAGAGCGCTTACAGCGCGC 657

QY 481 GATCTCTCAAGAGGACAGCTTGGCCACACCGCTGACCCACCTCTGACCATGAGGCGCCTGAGG 540
 Db 658 GACCCCGGAGAGACAGCTGAGCGGAGCGGCTGAGAGCGCTTACCTTGGAGGC 717

QY 541 TGCTGGCGCTTGGGCTTCTACCTTGGGAGATCAGCTGAGCTGGAGCGGAGTGGGAG 600
 Db 718 TGCTGGCGCTTGGGCTTCTACCTTGGGAGATCAGCTGAGCTGGAGCGGAGTGGGAG 777

QY 601 GAACAGACCCAGGACAGAGCTTGTGGAGACCGGCTGCGAG 644
 Db 778 GACCAACTCAGGACACTGAGCTTGTGGAGACCGAGCCAGCAGG 821

RESULT 11
 US-10-093-463-79
 ; Sequence 79, Application US/10093463
 ; Publication No. US20030208039A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Gusev, Vladimir
 ; APPLICANT: Pochart, Pascal
 ; APPLICANT: Zhong, Mei
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Mezei, Peter
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: Zernusen, Bryan
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Gangolli, Esha
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Pena, Carol
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Liu, Xiaohong

Matches 548; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGCGTTTCGACAGCGCCGCGGAT 60
 Db 139 ATCTCAGTGGGCTACGTGGAGACGACGCTGTTCTGAGGTTTCGACAGCGCCGCGAGT 198

QY 61 CCAGGATGAGCGCGGAGCGGCTGGTGGAGCAAGAGGGGCGCGATTTGGAGTGG 120
 Db 199 CCAGGAGAGGCGCGGCGCGGATAGAGAGGAGGGCGCGGATTTGGAGCGG 258

QY 121 ACCACGGGTACGCCAAGGCCAACACAGACTGACCGAGTGGCCCTGAGGAACTTGTCTC 180
 Db 259 AACACACAGATCTGCPAGACCAACACAGACTGACCGAGAGGCTCGGAACTGCGC 318

QY 181 CGCGCTTACAAACAGAGCGAGGCTGGTCTCACSCCTCCAGGAAATGATGCTGGAC 240
 Db 319 GGCTACTACAAACAGAGCGAGGCTGCTCACACCTCCAGTGGATGATGGCTGCGAC 378

QY 241 ATGGGGCCCGACGAGCGCTCTCCGGGGTATCACGACCGCGTACGACGCAAGGAT 300
 Db 379 GTGGGGCCCGACGAGCGGCTCTCCGGGGTATCACGAGGACGCTTACGACGCAAGGAT 438

QY 301 TACATCTCCCTGAACAGAGGACCTCGGCTCTCGAGAGCGCGGACACCTTGGTTCAGATC 360
 Db 439 TACATCGCTTGAACAGAGGACCTGAGCTCTCGAGCGCGGAGACACCTTGGTTCAGATC 498

QY 361 ACCAGCGCTTGTATGAGGAGGAGGATATGAGAGGATTCAGAGCTTACCTTGGAGGC 420
 Db 499 ACCAGCGCAAGTGGAGGCGGCGCTGTGGCGGAGCAGCTGAGAGCTTACCTTGGAGGC 558

QY 421 GAGTGCCTGGAGTGTCTCCGAGATATCTGGAGAGTGGAGAGAGCGCTTACAGCGCGCA 480
 Db 559 ACGTGCTGGAGTGGCTTCCGAGACACCTGAGAGCGGAGAGAGCGCTTACAGCGCGCG 618

QY 481 GATCTCTCAAGAGGACAGCTTGGCCACACCGCTGACCCACCTCTGACCATGAGGCGCCTGAGG 540
 Db 619 GACCCCGGAGAGACAGCTGAGCGGAGCGGCTGAGAGCGCTTACCTTGGAGGC 578

QY 541 TGCTGGCGCTTGGGCTTCTACCTTGGGAGATCAGCTGAGCTGGAGCGGAGTGGGAG 600
 Db 679 TGCTGGCGCTTGGGCTTCTACCTTGGGAGATCAGCTGAGCTGGAGCGGAGTGGGAG 738

QY 601 GAACAGACCCAGGACAGAGCTTGTGGAGACCGGCTGCGAG 644
 Db 739 GACCAAACTCAGGACCGGAGTGTGGAGACCGAGCCAGCAGG 782

RESULT 10
 US-10-044-090-576
 ; Sequence 576, Application US/10044090
 ; Publication No. US20020137081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olga Bandman
 ; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
 ; FILE REFERENCE: PA-0028 US
 ; CURRENT APPLICATION NUMBER: US/10/044,090
 ; CURRENT FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 850
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 576
 ; LENGTH: 1571
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020137081A1 1382902.13
 ; NAME/KEY: unsure
 ; LOCATION: 1568
 ; OTHER INFORMATION: a, t, c, g, or other
 ; US-10-044-090-576

Query Match 76.0%; Score 490.4; DB 14; Length 1571;
 Best Local Similarity 85.1%; Pred. No. 9.2e-128;

APPLICANT: Spytek, Kimberly
 APPLICANT: Gorman, Linda
 APPLICANT: Spaderna, Steven
 APPLICANT: Voss, Edward
 APPLICANT: Malvankar, Uriel
 APPLICANT: Anderson, David
 APPLICANT: Patturajan, Meera
 APPLICANT: Miller, Charles
 APPLICANT: Taupier, Raymond J. Jr.
 TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypeptide
 TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.
 FILE REFERENCE: 21402-290A (Cura 590AT)
 CURRENT APPLICATION NUMBER: US/10/093,463
 CURRENT FILING DATE: 2002-06-24
 PRIOR APPLICATION NUMBER: 60/273,675
 PRIOR FILING DATE: 2001-04-14
 PRIOR APPLICATION NUMBER: 60/338,092
 PRIOR FILING DATE: 2001-12-03
 PRIOR APPLICATION NUMBER: 60/274,281
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: 60/274,101
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: 60/325,681
 PRIOR FILING DATE: 2001-09-27
 PRIOR APPLICATION NUMBER: 60/304,354
 PRIOR FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/279,995
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: 60/294,899
 PRIOR FILING DATE: 2001-05-31
 PRIOR APPLICATION NUMBER: 60/287,424
 PRIOR FILING DATE: 2001-04-30
 PRIOR APPLICATION NUMBER: 60/299,027
 PRIOR FILING DATE: 2001-06-18
 PRIOR APPLICATION NUMBER: 60/309,198
 PRIOR FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: 60/281,194
 PRIOR FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: 60/274,194
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: 60/274,849
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 60/330,380
 PRIOR FILING DATE: 2001-10-18
 PRIOR APPLICATION NUMBER: 60/275,235
 PRIOR FILING DATE: 2001-03-12
 PRIOR APPLICATION NUMBER: 60/288,342
 PRIOR FILING DATE: 2001-05-03
 PRIOR APPLICATION NUMBER: 60/275,578
 PRIOR FILING DATE: 2001-03-13
 NUMBER OF SEQ ID NOS: 370
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 79
 LENGTH: 1175
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (21)..(1113)
 US-10-093-463-79

Query Match 75.4%; Score 486.6; DB 16; Length 1175;
 Best Local Similarity 84.7%; Pred. No. 1.1e-126;
 Matches 546; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCCGACAGCGCGCGCGATT 60
 Db 159 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCCGACAGCGCGCGCGATT 218
 QY 61 CCGAGGATGAGCCCGCGGAGCCGCTGGGTGGAGCAAGAGGGCGCGCAGTATGGGAGTGG 120
 Db 219 CCGAGGATGAGCCCGCGGAGCCGCTGGGTGGAGCAAGAGGGCGCGCAGTATGGGAGTGG 278

QY 121 ACCACGGGTACGCCAAGGCCCAACGACAGCACTACCGAGTGGCCCTGAGGAACTGCTC 180
 Db 279 GAGACACGGAACGCCAAGGGCCACGCGCAGATTTACCGAGTGAACCTGCGGACCTGCTC 338
 QY 181 CGCGCTACAAACACAGAGCGAGGCTGGGTCTCACSCCTCCACAGGGAATGAATGGTGGAC 240
 Db 339 CGCTATTACAAACAGAGCGAGCATGGTTCTCACACCATCCAGAGGAAGCATGGTGGAC 398
 QY 241 ATGGGCGCGGACGAGCGGCTCTCCGCGGGTATCACAGCAAGCGGTACGAGCGGCAAGGAT 300
 Db 399 GTGGGCGCGGACGAGCGGCTCTCCGCGAGGTATGAACAGTTTCGCTACGATGGCAAGGAT 458
 QY 301 TACATCTCCCTGAAGAGGAGCCTCGCTCTCGGACCGCGCGGACACCGTGGCTCAGATC 360
 Db 459 TACATCGCCCTGAACAGGAGCCTGCACTCTCGGACCGCGCGGACACAGCGGCTCAGATC 518
 QY 361 ACCAGCGCTTCTATAGGCGAGAGAAATATCAGAGGAGTTTACAGACTTACTTGAGAGGCG 420
 Db 519 TCCAGACCAAGTGGGAAGCGGACAAATATCTCAGAGAGGTTCAGGGCTTACCTGGAGGCG 578
 QY 421 GAGTCCCTGGAGTTGCTCCGCGAGTACTTGGAGATGGGAGGAGACGCTACAGCGCGCA 480
 Db 579 AAGTGCATGGAGTGGCTCCGCGAGACCTTGAGAACCGGAGAGGAGACCTTGAGCACCGCG 638
 QY 481 GATCCTCCAAAGGCGACACGTTGCCACCCACCCCATCTCTGACCATGAGGCCACCTGAGG 540
 Db 639 GATCCCCCAAGGCGACATGTGACCCAGCACCCCATCTCTGACCATGAGGCCACCTGAGG 698
 QY 541 TGCTGGGCGCTGGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 600
 Db 699 TGCTGGGCGCTGGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 758
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGAGACCGAGGCTGCGAGG 645
 Db 759 GACCAGACCCAGGACACGAGCTTGTGAGACCGAGGCTGCGAGG 803

RESULT 12
 US-09-969-708-235
 ; Sequence 235, Application US/09969708
 ; Patent No. US20020102532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Augustus, Meena
 ; TITLE OF INVENTION: Cancer
 ; TITLE OF INVENTION: Sets
 ; FILE REFERENCE: 689290-70
 ; CURRENT APPLICATION NUMBER: US/09/969,708
 ; CURRENT FILING DATE: 2001-10-03
 ; PRIOR APPLICATION NUMBER: US/60/237,606
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: US/60/237,608
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: US/60/237,425
 ; PRIOR FILING DATE: 2000-10-03
 ; NUMBER OF SEQ ID NOS: 658
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 235
 ; LENGTH: 1271
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 ; US-09-969-708-235

Query Match 75.3%; Score 485.6; DB 9; Length 1271;
 Best Local Similarity 84.6%; Pred. No. 2e-126;
 Matches 545; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
 QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCCGACAGCGCGCGCGATT 60
 Db 139 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCCGACAGCGCGCGCGATT 198
 QY 61 CCGAGGATGAGCCCGCGGAGCCGCTGGGTGGAGCAAGAGGGCGCGCAGTATGGGAGTGG 120
 Db 199 CCGAGGATGAGCCCGCGGAGCCGCTGGGTGGAGCAAGAGGGCGCGCAGTATGGGAGTGG 258

QY 121 ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 259 GAGACACAGATCTCCAAAGACCAACACACAGACTTACCGAGAGAGCTGCGGAACCTGGCC 318
QY 181 CGCGCTACACACAGAGCGAGCTGGTCTCAACCCCTCCAGGGAATGAATGGCTGGCAG 240
Db 319 GGTACTACACACAGAGCGAGCGGCTCTACACCCCTCCAGAGATGAAGCTGGCAG 378
QY 241 ATGGGGCCCGAGCGGAGCCCTCTCCCGGGGTATACACAGCAGCGGTACGAGCGCAAGAT 300
Db 379 GTGGGSCCGAGCGGCGCTCTCTCCGCGGCATGACCACTCCGCTACGACGCGCAAGAT 438
QY 301 TACATCTCCCTGNAACAGAGACCTGCTCTCCGCGCGGAGACACCGTGGCTCAGATC 360
Db 439 TACATCGCTCTGNAACAGAGACCTGAGCTCTCGACCGCGCGGAGACACCGGCTCAGATC 498
QY 361 ACCACGGCTTCTATGAGCGAGAGGAATATGAGAGGAGTTCAGGACCTTACCTGGAGGC 420
Db 499 ACCACGGCAAGTGGAGCGGCGCTGAGCGGAGCAGTGGAGAGCTTACCTGGAGGC 558
QY 421 GAGTGGCTGAGTGTCTCGAGATACCTTGGAGATGGAAGAGACGCTACAGCGCGCA 480
Db 559 CTGTGGCTGAGTGGCTTCCGAGATACCTGGAGACGGAAGAGAGCGCTGAGCGCGC 618
QY 481 GATCTCCAAAGGCACACAGTGGCCACACCCCTCTGACCATGAGGCCACCTTGAGG 540
Db 619 GACCCCGCAAGACACATGTGACCCACACCCCTCTGACCATGAGGCCACCTTGAGG 678
QY 541 TGCTGGGCGCTGGGCTTACCTCGGAGATCACCTGAGCGAGATCACCTGGAGCGGATGGGAG 600
Db 679 TGCTGGGCGCTGGGCTTACCTCGGAGATCACACTGAGCTGGAGCGGATGGCGAG 738
QY 601 GACAGACCCAGACACAGAGCTTGGAGACCGAGCGCTGAGG 644
Db 739 GACCAAACTCAGGACCCGAGCTTGGAGACCGAGACCGAGCAGG 782

RESULT 13
US-10-044-090-563
; Sequence 563, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 563
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 4847977CB1
; NAME/KEY: unsure
; LOCATION: 1350
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-563

Query Match 75.3%; Score 485.6; DB 14; Length 1377;
Best Local Similarity 84.6%; Pred. No. 2e-126;
Matches 545; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 1 ATCGCGGTGGAGTACGTAGACACACGCAATTCCTCGGTTCCGACAGCGCGCGCGATT 60
Db 228 ATCTCAGTGGCTACTGTGAGACACGAGTTCGTGGTTCCGACAGCGCGCGAGT 287
QY 61 CCGAGGATGGAGCCCGGAGACCGGTGGTGGAGCAAGGGGCGCGAGTATGGGATGG 120
Db 288 CCGAGGGGAGCCCGCGCGCGGTGGTGGAGAGGAGGGGCGCGGAGTATGGGACCGG 347

QY 121 ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 348 GAGACACAGATGTACAGCGCCAGGACAGGCTGACCGAGTGAACCTGCGGAACCTGGCG 407
QY 181 CGCGCTACACACAGAGCGAGGCTGGGTCTCAACCCCTCCAGGGAATGAATGGCTGGCAG 240
Db 408 GGTACTACACACAGAGCGAGGAGCGGCTCTCAACCCCTCCAGTGGATGTATGGCTGGCAG 467
QY 241 ATGGGGCCCGAGCGGAGCCCTCTCCCGGGGTATACACAGCAGCGGTACGAGCGCAAGAT 300
Db 468 CTGGGGCCCGAGCGGCGCTCTCTCCGCGGATGACCACTCCGCTTACGACGCGGATGAT 527
QY 301 TACATCTCCCTGAAACAGAGACCTGCTCGCTCTCGAGACCGCGCGGACACCGGCTCAGATC 360
Db 528 TACATCGCTTGAACAGAGACCTGCTCGCTCTCGAGACCGCGCGGACACCGGCTCAGATC 587
QY 361 ACCACGGCTTCTATGAGCGAGAGGAATATGAGAGGAGTTCAGGACCTTACCTGGAGGC 420
Db 588 ACCACGGCAAGTGGAGCGGCGCTGAGCGGAGCAGTGGAGAGCTTACCTGGAGGC 647
QY 421 GAGTGGCTGAGTGTCTCCGAGATACCTTGGAGAAATGGGAAGGAGACGCTACAGCGCGCA 480
Db 548 ACGTGGCTGAGTGGCTCCGAGATACCTTGGAGAACGGGAAGGAGACGCTGACGCGCGC 707
QY 481 GATCTCCAAAGGCACACAGTGGCCACACCCCTTCTGACCATGAGGCCACCTTGAGG 540
Db 708 GACACCCAAAGACACACAGTGAACCATCCCGTCTCTGACCATGAGGCCACCTTGAGG 767
QY 541 TGCTGGGCGCTGGGCTTCTACCTCGGAGATCACGCTGAGCTGGAGCGGAGTGGGAG 600
Db 768 TGCTGGGCGCTGGGCTTCTACCTCGGAGATCACATGAGCTGGAGCGGATGGCGAG 827
QY 601 GACAGACCCAGGACACAGAGCTTGTGGAGACCGAGCGCTGAGG 644
Db 828 GACCAAACTCAGGACACCGAGCTTGTGGAGACCGAGCGCAGG 871

RESULT 14
US-10-302-172-318/c
; Sequence 318, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. US20040053250A1el Arginine-rich Protein-like Nucleic Acids a
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 803.1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 318
; LENGTH: 2225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1140)..(1769)
US-10-302-172-318

Query Match 74.3%; Score 479.2; DB 13; Length 2225;
Best Local Similarity 84.0%; Pred. No. 1.3e-124;
Matches 541; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 1 ATCGCGGTGGAGTACGTAGACACACGCAATTCCTGCGGTTCCGACAGCGCGCGCGATT 60


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Db 963 ATCTCAGTGGGCTACGTGGAGCAACGAGTTCCTGGGTTTCAGACGCGCCGCGAGT 904
Qy 61 CCGAGGATGGAGCCGCGGGAGCCCTGGGTGGAGCAAGAGGGCGCGCAGTATTGGGAGTGG 120
Db 903 CCGAGAGGGAGCCCGCGCGCCGCTGGGTGGAGCAGGAGGGCGCGGAGTATTGGGACCGG 844
Qy 121 ACCAGSGGTACGCCAAGGCCAAGCAGACAGTACCGAGTGGGCCCTTGAGGAACTGCTC 180
Db 843 GAGACACAGAAGTACAAGCGCCAGCAGCAGGCTGACCGAGTGAACCTGCGGAACCTGCGC 784
Qy 181 CGCGCTACAAACAGAGCGAGCGCTGGGTCTCAGCCCTCCAGGGGAATGAATGGCTGCGAC 240
Db 783 GGCTACTACACAGAGCGAGCGGCTCTCAGCCCTCCAGAGGATGTTGGCTGCGAC 724
Qy 241 ATGGGGCCCGAGCAGACGCTCTCTCGGGGTATACACAGCAGCGGTAGCAGCGCAAGGAT 300
Db 723 CTGGGGCCGAGCGGGCGGCTCTCTCGGGGTATACCAAGTTGCGCTTACGAGCGCAAGGAT 664
Qy 301 TACATCTCCCTGAACGAGGAGCTGGCTCTCGGACCGCGGGGACACCGTGGCTCAGATC 360
Db 663 TACATCGCCCTGACAGAGATCTGGCTCTCTGGACCGCGGGGACACGGCGGCTCAGATC 604
Qy 361 ACCAGCGCTCTTATGAGGCAAGGAATATGAGAGGAGTTTCAGGACCTACTGGAGGGC 420
Db 603 ACCAGCGCAAGTGGAGGGCGCGCGTGGAGCGGAGCAGCGAGAGCTACTGGAGGGC 544
Qy 421 GAGTCCCTGGAGTCTCTCGCAGATCTTGGAGATGGAGAGGAGAGCGTACAGCGGCA 480
Db 543 ACGTGGGTGGAGTGGCTCCGAGATACCTGGAGAACGGAGAGAGCGCTGACGCGCG 484
Qy 481 GATCTCCAAAGGACACAGTTGGCCACCACCCCATCTCTGACCATGAGGCCACCCCTGAGG 540
Db 483 GAACACCCAAAGACACACAGTGACCCCAACCATCCCGTCTCTGACCATGAGGCCACCCCTGAGG 424
Qy 541 TGCTGGGCCCTGGGTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGGATGGGGAG 600
Db 423 TGCTGGGCCCTGGGTTCTACCTCGGAGATCAGCTGACCTGGCAGTGGGATGGGGAG 364
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGCTTGTGGAGACCAGGCCAGG 644
Db 363 GACCAAACTCAGGACACCGAGCTTGTGGAGACCAGGCCAGG 320
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RESULT 15

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US-09-971-429B-11
; Sequence 11, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 11
; TYPE: DNA
; LENGTH: 1533
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 1040584.5
US-09-971-429B-11
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Query Match 74.1%; Score 477.8; DB 10; Length 1533;

Best Local Similarity 84.8%; Pred. No. 3.1e-124;

Matches 547; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

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Qy 1 ATCCGCGTGGAGTACGTAGACGACGACGATTAATTCCTGCGGTTTCGACAGCGCCGCGGATT 60
Db 154 ATCCGAGTGGGCTACGTGGACGACGACGATTTCTGTCGGTTTCGACGACCGCCGCGAGT 213
Qy 61 CCGAGGATGGAGCCGCGGGAGCCCTGGGTGGAGCA - AGAGGGGCCCGCAGTATTGGGAGTGG 119
Db 214 CCAAGAGGGGAGCCGCGCGCGCTGGGTGGAGCAGCGGAGGGCGCGGAGTATTGGGACCG 273
Qy 120 GACCAGSGGTAGGCCAAGGCCAAGCAGACAGTACCGAGTGGGCCCTGAGGAACTGCTCT 179
Db 274 GGAGACACAGAAGTACAAGCGCGAGCAGACTGACCGAGTGAACCTCGGAACTTGGG 333
Qy 180 CGCGCTACAAACAGAGCGAGCGCTGGGTCTCAGSCCTCCAGGGGAATGAATGGCTGCGA 239
Db 334 CGGCTACTACAAACAGAGCGAGCGCGGCTCTCAGCCCTCCAGAGGATGATGCTGCTCGA 393
Qy 240 CATGGGGCCCGAGCAGGAGCGCTCTCTCGGGGTATACACAGCAGCGGTACGACGGCAAGGA 299
Db 394 CTGGGGCCCGAGCGGGCGGCTCTCTCGGGGTATACCAAGTTGCGCTACGACGGCAAGGA 453
Qy 300 TTACATCTCCCTGAACGAGGAGCCTGGCTCTCTGGACCGCGGGGACACCGTGGCTCAGAT 359
Db 454 TTACATCGCCCTGAATGAGGACCTGGCTCTCTGGACCGCGCGGACACCGCGGCTCAGAT 513
Qy 360 CACCCAGCGCTTCTATGAGGCAAGGAATATGAGAGGAGTTTCAGGACCTACTCTGAGGG 419
Db 514 CACCCAGCGCAAGTGGGAGGGCGCGCTGGAGCGGAGCAGCAGAGAGCCTACTCTGAGGG 573
Qy 420 CGAGTCCCTGGAGTTCTCTCGCAGATACCTGGAGATGGAGAGGAGACGCTACAGCGCGC 479
Db 574 CAGTGGGTGGAGTGGCTTCGAGATACCTTGAGAACGGAGAGAGAGCCTGACGCGCGC 633
Qy 480 AGATCTCTCAAAGGACACAGTTGCCCCACCAACCCCATCTCTGACCATGAGGCCACCCCTGAG 539
Db 634 GGAACACCCAAAGACACACAGTGACCCCAACCATCCCGTCTCTGACCATGAGGCCACCCCTGAG 693
Qy 540 GTGCTGGGCCCTGGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGGATGGGA 599
Db 694 GTGCTGGGCCCTGGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGGATGGCGA 753
Qy 600 GGAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGGCCCTGCGAGG 644
Db 754 GGACCAAACTCAGGACACCGAGCTTGTGGAGACCAGGCCAGG 798
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Search completed: June 18, 2004, 07:33:50

Job time : 1515 secs

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 18, 2004, 07:08:39 ; Search time 22.5 Seconds
(without alignments)

5514.981 Million cell updates/sec

Title: US-09-819-371-3
Perfect score: 1183
Sequence: 1 atcgccgtggagtagctagtaga.....tggagaccaggctgcaggg 645

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xih
-Q/cgn2_1/USPTO.spool/US09819371/runat_16062004_165857_7378/app_query.fasta_1.839
-DB=PIR_78 -QWTF=fastan -SUFFIX=pr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=Eits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09819371@cgn_1_1_25@runat_16062004_165857_7378 -NCPU=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1156	97.7	362	2 A60384	MHC class I histoc
2	1141	96.4	345	2 S07114	MHC class I histoc
3	1092	92.3	348	2 S29990	histocompatibility
4	952	80.5	340	2 S11143	class I histocompa
5	931	78.7	362	1 HLHUB2	MHC class I histoc
6	928	78.4	338	2 I56116	MHC HLA-B27-HS - h
7	927	78.4	354	2 I80170	class I histocompa
8	924	78.1	363	1 S42102	MHC class I histoc
9	923	78.0	362	2 I37515	MHC class I histoc
10	919	77.7	362	2 I54505	lymphocyte antigen
11	919	77.7	362	2 I59645	HLA-B-6701 - human
12	919	77.7	362	2 I54314	MHC HLA-B39N - hum
13	919	77.7	362	2 I68850	MHC class I histoc
14	917	77.5	355	2 I80169	class I histocompa

15	916	77.4	362	2 I61865	MHC HLA-Bw42, HLA-
16	915	77.3	362	2 I68724	MHC class I histoc
17	915	77.3	362	2 I59651	lymphocyte antigen
18	914	77.3	350	2 I68747	MHC class I lympho
19	914	77.3	354	2 S24440	class I histocompa
20	914	77.3	362	2 I84431	MHC HLA-B8 chain -
21	914	77.3	362	2 I72755	HLA-B*5602 - human
22	914	77.3	362	2 I62045	Gene HLA B-1517 pr
23	914	77.3	363	2 S07113	class I histocompa
24	913	77.2	361	2 I54418	MHC class I histoc
25	913	77.2	362	1 HLHUB7	MHC class I histoc
26	913	77.2	362	2 C35997	MHC class I histoc
27	913	77.2	362	2 I61863	MHC HLA-Bw46 - hum
28	913	77.2	362	2 I61859	MHC HLA-B14 chain
29	912	77.1	274	2 S24439	MHC class I histoc
30	912	77.1	358	2 S03538	class I histocompa
31	911	77.0	362	2 S06601	HLA-B*501 - human
32	910	76.9	354	2 I59308	class I histocompa
33	910	76.9	355	2 I80171	class I histocompa
34	910	76.9	362	2 JH0541	class I histocompa
35	910	76.9	362	2 I84488	lymphocyte antigen
36	910	76.9	362	2 I72753	HLA-B*5502 - human
37	910	76.9	362	2 I56130	HLA-B*5401 - human
38	910	76.9	363	2 S03537	class I histocompa
39	909	76.8	362	2 I72752	HLA-B*5501 - human
40	909	76.8	362	2 I36962	MHC class I protei
41	909	76.8	362	2 I59655	lymphocyte antigen
42	908	76.8	362	2 I72754	HLA-B*5601 - human
43	907	76.7	362	2 I61906	MHC class I histoc
44	907	76.7	366	2 I72113	MHC histocompatibi
45	907	76.7	366	2 I38507	MHC class I histoc

ALIGNMENTS

RESULT 1

A60384
MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Jul-1999
C/Accession: A60384; JI0147
R/Lury, D.; Epstein, H.; Holmes, N.
Int. Immunol. 2, 531-537, 1990
A/Title: The human class I MHC gene HLA-F is expressed in lymphocytes.
A/Reference number: A60384; MUID:91197889; PMID:1707859
A/Accession: A60384
A/Molecule type: DNA
A/Residues: 1-362 <LUR>
X/Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.
J. Exp. Med. 171, 1-18, 1990
A/Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I
A/Reference number: JI0147; MUID:90111605; PMID:1688605
A/Accession: JI0147
A/Molecule type: DNA
A/Residues: 1-362 <GER>
A/Cross-references: GB:X17093; NID:g32223; PIDN:CAA34947.1; PID:g312407
A/Experimental source: Lymphoblastoid cell line
C/Genetics:
A/Gene: GDB:HLA-F
A/Cross-references: GDB:125714
A/Map position: 6p21.3-6p21.3
A/Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 362/1
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
C/Keywords: Glycoprotein; heterodimer; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-111/Domain: alpha-1 <A1>
F:78-104/Region: hypervariable
F:112-203/Domain: alpha-2 <A12>
F:164-192/Region: hypervariable
F:204-295/Domain: alpha-3 <A13>
F:217-282/Domain: immunoglobulin homology <IMM> #status predicted
F:107/Binding site: carbohydrate (Asn) (covalent)

Score: 1092.00 Matches: 202
 Percent Similarity: 95.81% Conservative: 4
 Best Local Similarity: 93.95% Mismatches: 9
 Query Match: 92.31% Indels: 0
 DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x S29990 (1-348)

QY 1 ATCCGCTGAGTACGTAGACACGCAATTCCTCGGTTTCACAGCGCGCGCGATT 60
 Db 46 IleaValSerTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 65
 QY 61 CCGAGGTAGAGCCCGGAGCCGTGGTGGAGCAGAGAGCGCGCGCAGTATGGAGTGG 120
 Db 66 ProArgMetGluProArgAlaProTyrValGluGlnGluGlyProGlnTyrTrpGluArg 85
 QY 121 ACCACGGGTACGCGCAAGGCCAAGCAGACACTGACCGAGTGGCCCTGAGAACCTGCTC 180
 Db 86 ThrThrGlyTyrAlaLysAlaAsnAlaArgThrAspArgValAlaLeuArgLysLeu 105
 QY 181 CGCGCTACCAACAGCAGCGAGGTGGTCTCAGSCCCTCCAGGAATGAATGCTCGCAC 240
 Db 106 LeuArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 125
 QY 241 ATGGGCGCGACGCGCTCCTCCGCGGTATCACCAGCAGCGTACGACGCAAGGAT 300
 Db 126 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 145
 QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTGGACCGCGCGACACCGTGGTCTCAGATC 360
 Db 146 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaArgile 165
 QY 361 ACCAGCGCTTCTATGAGCAGAGGATATGCAGAGAGTTCAGGACCTACCTGGAGGGC 420
 Db 166 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 185
 QY 421 GAGTGCCTGAGTTCCTCCGAGATATCTGGAGAACTGGAGAGAGCGCTACAGCGCGCA 480
 Db 186 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 205
 QY 481 GATCCTCCAAAGGACACAGTTCGCCACACCCATCTCTGACCATGAGGCCACCTGAGG 540
 Db 206 AspProProlsAlaHisLeuAlaHisProValSerAspArgGluAlaThrLeuArg 225
 QY 541 TGCTGGCCCTGGCTCTACCTCCGAGATACAGTGCCTCGCAGCGGAGTGGGAG 600
 Db 226 CysTrpAlaLeuGlyPheTyrProAspGluIleThrLeuThrTrpGlnArgAspGlyGlu 245
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTGCAGGG 645
 Db 246 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 260

RESULT 4

S11143
 Class I histocompatibility antigen alpha chain - cotton-top tamarin
 C/Species: *Saguinus oedipus* (cotton-top tamarin)
 C/Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 23-May-1997
 R/Accession: S11143
 R/Watkins, D.I.; Chen, Z.W.; Hughes, A.L.; Evans, M.G.; Tedder, T.F.; Letvin, N.L.
 Nature 346, 60-63, 1990
 A/Title: Evolution of the MHC class I genes of a New World primate from ancestral homold
 A/Reference number: S10934; MUID:90309971; PMID:2114550
 A/Accession: S11143
 A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A/Molecule type: mRNA
 A/Residues: 1-340 <NAR>
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:212-277/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 1.7e-63 Length: 340
 Score: 952.00 Matches: 177
 Percent Similarity: 86.05% Conservative: 8

Best Local Similarity: 82.33% Mismatches: 30
 Query Match: 80.47% Indels: 0
 DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x S11143 (1-340)

QY 1 ATCCGCTGAGTACGTAGACACGCAATTCCTCGGTTTCAGACGCGCGCGCGATT 60
 Db 39 IleGlyValGlyTyrValAspAspThrLeuPheValArgPheAspSerAspProSer 58
 QY 61 CCGAGGTAGAGCCCGGAGCCGTGGTGGAGCAAGAGCGCGCGCAGTATGGAGTGG 120
 Db 59 ProArgMetGluProArgAlaProTyrValGluGlnGluArgProGluTyrTrpGluAsp 78
 QY 121 ACCACGGGTACGCCAAGGCCAAGCAGACTGACCGAGTGGCCCTCAGAGAACCTGCTC 180
 Db 79 GlnThrArgValValLysAlaAsnAlaGlnThrAspArgValLysLeuArgLysLeu 98
 QY 181 CGCGCTCAACACAGCAGGAGGCTGGTCTCAGSCCCTCCAGGGAATGAATGGCTCGCAC 240
 Db 99 ArgTyrTyrAsnGlnSerGluGlyGlySerHisThrLeuGlnGlyThrAsnGlyCysAsp 118
 QY 241 ATGGGCGCGACGCGCTCCTCCGCGGTATCACCAGCAGCGCTACGACGCAAGGAT 300
 Db 119 ValGlyProAspGlyArgPheLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 138
 QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTGGACCGCGCGGACACCGTGGTCTCAGATC 360
 Db 139 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle 158
 QY 361 ACCAGCGCTTCTATGAGCAGAGGAAATGCAGAGGATTCAGAGCTTACGACCTCGAGGGC 420
 Db 159 ThrGlnArgMetTyrGluSerGluLysTyrAlaGluGluPheSerThrTyrLeuLysGly 178
 QY 421 GAGTGCCTGAGTTCCTCCGAGATACTTGGAGATGGAGAGAGACCTACAGCGCGCA 480
 Db 179 GlyCysValGluTrpLeuHisArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 198
 QY 481 GATCCTCCAAAGGACACAGTTCGCCACACCCATCTCTGACCATGAGGCCACCTGAGG 540
 Db 199 ValProProlsAlaHisValAlaHisProIleSerAspHisGluAlaIleLeuArg 218
 QY 541 TGCTGGCCCTGGCTTTCACCTCGGAGATCAGCTGACCTGCGAGCGGATGGGAG 600
 Db 219 CysTrpAlaLeuGlyPheTyrProAlaGluIleMetLeuThrTrpGlnArgAspGlyGlu 238
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTGCAGGG 645
 Db 239 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 253

RESULT 5

HLHUB2
 MHC class I histocompatibility antigen HLA-B27 alpha chain precursor - human
 C/Species: *Homo sapiens* (man)
 C/Date: 13-Aug-1986 #sequence_revision 28-Apr-1995 #text_change 01-Dec-2000
 C/Accession: S07441; A25092; B25092; A94087; S3480; S4942; A90493; B24741; I55965; S5.
 R/Weiss, E.H.; Kuon, W.; Doerner, C.; Lang, M.; Riethmuller, G.
 Immunobiology 170, 367-380, 1985
 A/Title: Organization, sequence and expression of the HLA-B27 gene: a molecular approach
 A/Reference number: S07441; MUID:86138405; PMID:3912316
 A/Accession: S07441
 A/Molecule type: DNA
 A/Residues: 1-362 <WE1>
 A/Cross-references: EMBL:X03945
 A/Note: the authors translated the codon GAC for residue 61 as Ala and the codon CAG fo
 A/Note: this allele is designated B*27052 (formerly 27W)
 R/Seemann, G.H.A.; Rein, R.S.; Brown, C.S.; Ploegh, H.L.
 EMBO J. 5, 547-552, 1986
 A/Title: Gene conversion-like mechanisms may generate polymorphism in human class I gen
 A/Reference number: A91061; MUID:86220133; PMID:3011411
 A/Accession: A25092
 A/Molecule type: DNA
 A/Residues: 1-362 <SEE>

A;Cross-references: GB:X03665; NID:G32250; PIDN:CAA27302.1; PID:G871297
A;Note: this allele is designated B*27051 (formerly 27W)
A;Accession: B25092
A;Molecule type: DNA
A;Residues: 1-100, 'N', 102-103, 'IA', 106-362 <SE2>
A;Cross-references: GB:X03664; NID:G32236; PIDN:CAA27301.1; PID:G871296
A;Note: this allele is designated B*2702 (formerly 27K)
R;Soeys, H.; Rietmuller, G.; Weiss, E.; Neo, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 1428-1432, 1986
A;Title: Complete sequence of HLA-B*27 cDNA identified through the characterization of s
A;Reference number: A94087; MUID:86149317; PMID:3485286
A;Accession: A94087
A;Molecule type: mRNA
A;Residues: 25-205, 'V', 207-362 <SZO>
A;Cross-references: GB:MI2678
A;Note: this allele is designated B*27052 (formerly 27W)
R;Vilches, C.
submitted to the EMBL Data Library, June 1993
A;Reference number: S34180
A;Accession: S34180
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100, 'S', 102-137, 'D', 139, 'Y', 141-175, 'E', 177-362 <VIL>
A;Cross-references: EMBL:X73578
A;Note: this allele is designated B*2706
R;D'Amato, M.; Sorrentino, R.
submitted to the EMBL Data Library, May 1994
A;Description: Identification of a novel HLA-B*27 subtype by restriction analysis of a cy
A;Reference number: S44942
A;Accession: S44942
A;Molecule type: mRNA
A;Residues: 1-139, 'H', 141-362 <DAM>
A;Cross-references: EMBL:Z33453; NID:G486652; PIDN:CAA83876.1; PID:G486653
R;Ezqueria, A.; Bragado, R.; Vega, M.A.; Strominger, J.L.; Woody, J.; Lopez de Castro, J
Biochemistry 24, 1733-1741, 1985
A;Title: Primary structure of papain-solubilized human histocompatibility antigen HLA-B*2
A;Reference number: A90493; MUID:85226361; PMID:2408663
A;Accession: A90493
A;Molecule type: protein
A;Residues: 25-265, 'E', 267-295 <EZO>
R;Vega, M.A.; Ezqueria, A.; Rojo, S.; Aparicio, P.; Bragado, R.; Lopez de Castro, J.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 7394-7398, 1985
A;Title: Structural analysis of an HLA-B*27 functional variant: identification of residue
A;Reference number: A94070; MUID:86042671; PMID:2414775
A;Accession: B24741
A;Molecule type: protein
A;Residues: 86-100, 'N', 102-103, 'IA', 106-107, 171-181 <VEG>
R;Coppin, H.L.; McDevitt, H.O.
J. Immunol. 137, 2168-2172, 1986
A;Title: Absence of polymorphism between HLA-B*27 genomic exon sequences isolated from no
A;Reference number: I55965; MUID:87009855; PMID:3489755
A;Accession: I55965
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 25-298 <RES>
A;Cross-references: GB:MI4013; NID:G187743; PIDN:AAA59643.1; PID:G187744
R;Blasczyk, R.; Weber, M.; Salama, A.
submitted to the EMBL Data Library, January 1995
A;Reference number: S52291
A;Accession: S52291
A;Molecule type: DNA
A;Residues: 116-192 <BLA>
A;Cross-references: EMBL:X83737
R;Del Porto, P.; D'Amato, M.; Florillo, M.T.; Tuosto, L.; Piccolella, E.; Sorrentino, R.
J. Immunol. 153, 3093-3100, 1994
A;Title: Identification of a novel HLA-B*27 subtype by restriction analysis of a cytotoxi
A;Reference number: I37485; MUID:94375872; PMID:8089488
A;Accession: I37485
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-139, 'H', 141-362 <RE3>
A;Cross-references: EMBL:Z33453; NID:G486652; PIDN:CAA83876.1; PID:G486653
C;Comment: This allele for HLA-B correlates with the development of ankylosing spondylit

C;Genetics:
A;Gene: GDB:HLA-B
A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
A;Introns: 25/1; 114/1; 207/1; 299/1; 338/1; 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: ankylosing spondylitis; duplication; glycoprotein; heterodimer; transmembra
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-362/Product: class I histocompatibility antigen HLA-B*27 alpha chain #status predic
F;25-307/Domain: extracellular #status predicted <EXT>
F;125-114/Domain: alpha-1 <EX1>
F;115-206/Domain: alpha-2 <EX2>
F;220-285/Domain: immunoglobulin homology <IMM>
F;308-331/Domain: transmembrane #status predicted <TM>
F;332-362/Domain: intracellular #status predicted <INT>
F;110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;125-188,227-283/Disulfide bonds: #status experimental

Alignment Scores:	Pred. No.:	Length:	362
Score:	6.3e-62	Matches:	173
Percent Similarity:	85.12%	Conservative:	10
Best Local Similarity:	80.47%	Mismatches:	32
Query Match:	78.70%	Indels:	0
DB:	1	Gaps:	0

US-09-819-371-3 (1-645) x HLHUB2 (1-362)

QY	1	ATCGCGTGGAGTACGTAGACGACGCAATCTCGCGTTTCGACAGCGCCGCGGATT	60
DB	47	ThrValGlyTyrValAspAspThrLeuPheValPheAspSerAspAlaSer	66
QY	61	CCGAGGATGGAGCCCGCGGAGCGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	120
DB	67	ProArgGluGluProArgAlaProTrrpLeuGluGluGlyProGluTyrTrpAspArg	86
QY	121	ACCGAGGGGTACGCAAGGCGCAACGACAGCTACCGAGTGGCGCTGAGGACCTGTC	180
DB	87	GluThrGlnIleCysLeuAlaLysAlaGlnThrAspArgGluAspLeuArgThrLeuLeu	106
QY	181	CGCGCTCAACACGAGGAGGAGTGGTCTCAGCCCTCCAGGGAATCAATGGTGGCGAC	240
DB	107	ArgTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnAsnMetTyrGlyCysAsp	126
QY	241	ATGGGCGCCGACGCGCTCTCCGCGGTATACCGAGCGCGGACCGCTGAGGAGGAG	300
DB	127	ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp	146
QY	301	TCATCTCCCTGAACGAGGAGTGGCTCGCTCGAGCGCGGACACCGTGGCTCAGATC	360
DB	147	TyrIleAlaLeuAsnGluAspLeuSerTrpThrAlaAlaAspThrAlaGlnIle	166
QY	361	ACCGAGCGCTTCTATGAGCGAGGAGATATGAGGAGGAGTTCAGGACCTTACCTGAGG	420
DB	167	ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly	186
QY	421	GAGTGGCTGGAGTTCCTCGGAGACTTGGAGATGGAGGAGGAGGAGGAGGAGGAGG	480
DB	187	GluCysValGluThrLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla	206
QY	481	GATCTCTCAAAGGCGACCGTTCGCCACACCCCATCTCTGACCATGAGGAGGAGGAGG	540
DB	207	AspProProLysThrHisValThrHisProlleSerAspHisGluAlaThrLeuArg	226
QY	541	TGCTGGCGCTGGCTTTCACCTCGGAGATCAGCTGAGCTGCGAGCGGAGGAGGAGG	600
DB	227	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGly	246
QY	601	GAGCAGACCCGACGACGAGCTTGTGGAGACCGAGCGCTGCGAGG	645
DB	247	AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	261

RESULT 6

I56116
MHC HLA-B27-HS - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C/Accession: I56116
R:Choo, S.Y.; Fan, L.A.; Hansen, J.A.
J. Immunol. 147, 174-180, 1991
A/Title: A novel HLA-B27 allele maps B27 allotype specificity to the region around position 7
A/Reference number: I56116; MUID:91268545; PMID:1711072
A/Accession: I56116
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-338 <RES>
A/Cross-references: GB:M62852; NID:G187760; PIDN:AAA59647.1; PID:G187761
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:196-261/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1,056-61 Length: 338
Score: 928.00 Matches: 172
Percent Similarity: 86.05% Conservative: 13
Best Local Similarity: 80.00% Mismatches: 30
Query Match: 78.44% Indels: 0
DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x I56116 (1-338)

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QY 1 ATCCGCTGGAGTACGTAGACACGCAATCTCTCGGTTCCGAGCGCGCGGATT 60
Db 23 ILeThrValGlyTyrValAspThrLeuPheValArgPheAspSerAspAlaIAser 42
QY 61 CCGAGGATGGACCGCGGAGCGGTCGGTGGAGCAAGAGGGCGCGAGTATGGAGTGG 120
Db 43 ProArgGluGluProAAspGluProTrpIleGluGluGluGluGluGluGluGluGlu 62
QY 121 ACCACGGGTACGCCAAGCGCAACGACAGACTACCGAGTGGCGCTGAGCAACCTGCTC 180
Db 63 GluThrGlnIleCysAlaLysAlaGlnThrAspArgGluAspLeuArgThrLeuLeu 82
QY 181 CGCGCTCAACACGAGGAGCGTGGTCTCACSCCTCCGGAAGTAAATGGTGGCAG 240
Db 83 ArgTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnSerMetTyrGlyCysAsp 102
QY 241 ATGGGGCCGACGACGCGCTCTCCGGGGTATCACACGACGCGGTACGACGGCAAGGAT 300
Db 103 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnTyrAlaTyrAspGlyLysAsp 122
QY 301 TACATCTCCCTGAACGAGACCTCGCTCTCGACCGCGCGGACACCGTGGCTCAGATC 360
Db 123 TyrIleAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle 142
QY 361 ACCCAGCGCTTCTATGAGCGAGAGGAATATGACGAGGAGTTCAGGACCTACCTGAGGGC 420
Db 143 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly 162
QY 421 GAGTGGCTGGAGTCTCTCCGAGATCTTGGAGATGGAGAGGAGAGCGTACACGCGGCA 480
Db 163 GluCysValGluTyrLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 182
QY 481 GATCTCCAAAGGACACGATGGCCACACCCCTCTCTGACCATGAGCCACCTGAGG 540
Db 183 AspProProLysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 202
QY 541 TGCTGGGCGCTGGGCTTCTACCTCGGAGATCACGCTGACCTGGCAGCGGAGTGGGAG 600
Db 203 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 222
QY 601 GAACAGACCCAGGACACAGAGTGTGGAGACCGAGCTGCGAGG 645
Db 223 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 237

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RESULT 7
I56116

class I histocompatibility antigen - chimpanzee (fragment)
C/Species: Pan troglodytes (chimpanzee)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jan-2000
C/Accession: I80170
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkir
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A/Title: A uniquely high level of recombination at the HLA-B locus.
A/Reference number: I59308; MUID:94286544; PMID:8016085
A/Accession: I80170
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-354 <RES>
A/Cross-references: EMBL:U05581; NID:G454779; PIDN:AAA50184.1; PID:G454780
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:212-277/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1,256-61 Length: 354
Score: 927.00 Matches: 172
Percent Similarity: 86.05% Conservative: 13
Best Local Similarity: 80.00% Mismatches: 30
Query Match: 78.36% Indels: 0
DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x I80170 (1-354)

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QY 1 ATCCGCTGGAGTACGTAGACACGCAATCTCTCGGTTCCGAGCGCGCGGATT 60
Db 39 ILeAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaIle 58
QY 61 CCGAGGATGGACCGCGGAGCGGTCGGTGGAGCAAGAGGGCGCGAGTATGGAGTGG 120
Db 59 ProArgMetGluProArgAlaProTrpIleGluGlnGluGluGluGluGluGluGlu 78
QY 121 ACCACGGGTACGCCAAGCGCAACGACAGACTACCGAGTGGCGCTGAGCAACCTGCTC 180
Db 79 GluThrGlnIleSerLysThrAsnAlaGlnThrTyrArgValGlyLeuArgAsnLeuArg 98
QY 181 CGCGCTCAACACGAGGAGCGTGGTCTCACSCCTCCGGAAGTAAATGGTGGCAG 240
Db 99 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrTrpGlnThrMetTyrGlyCysAsp 118
QY 241 ATGGGGCCGACGACGCGCTCTCCGGGGTATCACACGACGCGGTACGACGGCAAGGAT 300
Db 119 ValGlyProAspGlyArgLeuLeuArgGlyTyrArgGlnPheAlaTyrAspGlyLysAsp 138
QY 301 TACATCTCCCTGAACGAGACCTCGCTCTCGACCGCGCGGACACCGTGGCTCAGATC 360
Db 139 TyrIleAlaLeuAsnLysAspLeuSerTrpThrAlaAlaAspThrAlaAlaGlnIle 158
QY 361 ACCCAGCGCTTCTATGAGCGAGAGGAATATGACGAGGAGTTCAGGACCTACCTGAGGGC 420
Db 159 ThrGlnArgLysTrpGluAlaAlaArgTrpAlaGluGlnLeuArgAlaTyrLeuGluGly 178
QY 421 GAGTGGCTGGAGTCTCTCCGAGATCTTGGAGATGGAGAGGAGAGCGTACACGCGGCA 480
Db 179 ThrCysValGluTyrLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 198
QY 481 GATCTCCAAAGGACACGATGGCCACACCCCTCTCTGACCATGAGCCACCTGAGG 540
Db 199 AspProProLysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 218
QY 541 TGCTGGGCGCTGGGCTTCTACCTCGGAGATCACGCTGACCTGGCAGCGGAGTGGGAG 600
Db 219 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 238
QY 601 GAACAGACCCAGGACACAGAGTGTGGAGACCGAGCTGCGAGG 645
Db 239 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 253

```

RESULT 8
S42102
MHC class I histocompatibility antigen HLA-B*73 alpha chain precursor - human

C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 26-May-1995 #text_change 22-Jun-1999
 C/Accession: I37512; I38486; S42102
 R/Vilches, C.; de Pablo, R.; Herrero, M.J.; Moreno, M.E.; Kreisler, M.
 Immunogenetics 40, 166, 1994
 A/Title: HLA-B*73: an atypical HLA-B molecule carrying a Bw6-epitope motif variant and a
 A/Reference number: I37512; MUID:94299292; PMID:7517915
 A/Accession: I37512
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-363 <RES>
 A/Cross-references: EMBL:X77658; NID:9457466; PIDN:CAA54739.1; PID:9457467
 A/Note: this allele is designated HLA-B*7301
 R/Farham, P.; Arnett, K.L.; Adams, E.J.; Barber, L.D.; Domana, J.D.; Stewart, D.; Hildeb
 Tissue Antigens 43, 302-313, 1994
 A/Title: The HLA-B*73 antigen has a most unusual structure that defines a second lineage
 A/Reference number: I38486; MUID:95026796; PMID:7524186
 A/Accession: I38486
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-363 <RE2>
 A/Cross-references: EMBL:U04787; NID:9439858; PIDN:AAAS3175.1; PID:9439859
 C/Genetics:
 A/Gene: GDB:HLA-B
 A/Cross-references: GDB:120048; OMIM:142830
 A/Map position: 6p21.3-6p21.3
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C/Keywords: glycoprotein; transmembrane protein
 F/1-24/Domain: signal sequence #status predicted <SIG>
 F/25-363/Product: MHC class I histocompatibility antigen HLA-B*73 alpha chain #status pre
 F/25-114/Domain: alpha-1 <EX1>
 F/115-206/Domain: alpha-2 <EX2>
 F/220-285/Domain: immunoglobulin homology <IMM>
 F/307-331/Domain: transmembrane #status predicted <TM>
 F/332-362/Domain: intracellular #status predicted <INT>
 F/110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/125-188,227-283/Disulfide bonds: #status predicted

Alignment Scores:
 Pred. No.: 2,1e-61 Length: 363
 Score: 924.00 Matches: 172
 Percent Similarity: 85.12% Conservative: 11
 Best Local Similarity: 80.00% Mismatches: 32
 Query Match: 78.11% Indels: 0
 DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x S42102 (1-363)

QY 1 ATCCCGGTGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCGCGGATT 60
 DB 47 ILeThrValGlyTyrValAspPheThrGlnPheValArgPheAspSerAspAlaSer 66
 QY 61 CCGAGGATGGAGCGCGGAGCCGTGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 120
 DB 67 ProArgGluGluProArgAlaProTriedGluGlnGlyProGluTyrTrpAspArg 86
 QY 121 ACCACGGGTACGCCAGGCCACGACGACTGACCGAGTGGCCCTGAGGACCTGCTC 180
 DB 87 AsnThrGlnIleCysLysAlaLysAlaGlnThrAspArgValGlyLeuArgAsnLeuArg 106
 QY 181 CGCCGCTACACACGAGCGGCTGGTCTCACSCCTCCAGGGAATGAATGGCTGCGAC 240
 DB 107 GlyTyrTyrAsnGlnSerGluAspGlySerHisThrTrpGlnThrMetTyrGlyCysAsp 126
 QY 241 ATGGGGCCGACGACCGCTCTCCGGGGTATCACGACGCGGTACGACGCGCAAGGAT 300
 DB 127 MetGlyProAspGlyArgLeuLeuArgGlyTyrAsnGlnPheAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCCTGACGAGGACTCGCTCTGGACCGCGGCGGACCGCTGCTCAGATC 360
 DB 147 TyrIleAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCCAGCGCTCTATGAGCGCAGGAATATGACGAGGAGTTTCAGGACCTACCTGGAGGC 420

Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
 QY 421 GAGTGCCTGAGTGTCTCCAGATACTTGGAGAAATGGGAGAGAGAGCGCTACAGCGGCA 480
 DB 187 GluCysValGluTrpLeuArgArgHisLeuGluAsnGlyLysGlnThrLeuGlnArgAla 206
 QY 481 GATCCTCCAAAGGCACACAGTTCGCCACCCCATCTCTCACCATGAGGCGCACCTCAGG 540
 DB 207 AspProProlysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 226
 QY 541 TGCTGGCCCTGGCTTCTACCTCGCGAGATACACGCTGACCTGCGACCGCGGTATGGGAG 600
 DB 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GAACAGACCCAGGACACAGAGTCTGTGGACAGCAGGCGCTCGAGGG 645
 DB 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 9
 I37515
 MHC class I histocompatibility antigen HLA-B*2706 alpha chain precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
 C/Accession: I37515
 R/Vilches, C.; de Pablo, R.; Kreisler, M.
 Immunogenetics 39, 219, 1994
 A/Title: Nucleotide sequence of HLA-B*2706.
 A/Reference number: I37515; MUID:94102824; PMID:8276469
 A/Accession: I37515
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-362 <RES>
 A/Cross-references: EMBL:X73578; NID:9975658; PIDN:CAA51980.1; PID:9975659
 C/Genetics:
 A/Gene: GDB:HLA-B
 A/Cross-references: GDB:120048; OMIM:142830
 A/Map position: 6p21.3-6p21.3
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F/220-285/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 2,5e-61 Length: 362
 Score: 923.00 Matches: 171
 Percent Similarity: 85.12% Conservative: 12
 Best Local Similarity: 79.53% Mismatches: 32
 Query Match: 78.02% Indels: 0
 DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x I37515 (1-362)

QY 1 ATCCCGGTGAGTACGTAGACGACGCAATTCCTCGGTTCGACAGCGCGCGGATT 60
 DB 47 ILeThrValGlyTyrValAspPheThrGlnPheValArgPheAspSerAspAlaSer 66
 QY 61 CCGAGGATGGAGCGCGGAGCCGTGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 120
 DB 67 ProArgGluGluProArgAlaProTriedGluGlnGlyProGluTyrTrpAspArg 86
 QY 121 ACCACGGGTACGCCAGGCCACGACGACTGACCGAGTGGCCCTGAGGACCTGCTC 180
 DB 87 GluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGluSerLeuArgThrLeuLeu 106
 QY 181 CGCCGCTACACACGAGCGGCTGGTCTCACSCCTCCAGGGAATGAATGGCTGCGAC 240
 DB 107 ArgTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnAsnMetTyrGlyCysAsp 126
 QY 241 ATGGGGCCGACGACCGCTCTCCGGGGTATCACGACGCGGTACGACGCGCAAGGAT 300
 DB 127 ValGlyProAspGlyArgLeuLeuArgGlyTyrAspGlnTyrAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCCTGACGAGGACTCGCTCTGGACCGCGGCGGACCGCTGCTCAGATC 360

147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166

361 ACCACGGCTTCTATGAGCAGCAGAGGAATATGACAGAGGAGTTCTCAGGACCTACCTGGAGGCG 420

167 ThrGlnArgLysTrpGluAlaAlaArgGluAlaGluGlnLeuArgAlaTyrLeuGluGly 186

421 GAGTGCTGGAGTTGCTCCGCAGATACTTGGAGATGGGAAGGAGACGCTACAGCGCGCA 480

187 GluCysValGluTrpLeuArgArgTyrLeuGluAsnGlyGluThrLeuGlnArgAla 206

481 GATCCTCCAAAGCAGACACAGCTTGCCACACCCCATCTCTGACCATGAGGCCACCTTGAGG 540

207 AspProProLysThrHisValThrHisHisProLysAspHisGluAlaThrLeuArg 226

541 TGCTGGGCGCTGGGCTTCTACCTCGCGAGATACACGCTGACCTGGCAGCGGATGGGAG 600

227 CysTrpAlaLeuGlyPheTyrProGlyGluIleThrLeuThrTrpGlnArgAspGlyGlu 246

601 GAACAGACCCAGCAGACACAGAGCTTGTGGAGACAGCGCTGCAGGG 645

247 AspGluThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 10

I54505

lymphocyte antigen - human

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000

C:Accession: I54505

R;Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.; Juji, T.; Kano, K.; Takiguchi, Y. 1993

A;Immunogenetics 37, 212-216, 1993

A;Title: Molecular analysis of HLA-B39 subtypes.

A;Reference number: I54505; MUID:93131294; PMID:8420828

A;Accession: I54505

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-362 <RES>

A;Cross-references: GB:M94052; NID:G184163; PIN:AA52658.1; PID:G184164

C;Superfamily: Class I histocompatibility antigen; immunoglobulin homology

F;220-285/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 4,97e-61 Length: 362

Score: 919.00 Matches: 170

Percent Similarity: 85.58% Conservative: 14

Best Local Similarity: 79.07% Mismatches: 31

Query Match: 77.68% Indels: 0

DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x I54505 (1-362)

QY 1 ATCCGCGTGAGTACGTAGACGACACCAATTCCTGCGTTTCGACGCGCGCGGATT 60

DB 47 ILeSerValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66

QY 61 CCAGGATGAGCCGCGGAGCCGCTGGTGAGCAGAGGCGCGGATTTGGAGTGG 120

DB 67 ProArgGluGluProArgAlaProTrpIleGluGlnGlyProGluTyrTrpAspArg 86

QY 121 ACCACGGGTACGCCAAGCGCCACGACAGCTACCGAGTGGCGCTTGAGAACCTCTCTC 180

DB 87 AsnThrGlnIleCysLysThrAsnThrGlnThrAspArgGluSerLeuAsnLeuArg 106

QY 181 CGCCGCTTACACAGACGAGGCTGGGTCTTCACGCCCTCCAGGGAATGAATGGCTGGCAC 240

DB 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysAsp 126

QY 241 ATGGGGGCGCCAGCGACGCCCTCTCCGCGGTATCCACGACGCGGTACGACGCGCAAGGAT 300

DB 127 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnPheAlaTyrAspGlyLysAsp 146

QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTCTGACCGCGCGGACACCGTGGCTCAGATC 360

DB 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166


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QY 361 ACCAGCGCTTCTATAGCGAGGAGATATGAGAGGAGTTCAGGACCTACCTGAGGGC 420
Db 167 ThrGlnArglystrpGluAlaAaArgValAlaGluGlnLeuArgThrTyrLeuGluGly 186
QY 421 GAGTGCCTGGAGTGTCTCCGAGATCTTGGAGATGGGAGAGACGCTACAGCGCGCA 480
Db 187 ThrCysValGluTrpLeuArgThrTyrLeuGluGlnGlyGlyGluThrLeuGlnArgAla 206
QY 481 GATCCTCCAAAGGACACAGTTCGCCACCCACCTCTTGACCATGAGGCGCCACCTGAGG 540
Db 207 AspProProlysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 226
QY 541 TGCCTGGCCCTGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 600
Db 227 CysTrpAlaLeuGlyPheThrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 246
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACACAGCGCTGCAGGG 645
Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 12
I54314
MHC HLA-B39N - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I54314
R:Ogawa, A.; Tokunaga, K.; Nakajima, F.; Kikuchi, A.; Karaki, S.; Kashiwase, K.; Ge, J.;
Hum. Immunol. 41, 241-247, 1994
A:Title: Identification of the gene encoding a novel HLA-B39 subtype. Two amino acid sub
A:Reference number: I54314; MUID:95189597; PMID:7533753
A:Accession: I54314
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:I22649; NID:g437369; PIDN:AAA69861.1; PID:g437370
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:I20048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:220-285/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 4.97e-61 Length: 362
Score: 919.00 Matches: 170
Percent Similarity: 85.58% Conservative: 14
Best Local Similarity: 79.07% Mismatches: 31
Query Match: 77.68% Indels: 0
DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x I54314 (1-362)
QY 1 ATCCGCGTGGAGTACGTAGACGACACGCAATTCTCGGTTCCGACAGCGCGCGCGATT 60
Db 47 IleSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
QY 61 CCGAGGATGAGAGCGCGGAGCCCTCGGTGGAGCAAGAGGCGCGCGAGTATGGAGTGG 120
Db 67 ProArgGluGluProArgAlaProTrpIleGlnGluGlyProGluTyrTrpAspArg 86
QY 121 ACCACGGGTACGCCAAGGCCAACGACAGACTCAGCGAGTGGCCCTGAGCAACCTGCTC 180
Db 87 AsnThrGlnIleCysLeuThrAsnThrGlnThrAspArgGluSerLeuA-GsnLeuArg 106
QY 181 CGCCGCTACAACAGAGCGAGCTGGGTCTCACCCCTCCAGGGAATGAATGGCTGGAC 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysAsp 126
QY 241 ATGGGCGCGAGGAGCGCTCTCCGCGGTATCACAGCACGCGTACGCGGCAAGGAT 300
Db 127 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnPheAlaTyrAspGlyLeuAsp 146
QY 301 TACATCTCCCTGAACAGAGACCTGGCTCTCTGGAGCCGCGCGGACACCGTGGCTCAGATC 360

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Db 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAlaSerThrAlaAlaGlnIle 166
QY 361 ACCAGCGCTTCTATAGCGAGGAGATATGAGAGGAGTTCAGGACCTACCTGAGGGC 420
Db 167 ThrGlnArglystrpGluAlaAaArgValAlaGluGlnLeuArgThrTyrLeuGluGly 186
QY 421 GAGTGCCTGGAGTGTCTCCGAGATCTTGGAGATGGGAGAGACGCTACAGCGCGCA 480
Db 187 ThrCysValGluTrpLeuArgThrTyrLeuGluGlnGlyGlyGluThrLeuGlnArgAla 206
QY 481 GATCCTCCAAAGGACACAGTTCGCCACCCACCTCTTGACCATGAGGCGCCACCTGAGG 540
Db 207 AspProProlysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 226
QY 541 TGCCTGGCCCTGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 600
Db 227 CysTrpAlaLeuGlyPheThrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 246
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACACAGCGCTGCAGGG 645
Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 13
I68850
MHC class I histocompatibility antigen precursor - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000
C:Accession: I68850; I38464
R:Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.; Ujji, T.; Kano, K.; Takig
Hum. Immunol. 37, 212-216, 1993
A:Title: Molecular analysis of HLA-B39 subtypes.
A:Reference number: I54505; MUID:93131294; PMID:8420828
A:Accession: I68850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:M94053; NID:g184165; PIDN:AAA52659.1; PID:g184166
R:Adams, E.J.; Martinez-Naves, E.; Arnett, K.L.; Little, A.M.; Tyan, D.B.; Parham, P
Tissue Antigens 45, 18-26, 1995
A:Title: HLA-B16 antigens: sequence of the ST-16 antigen, further definition of two B39
A:Reference number: I38464; MUID:95242308; PMID:7725307
A:Accession: I38464
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-362 <RES>
A:Cross-references: EMBL:U04243; NID:g458659; PIDN:AAA87396.1; PID:g458660
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:I20048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:220-285/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 4.97e-61 Length: 362
Score: 919.00 Matches: 170
Percent Similarity: 85.05% Conservative: 15
Best Local Similarity: 79.07% Mismatches: 30
Query Match: 77.68% Indels: 0
DB: 2 Gaps: 0

US-09-819-371-3 (1-645) x I68850 (1-362)
QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCTCGGTTCCGACAGCGCGCGCGATT 60
Db 47 IleSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
QY 61 CCGAGGATGAGAGCGCGGAGCCCTCGGTGGAGCAAGAGGCGCGCGAGTATGGAGTGG 120
Db 67 ProArgGluGluProArgAlaProTrpIleGlnGluGlyProGluTyrTrpAspArg 86
QY 121 ACCACGGGTACGCCAAGGCCAACGACAGACTCAGCGAGTGGCCCTGAGCAACCTGCTC 180
Db 87 AsnThrGlnIleCysLeuThrAsnThrGlnThrAspArgGluSerLeuA-GsnLeuArg 106
QY 181 CGCCGCTACAACAGAGCGAGCTGGGTCTCACCCCTCCAGGGAATGAATGGCTGGAC 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysAsp 126
QY 241 ATGGGCGCGAGGAGCGCTCTCCGCGGTATCACAGCACGCGTACGCGGCAAGGAT 300
Db 127 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnPheAlaTyrAspGlyLeuAsp 146
QY 301 TACATCTCCCTGAACAGAGACCTGGCTCTCTGGAGCCGCGCGGACACCGTGGCTCAGATC 180

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Db      87  GluThrGlnIleSerLysThrAsnThrGlnThrAspArgGluSerLeuArgAsnLeuArg 106
QY      181  CGCGCTACAAACAGAGAGGCTGGGTCTCAGCCCTCCAGGGAATGAATGGCTCGCAC 240
Db      107  GlyTyrTyranGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysAsp 126
QY      241  ATGGGGCCGACGAGCCCTCCCGGGTATCACCAGACCGGTCAGACGCGCAAGGAT 300
Db      127  ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnPheAlaTyrAspGlyLysAsp 146
QY      301  TACATCTCCCTGAGCAGGAGGACCTCGCTTCTGACCGCGCGACCGGCTCAGATC 360
Db      147  TyrIleAlaLeuAsnGluAspLeuSerSerTyrThrAlaAlaAspThrAlaGlnIle 166
QY      361  ACCAGCGCTTCTATAGGCGAGGAATATCGAGAGGATTCAGGACCTACCTGGAGGC 420
Db      167  ThrGlnArgLysTyrGluAlaAlaArgValAlaGlnGlnLeuArgThrTyrLeuGluGly 186
QY      421  GAGTGCCTGAGTGTCTCCGAGTACTTGGAGNAATGGAGAGGAGCGCTACAGCGCGCA 480
Db      187  ThrCysValGluTyrLeuArgTyrGlyLeuGlnGlyLysGluThrLeuGlnArgAla 206
QY      481  GATCCTCCAAAGGCACAGTGTCCCGACCCCATCTCTGACCATGAGGCGCACCCCTGAGG 540
Db      207  AspProLysThrHisValThrHisHisProLysSerAspHisGluAlaThrLeuArg 226
QY      541  TGCTGGCGCTGGCTTACCTCCGCGAGATCAGCTGACCTGACCGCGGATGGGAG 600
Db      227  CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
QY      601  GAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGCAGGG 645
Db      247  AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

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RESULT 14

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180169
Class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jan-2000
C:Accession: I80169
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544; PMID:8016085
A:Accession: I80169
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U05580; NID:9454777; PIDN:AAAS0183.1; PID:9454778
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
P:212-277/Domain: immunoglobulin homology <IMM>

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Alignment Scores:
Pred. No.: 7.01e-61 Length: 355
Score: 917.00 Matches: 171
Percent Similarity: 85.58% Conservative: 13
Best Local Similarity: 79.53% Mismatches: 31
Query Match: 77.51% Indels: 0
DB: 2 Gaps: 0

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US-09-819-371-3 (1-645) x I80169 (1-355)

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QY      1  ATFCGCGTGGAGTACGTAGACACGCAATTCCTCGCGTTTCGACGCGCGCGCGATT 60
Db      39  IleThrValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaSer 58
QY      61  CCGAGATGAGACCGCGGGAGCGGTGGTGGAGCAAGAGGGCGCGCAGTATGGAGTGG 120
Db      59  ProArgMetGluProArgAlaProTyrPheGluGlnGluGlyProGluTyrTrpAspArg 78
QY      121  ACCACGGGTACGCAAGGCCAACGACAGACTGACCGAGTGGCCCTCAGGAACCTGCTC 180

```

```

Db      79  GluThrArgAsnMetLysAlaSerAlaGlnThrAspArgGluAsnLeuArgIleAlaLeu 98
QY      181  CGCCCTCAACACAGAGAGGCTGGGTCTCAGCCCTCCAGGGAATGAATGGCTCGCAC 240
Db      99  ArgTyrTyranGlnSerGluAlaGlySerHisIleIleGlnArgMetTyrGlyCysAsp 118
QY      241  ATGGGGCCGACGAGCGCTCTCCCGGGTATCACCAGACCGGTCAGACGCGCAAGGAT 300
Db      119  MetGlyProAspGlyArgLeuLeuArgGlyTyrTyrGlnTyrAlaTyrAspGlyLysAsp 138
QY      301  TACATCTCCCTGAACAGGAGCTCGCTTCTGACCGCGCGGACACCGTGGCTCAGATC 360
Db      139  TyrIleAlaLeuAsnGluAspLeuSerSerTyrThrAlaAlaAspThrAlaGlnIle 158
QY      361  ACCAGCGCTTCTATAGGCGAGGAATATCGAGAGGATTCAGGACCTACCTGAGGCG 420
Db      159  ThrGlnArgLysTyrGluAlaAlaArgAlaAlaGluGlnArgAlaTyrLeuGluGly 178
QY      421  GAGTGCCTGAGTGTCTCCGAGTACTTGGAGNAATGGAGAGGAGCGCTACAGCGCGCA 480
Db      179  ThrCysValGluTyrLeuArgTyrGlyLeuGlnGlyLysGluThrLeuGlnArgAla 198
QY      481  GATCCTCCAAAGGCACAGTGTCCCGACCCCATCTCTGACCATGAGGCGCACCCCTGAGG 540
Db      199  AspProLysThrHisValThrHisHisProLysSerAspHisGluAlaThrLeuArg 218
QY      541  TGCTGGCGCTGGCTTACCTCCGCGAGATCAGCTGACCTGCGCGGATGGGAG 600
Db      219  CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 238
QY      601  GAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGCAGGG 645
Db      239  AspGlnThrGlnAspThrGluLeuValGluThrArgProGluGly 253

```

RESULT 15

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161865
MHC HLA-Bw42, HLA-Bw65 chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I61865; I61862; I79639
R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A:Title: Diversity and diversification of HLA-A,B,C alleles.
A:Reference number: I36956; MUID:89235215; PMID:2715640
A:Accession: I61865
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:M24034; NID:9187822; PIDN:AAAS9667.1; PID:9386904
A:Accession: I61862
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-34, 'A', 36-90, 'C', 92, 'TNT', 96-120, 'W', 122-136, 'Y', 138-139, 'F', 141-154, 'S',
A:Cross-references: GB:M24032; NID:9187816; PIDN:AAAS9664.1; PID:9386902
R:Bronson, S.K.; Pei, J.; Tailon-Miller, P.; Chorney, M.J.; Geraghty, D.E.; Chaplin, D
Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
A:Title: Isolation and characterization of yeast artificial chromosome clones linking t
A:Reference number: I59188; MUID:91156671; PMID:2000377
A:Accession: I79639
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 26-34, 'A', 36-90, 'C', 92, 'TNT', 96-120, 'W', 122-136, 'Y', 138-139, 'F', 141-154, 'S',
A:Cross-references: GB:M59840; NID:9187758; PIDN:AAAS9646.1; PID:9187759
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
A:Introns: 115/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: Glycoprotein; transmembrane protein
P:220-285/Domain: immunoglobulin homology <IMM>

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Alignment Scores:

Search completed: June 18, 2004, 07:39:52
Job time : 26.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 18, 2004, 06:01:58 ; Search time 15 Seconds
(without alignments)
4478.033 Million cell updates/sec

Title: US-09-819-371-3

Perfect score: 1183

Sequence: 1 atgcgcgtgagtagctaga.....tggagaccaggctgcaggg 645

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US09819371/runat.16062004.165856.7359/app.query.fasta.1.839
-DB=SwissProt.42 -QFMT=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -STAR=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORES=pt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pt -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USERS=US09819371 @CGN 1.1 13 @runat.16062004.165856.7359 -NCPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1156	97.7	362	1 HLA-F HUMAN	P30511 homo sapien
2	1141	96.4	346	1 IC28 PANTR	P36215 pan troglod
3	1092	92.3	348	1 HLA-F MACMU	P33617 macaca mula
4	931	78.7	362	1 1B27 HUMAN	P33989 homo sapien
5	924	78.1	363	1 1B73 HUMAN	Q31612 homo sapien
6	919	77.7	362	1 1B39 HUMAN	P30475 homo sapien
7	919	77.7	362	1 1B67 HUMAN	Q29836 homo sapien
8	916	77.4	362	1 1B42 HUMAN	P30480 homo sapien
9	915	77.3	362	1 1B47 HUMAN	P30485 homo sapien
10	914	77.3	362	1 1B08 HUMAN	P30460 homo sapien
11	913	77.2	362	1 1B07 HUMAN	P01889 homo sapien
12	913	77.2	362	1 1B14 HUMAN	P30462 homo sapien
13	913	77.2	362	1 1B37 HUMAN	P18463 homo sapien
14	913	77.2	362	1 1B46 HUMAN	P30484 homo sapien
15	912	77.1	362	1 1B02 PANTR	P13751 pan troglod
16	912	77.1	362	1 1B61 HUMAN	Q31610 homo sapien
17	911	77.0	362	1 1B40 HUMAN	Q04826 homo sapien
18	910	76.9	359	1 1B01 PANTR	P13750 pan troglod

19	910	76.9	362	1 1B03 GORGO	P30381 gorilla gor
20	910	76.9	362	1 1B54 HUMAN	P30492 homo sapien
21	909	76.8	362	1 1A02 PANTR	P16210 pan troglod
22	909	76.8	362	1 1B55 HUMAN	P30493 homo sapien
23	908	76.8	362	1 1B56 HUMAN	P30508 homo sapien
24	907	76.7	366	1 1C12 HUMAN	Q95365 homo sapien
25	906	76.6	362	1 1B38 HUMAN	P30379 gorilla gor
26	905	76.5	362	1 1B01 GORGO	P30464 homo sapien
27	905	76.5	362	1 1B15 HUMAN	P30447 homo sapien
28	905	76.5	366	1 1C08 HUMAN	P30505 homo sapien
29	904	76.4	362	1 1B78 HUMAN	P30498 homo sapien
30	903	76.3	362	1 1B02 GORGO	P30380 gorilla gor
31	903	76.3	362	1 1B48 HUMAN	P30486 homo sapien
32	902	76.2	366	1 1C07 HUMAN	P10321 homo sapien
33	901	76.2	365	1 1A23 HUMAN	P30447 homo sapien
34	900	76.1	362	1 1B35 HUMAN	P30685 homo sapien
35	900	76.1	362	1 1B22 HUMAN	Q29718 homo sapien
36	899	76.0	362	1 1B58 HUMAN	P10319 homo sapien
37	899	76.0	366	1 1C14 HUMAN	P30510 homo sapien
38	898	75.9	362	1 1B57 HUMAN	P18465 homo sapien
39	898	75.9	366	1 1C02 GORGO	P30385 gorilla gor
40	898	75.9	366	1 1C04 GORGO	P30387 gorilla gor
41	897	75.8	365	1 1A01 SAGOR	P30515 saginurus oe
42	896	75.7	362	1 1B53 HUMAN	P30491 homo sapien
43	896	75.7	366	1 1C03 HUMAN	P04222 homo sapien
44	895	75.7	362	1 1B59 HUMAN	Q29940 homo sapien
45	895	75.7	366	1 1C03 GORGO	P30386 gorilla gor

ALIGNMENTS

RESULT 1	HLAF HUMAN	STANDARD;	PRT;	362 AA.
ID	HLAF HUMAN			
AC	P30511;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last annotation update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CDA12).			
DE	HLA-F OR HLA-F OR HLA-5.4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=90111605; PubMed=1688605;			
RA	Garaghty D.E., Wei X., Orr H.T., Koller B.H.;			
RA	"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of			
RT	a class I coding sequence linked to a novel transcribed repetitive			
RT	element."			
RL	J. Exp. Med. 171:1-18(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=91197899; PubMed=1707659;			
RA	Lury D., Epstein H., Holmes N.;			
RA	"The human class I MHC gene HLA-F is expressed in lymphocytes."			
RL	Int. Immunol. 2:531-537(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	Shima S., Tamiya G., Oka A., Inoko H.;			
RA	"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."			
RA	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
CC	-/- FUNCTION: Involved in the presentation of foreign antigens to the			
CC	immune system.			
CC	-/- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-			
CC	microglobulin).			

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CC EMBL; X17093; CAA34947.1; -.
 DR EMBL; AF000521; BAB63337.1; -.
 DR PIR; A60384; A60384.
 DR HSSP; Q30201; 1A6Z.
 DR Genew; HGNC:4963; HLA-F.
 DR MIM; 143110; -.
 DR GO; GO:0030106; F.MHC class I receptor activity; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig_1.
 DR Pfam; PF00129; MHC_I_1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I_1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 362
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN F. ALPHA-1.
 FT DOMAIN 22 111
 FT EXTRACELLULAR ALPHA-1.
 FT DOMAIN 112 203
 FT EXTRACELLULAR ALPHA-2.
 FT DOMAIN 204 295
 FT EXTRACELLULAR ALPHA-3.
 FT DOMAIN 296 305
 FT CONNECTING PEPTIDE.
 FT TRANSMEM 306 329
 FT DOMAIN 330 362
 FT CYTOPLASMIC TAIL.
 FT DISULFID 122 185
 FT BY SIMILARITY.
 FT DISULFID 224 280
 FT BY SIMILARITY.
 FT CARBOHYD 107 107
 FT N-LINKED (GLCNAC. .) (BY SIMILARITY).
 SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Alignment Scores:

Pred. No.: 2,42e-71 Length: 362
 Score: 1156.00 Matches: 213
 Percent Similarity: 99.07% Conservative: 0
 Best Local Similarity: 99.07% Mismatches: 2
 Query Match: 97.72% Indels: 0
 DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x HLA_F_HUMAN (1-362)

QY 1 ATGCGCTGAGTACGTAGACGACGCAATTCCTGCGTTCACAGCGCGCGCGGAT 60
 Db 44 ILEAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 63
 QY 61 CCGAGGTGAGCGCGCGGAGCGTGGTGGAGCAAGAGCGCGCGGAGTGGAGTGG 120
 Db 64 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTrp 93
 QY 121 ACCACSGGTACGCAAGGCAAGCAGACGACTGACCGAGTGGCTGAGGAACTGCTC 180
 Db 84 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 103
 QY 181 CGCGCTACACACGACGAGGCTGGTCTCASCCTCCAGGAGTATGATGCTCGAC 240
 Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
 QY 241 ATGGGGCCGACGACGCGCTCTCCGCGGGTATCACCAGCAGCGGTACGACGGCAAGGAT 300
 Db 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
 QY 301 TACATCTCCCTGACGAGGACCTGGCTCTCTGACCGCGGCGGACCGGCTCAGATC 360
 Db 144 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
 QY 361 ACCCAGCGCTCTTATGAGGCGAGGAATATGACAGGAGTTCAGGACCTACCTGAGGCG 420

Db 164 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuGluGly 183
 QY 421 GAGTGCCTGAGTGTCTCGCAGATACCTTGGAGATGGAGAGAGAGCGCTACAGCCGCA 480
 Db 184 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 203
 QY 481 GATCTCTCAAGGACACGTTGCCACCCACCCCATCTCTGACCATGAGCCACCTGAGG 540
 Db 204 AspProProlYsAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 223
 QY 541 TGCTGGGCGCTGCTTCTACCTCGCGAGATCACGCTGACCTGACCTGGCAGCGGATGGGAG 600
 Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACACAGCGCTCCAGGG 645
 Db 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258

RESULT 2

1C28_PANTR STANDARD; PRT; 346 AA.
 ID 1C28_PANTR
 AC P16215;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE CHLA class I histocompatibility antigen, CH28 alpha chain precursor.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90201944; PubMed=1690682;
 RA Lawlor D.A., Warren E., Ward F.E., Parham P.;
 RT "Comparison of class I MHC alleles in humans and apes.";
 RL Immunol. Rev. 113:147-185(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88319000; PubMed=3412487;
 RA Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.;
 RT "HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.";
 RL Nature 335:268-271(1988).
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
 CC -!- SURUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).

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CC EMBL; M30685; AA87973.1; -.
 DR HSSP; Q30201; 1A6Z.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig_1.
 DR Pfam; PF00129; MHC_I_1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I_1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 346
 FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT CH28 ALPHA CHAIN.

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FT DOMAIN 22 111 EXTRACELLULAR ALPHA-1.
FT DOMAIN 112 203 EXTRACELLULAR ALPHA-2.
FT DOMAIN 204 295 EXTRACELLULAR ALPHA-3.
FT DOMAIN 296 305 CONNECTING PEPTIDE.
FT TRANSMEM 306 329
FT DOMAIN 330 346 CYTOPLASMIC TAIL.
FT DISULFID 122 185 BY SIMILARITY.
FT DISULFID 224 280 BY SIMILARITY.
FT CARBOHYD 107 107 N-LINKED (GLCNAC...) (BY SIMILARITY).
SQ SEQUENCE 346 AA; 39084 MW; F63E882D5C250971 CRC64;

Alignment Scores:
Pred. No.: 2,51e-70 Length: 346
Score: 1141.00 Matches: 211
Percent Similarity: 98.60% Conservative: 1
Best Local Similarity: 98.14% Mismatches: 3
Query Match: 96.45% Indels: 0
DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x 1C28_PANTR (1-346)
Qy 1 ATCCCGTGGAGTACGTAGACACACGCAATTCCTCGGTTCCGACGCGCGCGGATT 60
Db 44 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 63
Qy 61 CCGAGGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 64 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluArg 83
Qy 121 ACCACGGGTACGCGCAAGCGCAAGCGCAAGCGCAAGCGCGCGCGCGCGCGCGCG 180
Db 84 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
Qy 181 CGCGCTACACACGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
Qy 241 ATGGGGCCGACGCGACCGCTCTCCGCGGTTATCACACGACGCGCGCGCGCGCGCG 300
Db 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
Qy 301 TACATCTCCCTGAACGAGGACCTCGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 144 TyrIleSerLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrValAlaGlnIle 163
Qy 361 ACCACGCGCTCTATGAGCGAGAGAGATATCCAGAGGATTCAGGACCTACCTGAGGCG 420
Db 164 ThrGlnArgPheTyrGluAlaGluGluTyrAlaGluGluPheArgThrTyrLeuGluGly 183
Qy 421 GAGTGCCTGGAGTTGCTCCGCGAGATCTTGGAGATCGGAGGAGAGCGCTACAGCGCGCA 480
Db 184 GluCysLeuGluLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 203
Qy 481 GATCCTCCAAAGGCACACGTTGCCACACCCATCTCTGACCATGAGGCGACCCCTGAGG 540
Db 204 AspProLysAlaHisIleAlaHisProIleSerAspHisGluAlaThrLeuArg 223
Qy 541 TGCTGGCGCTGGCTTACCTCGGAGATCACGCTGAGTACGCTGCGCGCGGATGGGAG 600
Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
Qy 601 GAACAGACCCGAGGACACAGAGCTGTGTGAGACCGAGCGCTGCGAGG 645
Db 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258

```

RESULT 3

```

HLAF_MACMU
ID HLAF_MACMU STANDARD; PRT; 348 AA.
AC P33617;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F

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DE antigen) (leukocyte antigen F).
GN HLA-F OR HLA-F.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
ON NCBI_TaxID=9544;
RX SEQUENCE FROM N.A.
RA MEDLINE=93246295; PubMed=8482576;
RA "Oetting N., Bontrop R.E.;
RT "Characterization of the rhesus macaque (Macaca mulatta) equivalent
RT of HLA-F";
RL Immunogenetics 38:141-145 (1993).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z21819; CAA79885.1; -.
CC PIR; S29990; S29990.
CC DR HSSP; Q30201; 1A6Z.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003597; IG_c1.
CC DR InterPro; IPR003006; IG_MHC.
CC DR InterPro; IPR001039; MHC_I.
CC DR Pfam; PF00047; IG_1.
CC DR Pfam; PF00129; MHC_I; 1.
CC DR PRINTS; PR01638; MHCCLASSI.
CC DR ProDom; PD000050; MHC_I; 1.
CC DR SMART; SM00407; IGc1_1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC KW MHC I; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 21 BY SIMILARITY.
CC CHAIN 22 348 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC FT ALPHA CHAIN F.
CC FT DOMAIN 22 113 EXTRACELLULAR ALPHA-1.
CC FT DOMAIN 114 205 EXTRACELLULAR ALPHA-2.
CC FT DOMAIN 296 307 EXTRACELLULAR ALPHA-3.
CC FT TRANSMEM 308 331 CONNECTING PEPTIDE.
CC FT DOMAIN 332 348 CYTOPLASMIC TAIL.
CC FT DISULFID 124 187 BY SIMILARITY.
CC FT DISULFID 226 282 BY SIMILARITY.
CC FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 348 AA; 39300 MW; 77BD7E3B9B11E0F7 CRC64;

Alignment Scores:
Pred. No.: 5,34e-67 Length: 348
Score: 1092.00 Matches: 202
Percent Similarity: 95.81% Conservative: 4
Best Local Similarity: 93.95% Mismatches: 9
Query Match: 92.31% Indels: 0
DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x HLAF_MACMU (1-348)
Qy 1 ATCCCGTGGAGTACGTAGACACACGCAATTCCTCGGTTCCGACGCGCGCGGATT 60
Db 46 IleAlaValSerTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 65
Qy 61 CCGAGGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 66 ProArgMetGluProArgAlaProTyrValGluGlnGluGlyProGlnTyrTrpGluArg 85

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QY 121 ACCACGGGTACCCCAAGCCACACGACTGACGAGTGGCCCTGAGGAACCTGCTC 180
 Db 86 ThrThrGlyTyrAlaYsAlaAsnAlaA-gfthrAspArgValAlaLeuArgYsLeuLeu 105
 QY 181 CGCCGCTTACAACACAGACGAGCGTGGTCTCTACSCCCTCCAGCGAATGATGGCTCGAC 240
 Db 106 LeuArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 125
 QY 241 ATGGGCGCCGACGACGACCTCTCCCGGGGTATCACACGACGCGTACGACGCGCAGGAT 300
 Db 126 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyYsAsp 145
 QY 301 TACATCTCCCTGAACACGAGACCTCGCTCTCTGACCGCGCGGACACCCGTGGCTCAGATC 360
 Db 146 TyrIleSerLeuAsnGlnAspLeuArgSerTyrThrAlaAlaAspThrValAlaArgIle 165
 QY 361 ACCAGCGCTTATAGGACAGAGGAATATGACAGAGAGTTCAGGACCTACCTGGAGGCG 420
 Db 166 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluPheArgThrTyrLeuGluGly 185
 QY 421 GAGTGCTCGAGTGTCTCCACAGATCTTCGAGATGGGAGAGACGCTACAGCCGCGCA 480
 Db 186 GluCysLeuGluLeuLeuArgArgTyrLeuGluAsnGlyYsGlnThrLeuGlnArgAla 205
 QY 481 GATCCTCCAAAGGACACGTTGGCCACCCACCCATCTTGCATGAGGCCACCTGAGG 540
 Db 206 AspProProYsAlaHisLeuAlaHisHisProValSerAspArgGluAlaThrLeuArg 225
 QY 541 TGCTGGGCGCTGCTCTACCTCGGAGATCAGCTGACCGTACCGGAGCGGATGGGAG 600
 Db 226 CysTrpAlaLeuGlyPheTyrProAspGluIleThrLeuThrTyrGlnArgAspGlyGlu 245
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTCGACGG 645
 Db 246 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 260
 RESULT 4
 1B27 HUMAN STANDARD; PRT; 362 AA.
 AC P03989; P10317; P19373; P30467; Q08136; Q29846;
 AC Q29961;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-27 alpha chain precursor
 DE (MHC class I antigen B*27).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*2701).
 RP MEDLINE=86138405; PubMed=3912316;
 RA Weiss B.H., Kuon W., Doerner C., Lang M., Riethmuller G.;
 RT "Organization, sequence and expression of the HLA-B27 gene: a
 RT molecular approach to analyze HLA and disease associations.";
 RL Immunobiology 170:367-380(1985).
 RN [2]
 RP SEQUENCE OF 25-361 FROM N.A. (B*2701).
 RP MEDLINE=86149317; PubMed=3485286;
 RA Szoets H., Riethmuller G., Weiss E., Mee T.;
 RT "Complete sequence of HLA-B27 cDNA identified through the
 RT characterization of structural markers unique to the HLA-A, -B, and
 RT -C allelic series.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
 RN [3]
 RP SEQUENCE OF 25-295 (B*2701).
 RP MEDLINE=85226361; PubMed=2408663;
 RA Ezquerria A., Bragado R., Vega M.A., Strominger J.L., Woody J.,
 RA Lopez de Castro J.A.;
 RT "Primary structure of papain-solubilized human histocompatibility

antigen HLA-B27."; Biochemistry 24:1733-1741(1985).
 RN [4]
 RP SEQUENCE FROM N.A. (B*2701 AND B*2702).
 RP MEDLINE=86220133; PubMed=3011411;
 RA Seemann G.H.A., Rein R.S., Brown C.S., Ploegh H.L.;
 RT "Gene conversion-like mechanisms may generate polymorphism in human
 RT class I genes."; EMBO J. 5:547-552(1986).
 RN [5]
 RP SEQUENCE FROM N.A. (B*2702).
 RP MEDLINE=9608486; PubMed=7482496;
 RA Moses J.H., Marsh S.G.E., Arnett K.L., Adams E.J., Bodmer J.G.,
 RA Farham P.;
 RT "On the nucleotide sequences of B*2702 and B*2705."; Tissue Antigens 46:50-53(1995).
 RN [6]
 RP SEQUENCE OF 86-107 AND 171-181 (B*2702).
 RP MEDLINE=86042671; PubMed=2414775;
 RA Vega M.A., Ezquerria A., Rojo S., Aparicio P., Bragado R.,
 RA Lopez de Castro J.A.;
 RT "Structural analysis of an HLA-B27 functional variant: identification
 RT of residues that contribute to the specificity of recognition by
 RT cytolytic T lymphocytes."; Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
 RN [7]
 RP SEQUENCE FROM N.A. (B*2703).
 RP MEDLINE=88227491; PubMed=3286582;
 RA Choo S.Y., St John T., Orr H.T., Hansen J.A.;
 RT "Molecular analysis of the variant alloantigen HLA-B27d (HLA-B*2703)
 RT identifies a unique amino acid substitution."; Hum. Immunol. 21:209-219(1988).
 RN [8]
 RP SEQUENCE FROM N.A. (B*2704 AND B*2706).
 RP MEDLINE=96134006; PubMed=8550101;
 RA Rudvalis M., Bowness P., Wordsworth P.;
 RT "The nucleotide sequence of HLA-B*2704 reveals a new amino acid
 RT substitution in exon 4 which is also present in HLA-B*2706."; Immunogenetics 43:160-162(1996).
 RN [9]
 RP SEQUENCE FROM N.A. (B*2706).
 RP MEDLINE=94102824; PubMed=8276469;
 RA Vilches C., de Pablo R., Kreisler M.;
 RT "Nucleotide sequence of HLA-B*2706."; Immunogenetics 39:219-219(1994).
 RN [10]
 RP SEQUENCE FROM N.A. (B*2707).
 RP MEDLINE=91268545; PubMed=1711072;
 RA Choo Y.S., Fan L.A., Hansen J.A.;
 RT "A novel HLA-B27 allele maps B27 allospecificity to the region around
 RT position 70 in the alpha 1 domain."; J. Immunol. 147:174-180(1991).
 RN [11]
 RP SEQUENCE FROM N.A. (B*2708).
 RP MEDLINE=95064789; PubMed=7974468;
 RA Hildebrand W.H., Domina J.D., Shen S.Y., Marsh S.G.E., Bunce M.,
 RA Guttridge M.G., Darke C., Farham P.;
 RT "The HLA-B70i antigen is encoded by a new subtype of HLA-B27
 RT (B*2708)"; Tissue Antigens 44:47-51(1994).
 RN [12]
 RP SEQUENCE FROM N.A. (B*2709).
 RP TRISUE=Blood;
 RP MEDLINE=94375872; PubMed=8089488;
 RA Del Porto P., D'Amato M., Fiorillo M.T., Tuocto L., Piccolella E.,
 RA Sorrentino R.;
 RT "Identification of a novel HLA-B27 subtype by restriction analysis of
 RT a cytotoxic gamma/delta T cell clone."; J. Immunol. 153:3093-3100(1994).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
 RP MEDLINE=92405152; PubMed=1525820;
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;

"The three-dimensional structure of HLA-B*27 at 2.1-Å resolution suggests a general mechanism for tight peptide binding to MHC.";
Cell 110:1035-1048(1992).
[14]
X-RAY CRYSTALLOGRAPHY.
MEDLINE=92018187; PubMed=1922337;
Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
"The structure of HLA-B*27 reveals nonamer self-peptides bound in an extended conformation.";
Nature 353:321-325(1991).
[15]
X-RAY CRYSTALLOGRAPHY (2.1 ÅNGSTROMS) OF 25-300.
MEDLINE=22344622; PubMed=12244049;
Hulsmeier M., Hillig R.C., Volz A., Ruhl M., Schroder W., Saenger W., Ziegler A., Uchanska-Ziegler B.;
"HLA-B*27 subtypes differentially associated with disease exhibit subtle structural alterations.";
J. Biol. Chem. 277:47844-47853(2002).
[16]
3D-STRUCTURE MODELING OF 115-206.
MEDLINE=95148615; PubMed=7846047;
Rognan D., Scapozza L., Folkers G., Daese A.;
"Rational design of nonnatural peptides as high-affinity ligands for the HLA-B*2705 human leukocyte antigen.";
Proc. Natl. Acad. Sci. U.S.A. 92:753-757(1995).
-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of B-27 are known:
B*2701=B*2705, B*2702 (B27.2; B-27k; B27e), B*2703 (B27d), B*2704 (B*2706, B*2707, B*2708 (B7Qui) and B*2709 (B27-ci). The sequence shown is that of B*2701.
-!- DISEASE: HLA-B*27 is associated with the development of ankylosing spondylitis.

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EMBL; X03945; CAA27578.1; ALT_SEQ.
DR EMBL; X03664; CAA27301.1; -
DR EMBL; X03667; CAA27301.1; JOINED.
DR EMBL; L38504; AAA69724.1; -
DR EMBL; M54883; AAA59616.1; -
DR EMBL; X03665; CAA27302.1; -
DR EMBL; X03666; CAA27302.1; JOINED.
DR EMBL; M12967; AAA36221.1; -
DR EMBL; U27608; AAC50444.1; -
DR EMBL; U35734; AAC50447.1; -
DR EMBL; X73578; CAA51980.1; -
DR EMBL; M62852; AAA59647.1; -
DR EMBL; L19923; CAA59658.1; -
DR EMBL; Z33453; CAA83876.1; -
DR PIR; I37515; I37515.
DR PIR; I56116; I56116.
DR PIR; S07441; HLHUB2.
DR PDB; 1HSA; 15-OCT-92.
DR PDB; 1ROG; 30-SEP-94.
DR PDB; 1ROI; 30-SEP-94.
DR PDB; 1ROJ; 30-SEP-94.
DR PDB; 1ROK; 30-SEP-94.
DR PDB; 1ROL; 30-SEP-94.
DR PDB; 1LGE; 23-DEC-02.
DR Genew; HGNC:4932; HLA-B.
DR MIM; 142830; -
DR InterPro; IPR007110; Ig-like.

DR	InterPro; IPR003597; IG_c1.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR001039; MHC_I.
DR	Pfam; PF00047; IG_1.
DR	Pfam; PF00129; MHC_1.
DR	PRINTS; PR01638; MHCCLASSI.
DR	ProDom; PD000050; MHC_I; 1.
DR	SMART; SM00407; IGc1; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
DR	PROSITE; PS00290; IG_MHC; 1.
KW	MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism;
KW	3D-structure.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	TRANSMEM

Alignment Scores:

Pred. No.:	4,61e-56	Length:	362
Score:	931.00	Matches:	173
Percent Similarity:	85.12%	Conservative:	10
Best Local Similarity:	80.47%	Mismatches:	32
Query Match:	78.70%	Indels:	0
DB:	1	Gaps:	0

US-09-819-371-3 (1-645) x 1B27_HUMAN (1-362)

QY	1	ATCGCCGCTGGAGTACGTAGACACACGCAATTCCTCGGTTTCGACGCCGCCGCATT	60
Db	47	IleThrValGlyTyrValAspThrLeuPheValArgPheAspSerAspAlaAser	66
QY	61	CGAGATGAGCCGCGGAGCGCTGGTGAGCAGAGGGCGCGAGTAGTTCGGACTGG	120
Db	67	ProArgGluGluProArgAlaProTrpIleGluGlnGlyProGluTyrTrpAspArg	86
QY	121	ACCACCGGCTACGCCAACGCCACGACAGACTGACCGAGTGGCCCTCGAGGAACCTGCTC	180
Db	87	GluThrGlnIleCysIysAlaLysAlaGlnThrAspArgGluAspLeuArgThrLeuLeu	106
QY	181	CGCCGCTACMACAGAGCGAGGCTGGTCTCACSCCTCCAGGAAATGATGGCTCGCAC	240
Db	107	ArgTyrTyraGlnSerGluAlaGlySerHisThrLeuGlnAsnMetTyrGlyCysAsp	126
QY	241	ATGGGGCCCCAGCGAGCCCTCTCCGCGGTATCACACGACCGCTACGACGCCAAGAT	300
Db	127	ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp	146
QY	301	TACATCTCCCTGAACAGAGACCTGGCTCTGTGACCGCGGACACCGTGGCTCAGATC	360
Db	147	TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaIleGlnIle	166
QY	361	ACCAGCGCTCTATGAGGCAGAGGAATAATGACAGAGAGTTCAGGACCTACCTGGAGGC	420
Db	167	ThrGlnArgIysTrpGluAlaAlaArgValaGluGlnLeuArgAlaTyrLeuGluGly	186
QY	421	GAGTGCCTGGAGTTGCTCCGAGATACCTTGGAGNATGGAGAGGACGCTACAGCGGCA	480
Db	187	GluCysValGluTrpLeuArg-gTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla	206
QY	481	GATCCTCCAAGGCACACGTTGCCACACCCCACATCTCTGACCATGAGGCCACCTGAGG	540
Db	207	AspProProllysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg	226
QY	541	TGCTGGGCCCTGGGCTTCTACCTTGGGAGATACAGCTGACCTGGCAGCGGATGGGAG	600
Db	227	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu	246
QY	601	GAACAGACCCAGGACACAGAGCTGTGTGAGACACCGGCTCGAGGG	645

Db	247	AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	261
DB	1B73_HUMAN	STANDARD;	PRT; 363 AA.
AC	Q31612;		
DT	10-OCT-2003	(Rel. 42, Created)	
DT	10-OCT-2003	(Rel. 42, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	HLA class I histocompatibility antigen, B-73 alpha chain precursor		
DE	(MHC class I antigen B*73).		
GN	HLA-B OR HLAB		
OS	Homo sapiens (human)		
OC	Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (B*7301).		
RX	MEDLINE=95026796; PubMed=7524186;		
RA	Parham P., Arnett K.L., Adams E.J., Barber L.D., Domona J.D.,		
RA	Stewart D., Hildebrand W.H., Little A.-M.;		
RT	"The HLA-B73 antigen has a most unusual structure that defines a		
RT	second lineage of HLA-B alleles.";		
RL	Tissue Antigens 43:302-313(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A. (B*7301).		
RX	MEDLINE=94299292; PubMed=7517915;		
RA	Vilches C., de Pablo R., Herrero M.J., Moreno M.E., Kreisler M.;		
RA	"HLA-B73: an atypical HLA-B molecule carrying a Bw6-epitope motif		
RT	variant and a B pocket identical to HLA-B27.";		
RL	Immunogenetics 40:166-166(1994).		
RN	[3]		
RP	SEQUENCE FROM N.A. (B*7301).		
RX	MEDLINE=96164742; PubMed=8547229;		
RA	Hofmann H.J., Kristensen T.J., Jensen T.G., Graugaard B., Lamm L.U.;		
RA	"Antigenic characteristics and cDNA sequences of HLA-B73.";		
RL	Eur. J. Immunogenet. 22:231-240(1995).		
RN	[4]		
RP	SEQUENCE FROM N.A. (B*7301).		
RC	TISSUE=Blood;		
RA	MEDLINE=22512041; PubMed=12622774;		
RA	Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,		
RA	Madrigal J.A., Little A.-M.;		
RT	"Cloning and sequencing full-length HLA-B and -C genes.";		
RL	Tissue Antigens 61:20-48(2003).		
CC	-!- FUNCTION: Involved in the presentation of foreign antigens to the		
CC	immune system.		
CC	-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-		
CC	microglobulin).		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; U04787; AB53175.1; -		
DR	EMBL; X77658; CA54739.1; -		
DR	EMBL; L24373; AA96733.1; -		
DR	EMBL; AJ311601; CAC35319.1; -		
DR	PIR; I37512; S42102.		
DR	HSSP; P03989; 1HGA.		
DR	Genew; HGNC:4932; HLA-B.		
DR	MM; 142830; -		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003597; Ig_c1.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR001039; MHC_I.		
DR	Pfam; PF00047; Ig; 1.		
DR	Pfam; PF00129; MHC_I; 1.		

DR	PRINTS; PR01638; MHCCLASSI.		
DR	PRODOM; PD00050; MHC_I; 1.		
DR	SMART; SM00407; IGc1; 1.		
DR	PROSITE; PS0835; IG_LIKE; 1.		
DR	PROSITE; PS00290; IG_MHC; 1.		
KW	MHC I; Transmembrane; Glycoprotein; Signal.		
FT	SIGNAL	1	24
FT	CHAIN	25	363
FT	DOMAIN	25	114
FT	DOMAIN	115	206
FT	DOMAIN	207	298
FT	DOMAIN	299	308
FT	TRANSMEM	309	333
FT	DOMAIN	334	363
FT	CARBOHYD	110	110
FT	DISULFID	125	188
FT	DISULFID	227	283
SQ	SEQUENCE	363 AA;	40435 MW; 04522E97C1E11C40 CRC64;
Alignment Scores:			
Pred. No.:	1.38e-55	Length:	363
Score:	924.00	Matches:	172
Percent Similarity:	85.12%	Conservative:	11
Best Local Similarity:	80.00%	Mismatches:	32
Query Match:	78.11%	Indels:	0
DB:	1	Gaps:	0
US-09-819-371-3	(1-645) x 1B73_HUMAN	(1-363)	
QY	1	ATCGCCGTGGAGTACGTAGACGACGCAATCTCGGGTTCGACAGCGCCGCGCGATT	60
DB	47	ileThrValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaSer	66
QY	61	CGAGGATGGAGCGCGGAGCGGTGGTGGAGGAGGCGCGCGCAGTATTGGAGTGG	120
DB	67	ProArgGluGluProAlaProTrpIleGluGluGlyProGluTyrTrpAspArg	86
QY	121	ACCACGGGTACGCCAAGGCCAACGACAGACTCAGCAGTGGCGCTCAGGACCTGCTC	180
DB	87	AsnThrGlnIleCysLysAlaLysAlaGlnThrAspArgValGlyLeuArgAsnLeuArg	106
QY	181	CGCCGCTACACAGGAGGAGTGGTGGTCCACCCCTCCAGGGAATGAATGGCTGGCAC	240
DB	107	GlyTyrTyrAsnGlnSerGluAspGlySerHisThrTrpGlnThrMetTyrGlyCysAsp	126
QY	241	ATGGGCGCCGACGACGCGCTCTCCGCGGGTATCACCACGACGCGCTACGCGCAGGAT	300
DB	127	MetGlyProAspGlyArgLeuLeuArgGlyTyrAsnGlnPheAlaTyrAspGlyLysAsp	146
QY	301	TACATCTCCCTGAAGAGAGCCTCGCTCTCGACCGCGGGGACACCGTGGCTCAGATC	360
DB	147	TyrIleAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle	166
QY	361	ACCCAGCGTCTATGAGGACAGGAGATATGAGAGGAGTTCCAGGACCTACCTGAGGCGC	420
DB	167	ThrGlnArgGlyTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGly	186
QY	421	GAGTGGCTGGAGTGTCTCCGAGATACCTTGGAGATGGAGAGACGCTACGAGCGCGCA	480
DB	187	GluCysValGluTrpLeuArgArgHisLeuGluAsnGlyLysGluThrLeuGlnArgAla	206
QY	481	GATCCTCCAAAGGCACACGTTGCCACACCCCTCTGACCATGAGGCCACCTGAGG	540
DB	207	AspProProLysThrHisValThrHisLysProIleSerAspHisGluAlaThrLeuArg	226
QY	541	TGCTGGCGCTGGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG	600
DB	227	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu	246
QY	601	GAACAGCCAGGACACAGAGCTTGGAGACGACGCGCTGCGAGG	645
DB	247	AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	261


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RESULT 6
1B39 HUMAN
ID 1B39 HUMAN STANDARD; PRT: 362 AA
AC P30475; O02960; Q78217; P30476; P79504; Q29665; Q29697; Q29749;
AC Q29847; Q29852; Q29858; Q8HW0; Q8TP07;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B*39 alpha chain precursor
DE (MHC class I antigen B*39).
DE HLA-B OR HLAB
CN Homo sapiens (human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*3901 AND B*3902).
RX MEDLINE=93131294; PubMed=8420828;
RA Kato N., Karaki S., Kashiwase K., Mueller C., Akaza T., Juji T.,
RA Kano K., Takiguchi M.;
RT "Molecular analysis of HLA-B39 subtypes.";
RL Immunogenetics 37:212-216(1993).
RN [2]
RP SEQUENCE FROM N.A. (B*3902 AND B*3905).
RX MEDLINE=95242308; PubMed=7725307;
RA Adams E.J., Martinez-Naves E., Arnett K.L., Little A.-M.,
RA Tyan D.B., Parham P.;
RT "HLA-B16 antigens: sequence of the ST-16 antigen, further definition
of two B38 subtypes and evidence for convergent evolution of
B*3902.";
RL Tissue Antigens 45:18-26(1995).
RN [3]
RP SEQUENCE FROM N.A. (B*3904).
RX TISSUE=Peripheral blood;
RC TISSUE=Peripheral blood;
RX MEDLINE=95189597; PubMed=7533753;
RA Ogawa A., Tokunaga K., Nakajima F., Kikuchi A., Karaki S.,
RA Kashiwase K., Ge J., Hannestad K., Juji T., Takiguchi M.;
RT "Identification of the gene encoding a novel HLA-B39 subtype. Two
amino acid substitutions on the beta-sheet out of the peptide-binding
floor form a novel serological epitope.";
RL Hum. Immunol. 41:241-247(1994).
RN [4]
RP SEQUENCE FROM N.A. (B*3909).
RX TISSUE=Blood;
RC TISSUE=Blood;
RX MEDLINE=96435466; PubMed=8838352;
RA Ramos M., Postigo J.M., Vilches C., Layrisse Z., Lopez de Castro J.A.;
RT "Primary structure of a novel HLA-B39 allele (B*3909) from the Warao
Indians of Venezuela. Further evidence for local HLA-B diversification
in South America.";
RL Tissue Antigens 46:401-404(1995).
RN [5]
RP SEQUENCE FROM N.A. (B*3906).
RX MEDLINE=96387677; PubMed=8795147;
RA Zhao W., Fernandez-Vina M.A., Lazaro A.M., Araujo H.A., Miller S.,
RA Stastny P.;
RT "Full cDNA of a novel HLA-B39 subtype, B*3906.1";
RL Tissue Antigens 47:435-437(1996).
RN [6]
RP SEQUENCE FROM N.A. (B*3906).
RX Zhang L., Ellexson M.E., Hildebrand W.H.;
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (B*3910).
RX MEDLINE=97142356; PubMed=8988545;
RA Wells R.S., Parham P.;
RT "A novel recombinant HLA-B*39 allele (B*3910) in a South African
Zulu.";
RL Tissue Antigens 48:595-597(1996).
RN [8]
RP SEQUENCE FROM N.A. (B*3910).
RX MEDLINE=97378991; PubMed=9234488;
RA Vilches C., Bunce M., de Pablo R., Moreno M.E., Puente S., Sanz L.,

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RA Kreieler M.;
RT "The novel HLA-Cw*1802 allele is associated with B*5703 in the Bubi
population from Equatorial Guinea.";
RL Tissue Antigens 49:644-648(1997).
RN [9]
RP SEQUENCE FROM N.A. (B*3901).
RA Kashiwase K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A. (B*3924).
RC TISSUE=Peripheral blood;
RX MEDLINE=22447027; PubMed=12558815;
RA Escarot E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;
RT "Complementary DNA sequence of the HLA-B*3924 allele.";
RL Eur. J. Immunogenet. 30:11-12(2003).
RN [11]
RP SEQUENCE OF 10-362 FROM N.A. (B*3908).
RX MEDLINE=96435470; PubMed=8838356;
RA Adams E.J., Little A.-M., Arnett K.L., McAuley J.E., Williams R.C.,
RA Parham P.;
RT "Three new HLA-B alleles found in Mexican-Americans.";
RL Tissue Antigens 46:414-416(1995).
RN [12]
RP SEQUENCE OF 26-206 FROM N.A. (B*3912).
RX MEDLINE=99299758; PubMed=10372543;
RA Marcos C.Y., Fernandez-Vina M.A., Lazaro A.M., Moraes M.E.,
RA Moraes J.R., Stastny P.;
RT "Novel HLA-A and HLA-B alleles in South American Indians.";
RL Tissue Antigens 53:476-485(1999).
RN [13]
RP SEQUENCE OF 26-206 FROM N.A. (B*3912).
RX MEDLINE=20066996; PubMed=10600013;
RA Lazaro A.M., Moraes M.E., Marcos C.Y., Moraes J.R.,
RA Fernandez-Vina M.A., Stastny P.;
RT "Evolution of HLA-class I compared to HLA-class II polymorphism in
Tereña, a South-American Indian tribe.";
RL Hum. Immunol. 60:1138-1149(1999).
RN [14]
RP SEQUENCE OF 26-206 FROM N.A. (B*3923).
RX MEDLINE=21160452; PubMed=11360515;
RA Akesaka T., Kashiwase K., Ishikawa Y., Tanaka H., Shimizu M.,
RA Kawai S., Akaza T., Takahashi T., Juji T.;
RT "Allele frequency of HLA-B39 in the Japanese population and
identification of a novel B39 allele, B*3923.";
RL Tissue Antigens 57:169-172(2001).
RN [15]
RP SEQUENCE OF 60-196 FROM N.A. (B*3907).
RX MEDLINE=95317819; PubMed=7797264;
RA Garber T.L., Butler L.M., Trachtenberg E.A., Erlich H.A., Rickards O.,
RA De Stefano G., Watkins D.I.;
RT "HLA-B alleles of the Cavapa of Ecuador: new B39 and B15 alleles.";
RL Immunogenetics 42:19-27(1995).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of B-39 are known: B*3901
CC (B39.1), B*3902 (B9.2), B*3903, B*3904 (B39N), B*3905 (ST-16),
CC B*3906 (B39G), B*3907 (B39uW3), B*3909, B*3910, B*3912 (B3901v),
CC B*3923 (B39022v1) and B*3924. The sequence shown is that of
CC B*3901.
CC -----
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CC -----
CC EMBL; M94052; AAA52658.1; --
CC EMBL; M94051; AAA52660.1; --
DR

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DR EMBL; L36318; AAA73942.1; -
DR EMBL; L22649; AAA69861.1; -
DR EMBL; U23480; AAC50392.1; -
DR EMBL; L42024; AAB59484.1; -
DR EMBL; U29083; AAC32741.1; -
DR EMBL; U56246; AAB01985.1; -
DR EMBL; Y09058; CAA70261.1; -
DR EMBL; AB091216; BAC11810.1; -
DR EMBL; AB091218; BAC11811.1; -
DR EMBL; AF428252; AAB63555.1; -
DR EMBL; L42280; AAB51452.1; -
DR EMBL; U76395; AAB39108.1; -
DR EMBL; U76394; AAB39108.1; JOINED.
DR EMBL; AB032097; BAA84116.1; -
DR EMBL; U15640; AAB74047.1; -
DR PIR; I38876; I38876.
DR PIR; I54314; I54314.
DR PIR; I54505; I54505.
DR PIR; I68850; I68850.
DR PIR; I84488; I84488.
DR HSP; P30460; IAGD.
DR Genew; HGNC:4932; HLA-B.
DR MM; 142830; -.
DR GO; 0005887; C: integral to plasma membrane; NAS.
DR GO; 0003006; F: MHC class I receptor activity; NAS.
DR GO; 0006955; P: immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
DR MHC_I; Transmembrane, Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT
FT FT
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT VARIANT 33 33
FT VARIANT 35 35
FT VARIANT 35 35
FT FT
FT FT
FT FT
Alignment Scores:
Pred. No.: 3, 01e-55
Score: 919.00
Percent Similarity: 85.58%
Best Local Similarity: 79.07%
Query Match: 77.68%
DB: 1
Gaps: 0
US-09-819-371-3 (1-645) x 1B39_HUMAN (1-362)
QY 1 ATCCCGTGGAGTACGTAGACACACGCAATCTCGGTGCGTTCGACACGCGCGCGGCGATT 60
D 47 IISerValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
QY 61 CCGAGATGGAGCCCGGAGCCGCGGTGGGTGGAGCAAGAGGGCGCGCAGTATTGGGAGTGG 120

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Db 67 ProArgGluGluProArgAlaProTyrPheGlnGluGluGlyProGluTyrTrpAspArg 86
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Db 87 AsnThrGlnIleCysLysThrAsnThrGlnThrAspArgGluSerLeuArgAsnLeuArg 106
QY 181 CGCGCTCAACACGAGAGCGAGCTGGGTCTCACCSCCTCCAGGGAATGAATGGTGGCAG 240
Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysasp 126
QY 241 ATGGGGCCCGACGAGCGCTCTCCGGGGTATCACCAGCACGCGGTACGACGGCAAGGAT 300
Db 127 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnPheAlaTyrAspGlyLysasp 146
QY 301 TACATCTCCCTGAACGAGAGCTGGCTCTCGGACCGCGCGGAGACACCGTGGCTCAGATC 360
Db 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
QY 361 ACCCAGCGCTTCTATGAGGCGAGAGGAATATCAGAGGAGTTTCAGACCTTACTGGAGGCG 420
Db 167 ThrGlnArgLysTrpGluAlaAlaArgValaGluGlnLeuArgThrTyrLeuGluGly 186
QY 421 CAGTGCCTGGAGTTGCTCCGCAGATACTTGGAGAAATGGAGAGACCTTACGCGCGCA 480
Db 187 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
QY 481 GATCTCTCAAGGCGACAGCTTCCACCCACCCCTCTCTGACCATGAGCCACCTGAGG 540
Db 207 AspProLysThrHisValThrHisProIleSerAspHisGluAlaThrLeuArg 226
QY 541 TGCTGGCGCTGGCTTCTACCTCGCGAGATCAGCTGACCTGCGACGCGGATGGGAG 600
Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
QY 601 GAACAGACCCAGCACAGACTTGTGAGACCCAGCGCTGCGAGG 645
Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261
RESULT 7
1B67_HUMAN
ID 1B67_HUMAN STANDARD; PRT: 362 AA.
AC Q29836; Q29678; Q8NSC5; Q9SIA6; Q9BD38;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-67 alpha chain precursor
DE (MHC class I antigen B*67).
GN HLA-B OR HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (B*6701).
RX MEDLINE=94294981; PubMed=7517584;
RA Little A.-M., Domene J.D., Hildebrand W.H., Shen S.Y., Barber L.D.,
RA Marsh S.G.E., Bias W.B., Parham P.;
RT "HLA-B*67: a member of the HLA-B16 family that expresses the ME1
RT epitope.";
RL Tissue Antigens 43:38-43(1994).
RN [2]
RP SEQUENCE OF 26-205 FROM N.A. (B*6701).
RC TISSUE=Blood;
RA Petersdorf E.;
RT "Molecular diversity of HLA-B.";
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (B*6702).
RA Iglehart B.A., Leffell M.S.;
RT "HLA-B*6702 (Promoter-3' UTR).";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]

```

SEQUENCE OF 26-206 FROM N.A. (B*6702).
 RA Baldaasare L.A., Hurlay C.K.;
 RT "Novel HLA-B allele (HLA-B*67012 variant).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -|- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -|- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- POLYMORPHISM: The following alleles of B-67 are known: B*6701
 CC (B-67LAV) and B*6702. The sequence shown is that of B*6701.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; L17005; AAC37548.1; -;
 CC EMBL; U18789; AAB60360.1; -;
 CC EMBL; AF487379; AAL93257.1; -;
 CC EMBL; AF321835; AAK09378.1; -;
 CC EMBL; AF321834; AAK09378.1; JOINED.
 CC EMBL; AY050196; AAL18235.1; -;
 CC EMBL; AY050195; AAL18235.1; JOINED.
 CC PIR; I59645; I59645.
 CC HSSP; P30460; 1AGD.
 CC Genew; HGNC:4932; HLA-B.
 CC MIN; 142830;
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig cl.
 CC InterPro; IPR003006; Ig MHC.
 CC InterPro; IPR001039; MHC_I.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00129; MHC_I; 1.
 CC PRINTS; PR01638; MHCCLASSI.
 CC ProDom; PD000050; MHC_I; 1.
 CC SMART; SM00407; IGC1; 1.
 CC PROSITE; PS00835; IG LIKE; 1.
 CC PROSITE; PS00290; IG MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-67 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT VARIANT 69 69 E -> G (in allele B*6702).
 FT VARIANT 76 76 /FTID=VAR_016536.
 FT VARIANT 76 76 I -> V (in allele B*6702).
 FT VARIANT 87 87 /FTID=VAR_016537.
 FT VARIANT 87 87 N -> E (in allele B*6702).
 FT VARIANT 90 90 /FTID=VAR_016538.
 FT VARIANT 90 90 I -> K (in allele B*6702).
 FT VARIANT 93 93 /FTID=VAR_016539.
 FT VARIANT 93 93 A -> R (in allele B*6702).
 FT VARIANT 97 97 /FTID=VAR_016540.
 FT VARIANT 97 97 T -> A (in allele B*6702).
 FT VARIANT 100 100 /FTID=VAR_016541.
 FT VARIANT 100 100 E -> V (in allele B*6702).
 FT VARIANT 100 100 /FTID=VAR_016542.
 SQ SEQUENCE 362 AA; 40342 MW; 3F6A17FC10230F70 CRC64;
 Alignment Scores:
 Pred. No.: 3.01e-55 Length: 362

Score: 919.00 Matches: 171
 Percent Similarity: 86.05% Conservative: 14
 Best Local Similarity: 79.53% Mismatches: 30
 Query Match: 77.68% Indels: 0
 DB: 1 Gaps: 0
 US-09-819-371-3 (1-645) x 1B67_HUMAN (1-362)
 QY 1 ATCGCGCTGAGTACGTAGACACACCAATTCCTGCGTTTCGACAGCGCCCGCGATT 60
 Db 47 ILESerValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAsp 66
 QY 61 CGAGATGAGCCCGGAGCCGTGGTGGAGCAAGAGGGCCCGAGTATTGGAGTGG 120
 Db 67 ProArgGluGluProArgAlaProTrpLeuGluGluGlyProGluTyrTrpAspArg 86
 QY 121 ACCAGSGGTACGCCAAGCCCAACGACACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
 Db 87 AenThrGlnIleTyrIysAlaGlnThrAspArgGluSerIeuArgAsnLeuArg 106
 QY 181 CGCGCTACACACAGAGCGAGTGGTCTTCACSCCTCCAGGGAATGAATCGTCGCGAC 240
 Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysAsp 126
 QY 241 ATGGGGCCGACGAGCGCCCTCTCCGGGTATCACCGACGCGCTAGACGCGCAAGGAT 300
 Db 127 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnPheAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCCTGAACGAGGACCTGCGCTCTCGAGACCGCGCGGACACCGTGGCTCAGATC 360
 Db 147 TyrIleAlaLeuAsnGluAspLeuSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCAGCGCTTATGAGCAGAGGAATATGAGAGGAGTTCAGGACCTACCTGGAGGCG 420
 Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgThrTyrLeuGluGly 186
 QY 421 GAGTGGCTGGAGTGTCTCCGAGATCTTGGAGATGGGAAGAGACGCTACAGCGCGCA 480
 Db 187 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
 QY 481 GATCTCTCAAAGGCACACGTTGCCACACCCCATCTTGACATGAGGCCACCTGAGG 540
 Db 207 AspProLysThrHisValThrHisHisProLysSerAspHisGluAlaThrLeuArg 226
 QY 541 TGTGTGGCGCTGGCTTCTACCTCGGAGATCACGCTGAGGAGACCGCTGCGGAGTGGGAG 600
 Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGAGCGCTGCGAGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261
 RESULT 8
 1B42 HUMAN
 ID 1B42 HUMAN STANDARD; PRT; 362 AA.
 AC P30480; P79555;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-42 alpha chain precursor
 DE (MHC class I antigen B*42).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*4201).
 RX MEDLINE=89235215; PubMed=2715640;
 RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles";
 RU J. Immunol. 142:3937-3950(1989).
 RN [2]

US-09-819-371-3 (1-645) x 1B42_HUMAN (1-362)

QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCACAGCCGCCGCGGATT 60
D 47 ILSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
QY 61 CCGAGGATGAGCCGCGGAGCGTGGTGAGCAAGAGCGCGCGGAGTATTGGAGTGG 120
D 67 ProArgGluGluProArgAlaProTyrIleGluGluGluGlyProGluTyrTTPAspArg 86
QY 121 ACCACGCGGTACGCCAAGCGCAACGACAGACGACGAGTGGCCCTGAGGACCTGCTC 180
D 87 AsnThrGlnIleTyrIlyAlaGlnAlaGlnThrAspArgGluSerLeuArgAsnLeuArg 106
QY 181 CGCGCTACACAGAGCGAGGTGGTCTCCACCCCTCCAGGAAATGAATGGTGGCAG 240
D 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnSerMetTyrGlyCysAsp 126
QY 241 ATGGGGCGCCGACGACGCGCTCTCCCGCGGTATCACACGACGCGGTACGACGCGCAAGGAT 300
D 127 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnTyrAlaTyrAspGlyLysAsp 146
QY 301 TACATCTCCCTGAACGAGGACCTGCGCTCGTGGAGCGCGCGGACCGGCTCAGATC 360
D 147 TyrIleAlaLeuAsnGluAspLeuArgSerTyrThrAlaAlaAspThrAlaAlaGlnIle 166
QY 361 ACCCAGCGCTTCTATGAGGAGGAGGATATGCGAGGAGTTCAGGACCTACCTGGAGGCG 420
D 167 ThrGlnArgLysTyrGluAlaAlaArgValAlaGluGlnAspArgAlaTyrLeuGluGly 186
QY 421 GAGTGGCTGGAGTTCCTCCGCGATATCTTGAGAGATGGAGGAGCGCTACAGCGCGCA 480
D 187 ThrCysValGluTyrLeuArgArgTyrLeuGluAsnGlyLysAspThrLeuGluArgAla 206
QY 481 GATCTCCAAAGGACACGCTTGGCCACACCCATCTCTGACCATGAGGCGGACCTCAGG 540
D 207 AspProProLysThrHisValThrHisProIleSerAspHisGluAlaThrLeuArg 226
QY 541 TCTGGCGCTGGCTTCTACCTCGGAGATACCGTGGAGTTCAGCTGCGAGCGGAGTGGGAG 600
D 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTyrGlnArgAspGlyGlu 246
QY 601 GAACAGACCCAGGACACAGAGCTTGTGAGACACCGGCTGCGAGG 645
D 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 9

1B47_HUMAN

ID 1B47_HUMAN STANDARD; PRT; 362 AA.

AC P30485; O19555; 077933; Q95392; Q9GIL3;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE HLA class I histocompatibility antigen, B-47 alpha chain precursor

DE (MHC class I antigen B*47) (Bw-47).

GN HLA-B OR HLA-B

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (B*4701).

RX MEDLINE=88152906; PubMed=3257938;

RA Zemmour J., Ennis P.D., Parham P., Dupont B.;

RT "Comparison of the structure of HLA-Bw47 to HLA-B13 and its

RT relationship to 21-hydroxylase deficiency.";

RL Immunogenetics 27:281-287(1988).

RN [2]

RP SEQUENCE FROM N.A. (B*4701).

RC TISSUE=Blood;

RX MEDLINE=22512041; PubMed=12622774;

RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,

RA Madrigal J.A., Little A.-M.;

RD

RP SEQUENCE FROM N.A. (B*4202).

RX MEDLINE=97387746; PubMed=9243763;

RA Lardy N.M., Onting N., van de Weerd M.J., van de Horst A.R.,

RA Waal L.P., Bontrop R.E.;

RT "Full-length cDNA nucleotide sequence of the HLA-B*4202 allele.";

RL Tissue Antigens 50:83-84(1997).

RN [3]

RP SEQUENCE FROM N.A. (B*4201).

RC TISSUE=Blood;

RX MEDLINE=22512041; PubMed=12622774;

RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,

RA Madrigal J.A., Little A.-M.;

RT "Cloning and sequencing full-length HLA-B and -C genes.";

RL Tissue Antigens 61:20-48(2003).

CC -!- FUNCTION: Involved in the presentation of foreign antigens to the

CC immune system.

CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-

CC microglobulin).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- POLYMORPHISM: The following alleles of B-42 are known: B*4201

CC (Bw-42) and B*4202. The sequence shown is that of B*4201.

CC -----

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CC -----

DR ENBL; M24034; AAA59667.1; --

DR ENBL; U88407; AAC16437.1; --

DR ENBL; AJ309194; CAC38393.1; --

DR PIR; I61865; I61865.

DR HSP; P30460; IAGD.

DR Genew; HGNC:4932; HLA-B.

DR MIM; 142830; --

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR001039; MHC_I.

DR Pfam; PF00047; Ig; 1.

DR Pfam; PF00129; MHC_I; 1.

DR PRINTS; PR01638; MHCCLASSI.

DR ProDom; PD000050; MHC_I; 1.

DR SMART; SM00407; Igcl; 1.

DR PROSITE; PS00835; IG_LIKE; 1.

DR PROSITE; PS00290; IG_MHC; 1.

DR MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.

KW SIGNAL

FT CHAIN

FT 1 24

FT 25 362

FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

FT B-42 ALPHA CHAIN.

FT EXTRACELLULAR ALPHA-1.

FT EXTRACELLULAR ALPHA-2.

FT EXTRACELLULAR ALPHA-3.

FT CONNECTING PEPTIDE.

FT CYTOPLASMIC TAIL.

FT N-LINKED (GLCNAC. . .) (BY SIMILARITY).

FT BY SIMILARITY.

FT BY SIMILARITY.

FT Y -> H (in allele B*4202).

FT /FTID=VAR_016460.

FT C9155AB015DEALBE CRC64;

FT SEQUENCE 362 AA; 40333 MW; 40333 MW;

FT Alignment Scores:

FT Pred. No.: 4, 81e-55

FT Score: 916.00

FT Percent Similarity: 86.51%

FT Best Local Similarity: 78.60%

FT Query Match: 77.43%

FT DB: 1

RT "Cloning and sequencing full-length HLA-B and -C genes."; RT
 RN Tissue Antigens 61:20-48(2003). [3]
 RP SEQUENCE OF 1-302 FROM N.A. (B*4702).
 RC TISSUE=Peripheral blood;
 RX MEDLINE=97316881; PubMed=9174155;
 RA Fischer G.F., Broer E., Rae I., Leitner D., Mayr W.R.;
 RT "Nucleotide sequence analysis of an HLA-B*47 variant (HLA-B*4702).";
 RL Tissue Antigens 49:540-542(1997). [4]
 RN SEQUENCE OF 26-206 FROM N.A. (B*4703).
 RP MEDLINE=20548605; PubMed=11098929;
 RX Ellis J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H.,
 RA Hurley C.K.;
 RT "Diversity is demonstrated in class I HLA-A and HLA-B alleles in
 RT Cameroon, Africa: description of HLA-A*03012, *2612, *3006 and HLA-
 RT B*1403, *4016, *4703.";
 RL Tissue Antigens 56:291-302(2000). [5]
 RN SEQUENCE OF 26-206 FROM N.A. (B*4703).
 RP Kosman C.A., Hurley C.K.;
 RA "Novel HLA class I B locus alleles.";
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- POLYMORPHISM: The following alleles of B-47 are known: B*4701,
 CC B*4702 and B*4703. The sequence shown is that of B*4701.
 CC
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 CC
 CC -----
 CC EMBL: M19756; AAA52664.1; --
 CC EMBL: AJ308398; CAC33087.2; --
 CC EMBL: AJ295141; CAC17463.2; --
 CC EMBL: Y09118; CAA70335.1; --
 CC EMBL: AF016843; AAB70513.1; --
 CC EMBL: AF016842; AAB70513.1; JOINED.
 CC EMBL: AF017164; AAC23752.1; --
 CC EMBL: AF017163; AAC23752.1; JOINED.
 CC PIR: I58724; I68724.
 CC HSP: P03989; IHS4.
 CC Genew: HGNC:4932; HLA-B.
 CC MIM: 142830; --
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003597; Ig cl.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR001039; MHC_I.
 CC Pfam: PF00047; Ig_1.
 CC Pfam: PF00129; MHC_1.
 CC PRINTS: PR01638; MHCCLASS1.
 CC ProDom: PD000050; MHC_I_1.
 CC SMART: SM00407; Igcl_1.
 CC PROSITE: PS00835; IG_LIKE; 1.
 CC PROSITE: PS00290; IG_MHC; 1.
 CC MHC_I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 KW SIGNAL 1 24
 FT CHAIN 25 362
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-47 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206
 FT EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298
 FT EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309
 FT CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT CYTOPLASMIC TAIL.
 FT DOMAIN 334 362
 FT N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 110 110

FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT VARIANT 101 101 D -> S (in allele B*4702 and allele
 FT B*4703).
 FT /FTid=VAR_016474.
 FT VARIANT 104 104 T -> N (in allele B*4702 and allele
 FT B*4703).
 FT /FTid=VAR_016475.
 FT VARIANT 106 107 LR -> RG (in allele B*4702).
 FT /FTid=VAR_016476.
 FT SQ SEQUENCE 362 AA; 40571 MW; E3D3E4CBF8C15EAE CRC64;
 Alignment Scores:
 Pred. No.: 5,63e-55 Length: 362
 Score: 915.00 Matches: 170
 Percent Similarity: 84.19% Conservative: 11
 Best Local Similarity: 79.07% Mismatches: 34
 Query Match: 77.35% Indels: 0
 DB: 1 Gaps: 0
 US-09-819-371-3 (1-645) x 1B47_HUMAN (1-362)
 QY 1 ATCGCGGTGGAGTACGTAGACACGCAATTCTCTGGTTCGACGCGCGCCGCGATT 60
 Db 47 IIEThrValGlyTyrValAspThrLeuPheValArgPheAspSerAspAlaThrSer 66
 QY 61 CCGAGATGGAGCCCGGAGCCGTGGTGGAGCAAGAGGGGCCCGAGTATTGGAGTGG 120
 Db 67 ProArgLysGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAspArg 86
 QY 121 ACACSGGGTAGCCCAAGCCCAACGACGACTGACCGAGTGGCCCTCAGGAACCTGCTC 180
 Db 87 GluThrGlnIleSerLysThrAsnThrGlnThrTyrArgGluAspLeuArgThrLeuLeu 106
 QY 181 CGCCGCTACAAACAGAGGAGGCTGGTCTCACSCCTCCAGGGGAATGAATGGTGGAC 240
 Db 107 ArgTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetPheGlyCysAsp 126
 QY 241 ATGGGCGCGAGCGAGCGCTCTCTCCGGGTATACACGACGCGCTACGACGCGCAGGAT 300
 Db 127 ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCCTGAACGAGGACCTGGCTCTCGACCGCGCGCGGACACCGTGGCTCAGATC 360
 Db 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpTrpAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCACGCGCTTCTATGAGCAGAGGAATATGAGAGGAGTTCAGGACCTACCTGAGGGC 420
 Db 167 ThrGlnArgLysTrpGluAlaAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGly 186
 QY 421 GAGTGGCTGAGTTCCTCCGCGAGATCTTGGAGATGGGAGAGACGCTACAGCGCGCA 480
 Db 187 GluCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
 QY 481 GATCCTCCAAAGGCACACGTTGCCACACCCCATCTCTGACCATGAGCCACCTGAGG 540
 Db 207 AspProLysThrHisValThrHisHisSerPheSerAspHisGluAlaThrLeuArg 226
 QY 541 TGCTGGGCGCTGGCTTACCTCGCGAGATCACGCTGAGGAGTTCAGGCGGGATGGGAG 600
 Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GAACAGACCCAGACACAGAGCTTGTGGAGACAGGCGCTGCGAGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261
 RESULT 10
 1B08 HUMAN
 ID 1B08 HUMAN STANDARD; PRT; 362 AA.
 AC P30450; O62901; Q95730; Q98140; P79542; Q95369; Q95700; Q9GJ20;
 AC Q9MY28; Q9MYE4; Q9TQ6; Q9TQ62; Q9TQ70;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)

DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism;
 3D-structure.
 FT CHAIN 1 24
 FT CHAIN 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT DOMAIN 310 333
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT VARIANT 87 87
 FT VARIANT 91 91
 FT VARIANT 101 101
 FT VARIANT 101 101
 FT VARIANT 119 119
 FT VARIANT 121 121
 FT VARIANT 121 121
 FT VARIANT 121 121
 FT VARIANT 137 138
 FT VARIANT 138 138
 FT VARIANT 140 140
 FT VARIANT 176 176
 FT VARIANT 180 180
 FT VARIANT 180 180
 FT STRAND 27 36
 FT TURN 39 40
 FT STRAND 45 52
 FT TURN 53 54
 FT STRAND 55 61
 FT TURN 62 63
 FT STRAND 70 71
 FT HELIX 74 76
 FT TURN 77 78
 FT HELIX 81 108

Alignment Scores:
 Pred. No.: 6.58e-55 Length: 362
 Score: 914.00 Matches: 168
 Percent Similarity: 86.0% Conservative: 17
 Best Local Similarity: 78.14% Mismatches: 20
 Query Match: 77.28% Indels: 0
 DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x 1B08_HUMAN (1-362)

QY 1 ATCCGCGTGGAGTACGACGCAATTCCTCGGTTGACAGCGCCGCGGATT 60
 Db 47 HleSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
 QY 61 CCAGAGATGGACCGCGGAGCGTGGTGGAGCAAGAGCGGCCGACGATTTGGAGTGG 120
 Db 67 ProArgGluGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAspArg 86
 QY 121 ACCAGSGGTACGCCAGGCCACGACGACGACGACGACGACGACGACGACGACGACG 180
 Db 87 AsnThrGlnIlePheLeuThrAsnThrGlnThrAspArgGluSerLeuArgAsnLeuArg 106
 QY 181 CGCCGCTACACACAGACGAGCGTGGTCTCACSCCCTCCAGGGAATGAATGGTCTGCAC 240

Db 107 GlyTyrTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnSerMetTyrGlyCysasp 126
 QY 241 ATGGGCGCCGACGAGCGCTCTCCGCGGGTATACACGACGCGGTACGACGCGGAGGAT 300
 Db 127 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnTyrAlaTyrAspGlyLysasp 146
 QY 301 TACACTCTCCGACGAGGACCTGCGCTCTCCGCGGGTATACACGACGCGGTACGACG 360
 Db 147 TyrIleAlaLeuAsnGlnAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCAGCGCTTCTATGAGCAGGAGGAATATGACGAGAGTTCAGCACCTTACCTGGAGGC 420
 Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnAspArgAlaTyrLeuGluGly 186
 QY 421 GAGTGCCTGGAGTTCCTCCGCGGATACCTTGGAGATGGAGAGGACGCTACAGCGCGCA 480
 Db 187 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysAspThrLeuGluArgAla 206
 QY 481 GATCCTCCAAAGCAGACACGCTGCCACACCCCATCTCTGACCATGAGCCACCTGAGG 540
 Db 207 AspProProlysThrHisValThrHisHisProlSerAspHisGluAlaThrLeuArg 226
 QY 541 TGCTGGGCGCTGGCTTCTACCTCGCGGAGATACGCTGACCTGGCAGCGGATGGGGAG 500
 Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GAACACAGCCAGACACGAGCTTGTGGAGACAGCGCTGCGAGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 11
 1B07_HUMAN STANDARD; PRT; 362 AA.
 ID 1B07_HUMAN STANDARD; PRT; 362 AA.
 AC P01889; Q29638; Q29861; Q29854; Q31613; Q9GIX1; Q9TP95;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-7 alpha chain precursor
 DE (MHC class I antigen B*7).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*0702).
 RX MEDLINE=90207291; PubMed=2320591;
 RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;
 RT "Rapid cloning of HLA-A,B cDNA by using the polymerase chain
 reaction: frequency and nature of errors produced in amplification.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (B*0702).
 RX MEDLINE=90315860; PubMed=2700944;
 RA Parham P., Benjamin R.J., Chen B.P., Clayberger C., Ennis P.D.,
 RA Krensky A.M., Lawlor D.A., Littman D.R., Norment A.M., Orr H.T.,
 RA Salter R.D., Zemmour J.;
 RT "Diversity of class I HLA molecules: functional and evolutionary
 interactions with T cells.";
 RL Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989).
 RN [3]
 RP SEQUENCE FROM N.A. (B*0702).
 RX MEDLINE=85287366; PubMed=2993161;
 RA Sood A.K., Fan J., Biro P.A., Pereira D., Srivastava R., Reddy V.B.,
 RA Ducman B.W., Weissman S.M.;
 RT "Structure and polymorphism of class I MHC antigen mRNA.";
 RL Immunogenetics 22:101-121(1985).
 RN [4]
 RP SEQUENCE FROM N.A. (B*0702).
 RX Elixson M.E., Zhang L., Hildebrand W.H.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]

RP RX MEDLINE=94148707; PubMed=8106270;
RA Bergmans A., Tijssen H., Lardy J., Reekers P.;
RT "Complete nucleotide sequence of HLA-B*0703, a B7-variant (BPOT).";
RL Hum. Immunol. 36:159-162(1995).
RN [6]
RP SEQUENCE FROM N.A. (B*0703).
RX MEDLINE=95381233; PubMed=7652739;
RA Kubens B.S., Arnett K.L., Adams E.J., Parham P., Grosse-Wilde H.;
RT "Definition of a new HLA-B7 subtype (B*0704) by isoelectric focusing,
family studies and DNA sequence analysis.";
RL Tissue Antigens 45:322-327(1995).
RN [7]
RP SEQUENCE FROM N.A. (B*0705).
RX MEDLINE=95184211; PubMed=7878659;
RA Arnett K.L., Adams E.J., Domena J.D., Parham P.;
RT "Structure of a novel subtype of B7 (B*0705) isolated from a Chinese
individual.";
RL Tissue Antigens 44:318-321(1994).
RN [8]
RP SEQUENCE FROM N.A. (B*0703 AND B*0705).
RX MEDLINE=96128250; PubMed=8537119;
RA Smith K.D., Epperson D.F., Lutz C.T.;
RT "Alloreactive cytotoxic T-lymphocyte-defined HLA-B7 subtypes differ in
peptide antigen presentation.";
RL Immunogenetics 43:27-37(1996).
RN [9]
RP SEQUENCE FROM N.A. (B*0706).
RX MEDLINE=96369317; PubMed=8773323;
RA Sanz L., Vilches C., de Pablo R., Bunce M., Moreno M.E., Kreisler M.;
RT "Haplotypic association of two new HLA class I alleles: Cw*15052 and
B*0706: evolutionary relationships of HLA-Cw*15 alleles.";
RL Tissue Antigens 47:329-332(1996).
RN [10]
RP SEQUENCE FROM N.A. (B*0718).
RA Bettinotti M.P., Hadzikadic L., Dhillon G., Barracchini K.,
RA Marincola F.M.;
RT "A new HLA-B allele.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A. (B*0702).
RA Marsh S.G.E.;
RT "Intron sequences of HLA class I.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A. (B*0702).
RC TISSUE=Blood;
RX MEDLINE=22512041; PubMed=12622774;
RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
RA Madrigal J.A., Little A.-M.;
RT "Cloning and sequencing full-length HLA-B and -C genes.";
RL Tissue Antigens 61:20-48(2003).
RN [13]
RP SEQUENCE OF 26-206 FROM N.A. (B*0724).
RC TISSUE=Peripheral blood;
RX MEDLINE=21442086; PubMed=11556973;
RA Middleton D., Curran M.D., Anholts J.D., Reilly E.R., Schreuder G.M.;
RT "Characterisation of a new HLA-B allele, HLA-B*0724.";
RL Tissue Antigens 57:471-473(2001).
RN [14]
RP SEQUENCE OF 25-295 (B*0702).
RX MEDLINE=80088278; PubMed=518865;
RA Orr H.T., Lopez de Castro J.A., Lancet D., Strominger J.L.;
RT "Complete amino acid sequence of a papain-solubilized human
histocompatibility antigen, HLA-B*7. 2. Sequence determination and
search for homologues.";
RL Biochemistry 18:5711-5720(1979).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of B-7 are known: B*0702

(B7.2), B*0703 (BPOT), B*0704, B*0705, B*0706 (B7_L79), B*0718 and
B*0724. The sequence shown is B*0702.

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DR EMBL; M32317; AAA36230.1; -;
DR EMBL; M16102; AAA59622.1; ALT_SEQ.
DR EMBL; U29057; AAA91229.1; -;
DR EMBL; X64454; CAA45785.1; -;
DR EMBL; U04245; AAA87398.1; -;
DR EMBL; L33922; AAA65639.1; -;
DR EMBL; U21052; AAA92563.1; -;
DR EMBL; U21053; AAA92564.1; -;
DR EMBL; X91749; CAA62864.1; -;
DR EMBL; AF189017; AAF01052.1; -;
DR EMBL; AJ309047; CAC35468.1; -;
DR EMBL; AJ292075; CAC33440.1; -;
DR EMBL; AJ401222; CAC10402.1; -;
DR PIR; B35997; HLHUB7.
DR PIR; I59651; I59651.
DR PIR; S60601; S60601.
DR HSSP; P30460; IAGD.
DR Genew; HGNC:4932; HLA-B.
DR MIM; 142830; -;
DR GO; GO:0005887; C: integral to plasma membrane; NAS.
DR GO; GO:0030106; F: MHC class I receptor activity; NAS.
DR GO; GO:0006955; P: immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG_1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl_1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 362
FT B-7 ALPHA CHAIN.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT VARIANT 93 95
FT VARIANT 118 119
FT VARIANT 121 121
FT VARIANT 139 138
FT VARIANT 180 180
FT VARIANT 187 187
FT VARIANT 306 306
FT VARIANT 15 18
FT CONFLICT 15 18

HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-7 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .).
AQA -> TNT (in allele B*0703).
FTID=VAR_016351.
TL -> II (in allele B*0718).
S -> R (in allele B*0718).
FTID=VAR_016352.
FTID=VAR_016353.
D -> N (in allele B*0705 and allele
B*0706).
FTID=VAR_016354.
R -> D (in allele B*0704).
FTID=VAR_016355.
E -> L (in allele B*0724).
FTID=VAR_016616.
V -> I (in allele B*0705).
FTID=VAR_016356.
AALA -> GPW (IN REF. 3).

RESULT 12

FT	DOMAIN	334	362	CYTOPLASMIC TAIL.
FT	CARBOHYD	110	110	N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT	DISULFID	125	188	BY SIMILARITY.
FT	DISULFID	227	233	BY SIMILARITY.
FT	VARIANT	35	35	S -> A (in allele B*1402 and allele B*1403).
FT	VARIANT	180	180	/FTID=VAR 016364.
FT	VARIANT	180	180	L -> R (in allele B*1403).
FT	SEQUENCE	362 AA; 40358 MW; 9039122CC400337F CRC64;		/FTID=VAR 016654.
Alignment Scores:				
Pred. No.:	7.69e-55	Length:	362	
Score:	913.00	Matches:	169	
Percent Similarity:	85.12%	Conservative:	14	
Best Local Similarity:	78.60%	Mismatches:	32	
Query Match:	77.18%	Indels:	0	
DB:	1	Gaps:	0	
US-09-819-371-3 (1-645) x 1B14 HUMAN (1-362)				
QY	1	ATCGCGGTGGAGTACGTAGACACGCAATTCCTCGGTTCGACAGCGCCGCCGATT	60	
Db	47	IleSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaIaSer	66	
QY	61	CGAGGATGAGCGCGGGAGCGGTGGTGGACAGAGCGGCCGACGATTGGGATGG	120	
Db	67	ProArgGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAspArg	86	
QY	121	ACCACGGGTACGCCAAGCCACGACGACGACGACGACGACGACGACGACGACGAC	180	
Db	87	AsnThrGlnIleCysIleThrAsnThrGlnThrAspArgGluSerLeuArgAsnLeuArg	106	
QY	181	CGCGGTACACACGAGCGAGGTGGTGTACGCCCTCAGGGAATGAATGGTGGCAG	240	
Db	107	GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnTrpMetTyrGlyCysAsp	126	
QY	241	ATGGGGCCGACGAGCGCTCTCCCGGGTATCACGACGACGACGACGACGACGACGAT	300	
Db	127	ValGlyProAspGlyArgLeuLeuArgGlyTyrAsnGlnPheAlaTyrAspGlyAsp	146	
QY	301	TACATCTCCGTGACGAGGACCTCGCTCTGACCGCGCGGACACCGCTGGCTGATC	360	
Db	147	TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle	166	
QY	361	ACCAGCGCTTATGAGCGAGGAGATATGACGAGGATTCAGGACCTACCTGAGGCG	420	
Db	167	ThrGlnArgIleTrpGluAlaAlaArgGluAlaGlnLeuArgAlaTyrLeuGluGly	186	
QY	421	GAGTGGCTGAGTGTCTCCGAGATCTTGGAGATGGGAGGAGGACGCTACAGCGCGCA	480	
Db	187	ThrCysValGluTrpLeuArgArgHisLeuGluAsnGlyIleThrLeuGlnArgAla	206	
QY	481	GATCCTCCAAAGGACACGTTGGCCACCCACCCATCTCTGACCATGAGGACCCCTGAGG	540	
Db	207	AspProIleThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg	226	
QY	541	TGCTGGCCCTGGCTTCTACCTCGGAGATCACGCTGACCTGACCTGGGAGGATGGGAG	600	
Db	227	CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu	246	
QY	601	GAACAGACCCAGGACACAGAGCTTGTGGAGACGACGCGCTGCAGGG	645	
Db	247	AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly	261	

RESULT 13
1B37_HUMAN
ID 1B37_HUMAN STANDARD; Q95HAB; PRT; 362 AA.
AC P18463; O19627; Q95HAB; Q95HAB; Q95HAB; Q95HAB;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-37 alpha chain precursor

DE GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*3701).
RX MEDLINE=90207291; PubMed=2320591;
RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;
RT "Rapid cloning of HLA-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A. (B*3704).
RX TISSUE=Peripheral blood;
RA Estefania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;
RT "Complementary DNA sequence of the novel HLA-B*3704 allele.";
Tissue Antigens 59:142-144(2002).
RN [3]
RP SEQUENCE FROM N.A. (B*3705).
RX MEDLINE=22131942; PubMed=12135437;
RA Pyo C.-W., Han H., Kim T.G.;
RT "Identification of a new HLA-B allele, B*3705 containing a Bw6
sequence motif.";
Tissue Antigens 59:335-337(2002).
RN [4]
RP SEQUENCE OF 1-322 FROM N.A. (B*3701).
RX Hurley C.K., Bei M., Rodriguez S., Johnson A.;
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 26-206 FROM N.A. (B*3704).
RX Gans C.P., Hurley C.K.;
RT "Novel HLA-B allele.";
Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN -!- FUNCTION: Involved in the presentation of foreign antigens to the
immune system.
RN -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
RN -!- SUBCELLULAR LOCATION: Type I membrane protein.
RN -!- POLYMORPHISM: The following alleles of B-37 are known: B*3701,
B*3704 and B*3705. The sequence shown is that of B*3701.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M32320; AAA36233.1; -
DR EMBL; AF389378; AAL26324.1; -
DR EMBL; AF418978; AAL07502.1; -
DR EMBL; AF284828; AAK82990.1; -
DR EMBL; AF284826; AAK82990.1; JOINED.
DR EMBL; AF284827; AAK82990.1; JOINED.
DR EMBL; U11267; AAA19927.1; -
DR EMBL; AF303102; AAG21400.1; -
DR EMBL; AF303101; AAG21400.1; JOINED.
DR PIR; C35997; C35997.
DR HSSP; P03989; ILSA.
DR Genew; HGNC:4932; HLA-B.
DR MIM; 142830; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG_1.
DR Pfam; PF00129; MHC_I.
DR PRINTS; PR01638; MHCCLASS1.
DR ProDom; PD000050; MHC_I; 1.

DR SMART; SM00407; IG1; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 B-37 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT VARIANT 104 104 T -> N (in allele B*3705).
 FT VARIANT 106 107 /FTID=VAR_016408.
 FT VARIANT 106 107 LR -> RG (in allele B*3705).
 FT VARIANT 195 195 /FTID=VAR_016409.
 FT VARIANT 195 195 Y -> H (in allele B*3704).
 FT VARIANT 195 195 /FTID=VAR_016410.
 SQ SEQUENCE 362 AA; 40456 MW; FAB4375F05474725 CRC64;
 Alignment Scores:
 Pred. No.: 7,698-55 Length: 362
 Score: 913.00 Matches: 169
 Percent Similarity: 85.58% Conservative: 15
 Best Local Similarity: 78.60% Mismatches: 31
 Query Match: 77.18% Indels: 0
 DB: 1 Gaps: 0
 US-09-819-371-3 (1-645) x 1B37_HUMAN (1-362)
 QY 1 ATGCGCGTGGAGTACGTAGACGACGCAATCTCTGCGGTTCGACAGCGCGCGCGGATT 60
 DB 47 ILeSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAsaSer 66
 QY 61 CGAGGATCGAGCGCGCGCGCGCGTGGTGGAGCAGAGGCGCGCAGTATTGGAGTGG 120
 DB 67 ProArgThrGluProArgAlaProIleGluGlnGluGlyProGluTyrTrpAspArg 86
 QY 121 ACCACGGGTACGCCAAGCCCAACACACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
 DB 87 GluThrGlnIleSerLysThrAsnThrGlnThrTyrArgGluAspLeuArgThrLeuLeu 106
 QY 181 CGCGCTACACAGCAGCGAGCGTGGTCTCCCGGGTATCACACGCGTACGCGCAAGGAT 240
 DB 107 ArgTyrTyrAsnGlnSerGluAlaGlySerHisThrIleGlnArgMetSerGlyCysAsp 126
 QY 241 ATGGGCGCGCGAGCGCGCTCTCTCCGCGGTATCACACGCGTACGCGCAAGGAT 300
 DB 127 ValGlyProAspGlyArgLeuLeuArgGlyTyrAsnGlnPheAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCCTGAACAGGACCTGCGCTCTGAGCGCGCGCGGACACCGTGGCTCAGATC 360
 DB 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCACGCGTCTTATCAGCAGCAGGGAATATGACAGAGGAGTTCAGGACCTACCTGAGGCG 420
 DB 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnAspArgAlaTyrLeuGluGly 186
 QY 421 GAGTGCCTGGAGTGTCTCCGCGATACCTTGGAGAATGGGAAGGAGACGCTACGCGCGCA 480
 DB 187 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
 QY 481 GATCTCCAAAGCAGCAGCTGGCCACCCACCTCTGACCATGAGCGCACCTCTGAGG 540
 DB 207 AspProLysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 226
 QY 541 TGTGCGCGCTGGCGCTTACCTCGCGAGATCACGCTGAGGATCACGCTGAGCGGAGTGGGAG 600
 DB 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246

QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGCAGGCGCTGACGG 645
 DB 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261
 RESULT 14
 1B46_HUMAN
 ID 1B46_HUMAN STANDARD; PRT; 362 AA.
 AC P30484; O9TPR2;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-46 alpha chain precursor
 DE (MHC class I antigen B*46) (Bw-46).
 DE HLA-B OR HLAB
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*4601).
 RX MEDLINE=89235215; PubMed=2715640;
 RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles.";
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (B*4601).
 RX TISSUE=Blood;
 MEDLINE=22512041; PubMed=12622774;
 RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
 RA Madrigal J.A., Little A.-M.;
 RT "Cloning and sequencing full-length HLA-B and -C genes.";
 RL Tissue Antigens 61:20-48(2003).
 RN [3]
 RP SEQUENCE OF 26-206 FROM N.A. (B*4602).
 RX MEDLINE=20340078; PubMed=10885569;
 RA Akesaka T., Kashiwase K., Shimamura M., Ishikawa Y., Tanaka H.,
 RA Fujii M., Akaza T., Honda K., Yuasa S., Takahashi T., Fuji T.;
 RT "Identification of a novel HLA-B46 allele, B*4602, in Japanese.";
 RL Tissue Antigens 55:460-462(2000).
 CC -1- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- POLYMORPHISM: The following alleles of B-46 are known: B*4601
 CC and B*4602. The sequence shown is that of B*4601.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M24033; AAA59665.1; -;
 CC EMBL; AJ310508; CAC34573.1; -;
 CC EMBL; AB032091; BAA84111.1; -;
 CC PIR; I61863; I61863.
 CC HSP; P30685; I49E.
 CC Genew; HGNC:4932; HLA-B.
 CC MIM; 142830; -;
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig_C1.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR001039; MHC_I.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00129; MHC_I; 1.
 CC PRINTS; PR01638; MHCCLASSI.
 CC PRODOM; PD000050; MHC_I; 1.
 CC SMART; SM00407; IG1; 1.
 CC PROSITE; PS50835; IG_LIKE; 1.

DR PROSITE, PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 362

FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT DOMAIN 115 206 B-46 ALPHA CHAIN.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 299 309 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 310 333 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 334 362 CONNECTING PEPTIDE.
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT VARIANT 98 D -> G (in allele B*4602).
 FT SEQUENCE 362 AA; 40440 MW; 481B4C6876CB0E85 CRC64;
 FT SEQUENCE 362 AA; 40440 MW; 481B4C6876CB0E85 CRC64;

Alignment Scores:
 Pred. No.: 7,59e-55 Length: 362
 Score: 913.00 Matches: 171
 Percent Similarity: 85.58% Conservative: 13
 Best Local Similarity: 79.53% Mismatches: 31
 Query Match: 77.18% Indels: 0
 DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x 1B46_HUMAN (1-362)

QY 1 ATCCGCGTGGAGTACGTACGACGACGCGCAATCTCTCGGTTCGACGAGCGCGCCGCGATT 60
 Db 47 IleAlaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaAsp 66
 QY 61 CCAGAGTATGAGCGCGGAGCGCGTGGTGGTGGAGAGAGCGCGCGCGATTTGGAGTGG 120
 Db 67 ProArgMetAlaProArgAlaProTrieGluGlnGluGlyProGluTyrTrpAspArg 86
 QY 121 ACCACGGGTACCCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 180
 Db 87 GluThrGlnLysTyrLysArgGlnAlaGlnThrAspArgValSerLeuArgAsnLeuArg 106
 QY 181 CGCGCTTACACACGAGCGAGCGTGGTCTCTACGCGCTCCAGCGATGAATGGCTGCGAC 240
 Db 107 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnArgMetTyrGlyCysAsp 126
 QY 241 ATGGGCGCGACGAGCGCTCTCCGCGGTATACACGACGCGTACGACGCGCAGGAT 300
 Db 127 ValGlyProAspGlyArgLeuLeuLeuArgGlyHisAspGlnSerAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCTTACGAGGACCTCGCTCTCTGACCGCGCGACACCGCTGCTCAGATC 360
 Db 147 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCGAGCGCTTATGAGGAGGAGGAAATATGAGAGGAGTTCAGGACCTACCTGGAGGCG 420
 Db 167 ThrGlnArgLysTyrGluAlaAlaArgGluAlaGluGlnTrpArgAlaTyrLeuGluGly 186
 QY 421 GAGTGGCTGGAGTGTCTCCGAGATATCTGGAGATGGGAGGAGGAGGAGGAGGAGGAG 480
 Db 187 LeuGlyValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
 QY 481 GATCTCTCAGAGGACGAGTGGCGCCACGACCGACCGATCTCTGACCATGAGGCGCCCTGAGG 540
 Db 207 AspProLysThrHisValThrHisPheProIleSerAspHisGluAlaThrLeuArg 226
 QY 541 TGCTGGCGCTGGGCTTCTACCTCGGAGATACCGTGGAGTACCTGGCGAGCGGATGGGAG 600
 Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GAACAGACCCAGGACACAGCTGTGGAGACACGAGGCTGCGAGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 15

1B02_PANTR
 ID -1B02_PANTR STANDARD; PRT; 362 AA.
 AC P137E1, 1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE CHLA class I histocompatibility antigen, B-2 alpha chain precursor.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89030641; PubMed=2460344;
 RA Mayer W.B., Jonker M., Klein D., Ivanyi P., van Seventer G.,
 RA Klein J.;
 RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
 trans-species mode of evolution.";
 RL EMBO J. 7:2765-2774(1988).
 RN [2]
 RP REVISIONS.
 RA Mayer W.;
 RL Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; X13116; CAA31508.1; --
 DR HSP; P30685; I49E.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362

CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 B-2 ALPHA CHAIN.
 EXTRACELLULAR ALPHA-1.
 EXTRACELLULAR ALPHA-2.
 EXTRACELLULAR ALPHA-3.
 CONNECTING PEPTIDE.
 CYTOPLASMIC TAIL.
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC. .) (BY SIMILARITY).
 SEQUENCE 362 AA; 40488 MW; FFD2991044DA83 CRC64;

Alignment Scores:
 Pred. No.: 8,99e-55 Length: 362
 Score: 912.00 Matches: 169
 Percent Similarity: 85.58% Conservative: 15
 Best Local Similarity: 78.60% Mismatches: 31
 Query Match: 77.09% Indels: 0
 DB: 1 Gaps: 0

US-09-819-371-3 (1-645) x 1B02_PANTR (1-362)

Search completed: June 18, 2004, 07:36:45
Job time : 19 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 18, 2004, 06:17:44 ; Search time 64 seconds

(without alignments)

6359.664 Million cell updates/sec

Title: US-09-819-371-3

Perfect score: 1183
Sequence: 1 atccgcgtggagtagctagtaga.....tggagaccagcctgcagg 645

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlh
-O=/cgn2 1/USPTO.spool/US09819371/runat 16062004 165856 7369/app query.fasta 1.839
-DB=SPREMBL 25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09819371@cgn 1 1.87 @runat 16062004 165856 7369 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPREMBL 25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteria:
17: sp_archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1156	97.7	324	7	Q861F0	Q861F0 homo sapien

2	1156	97.7	324	7	Q861E9	Q861E9 homo sapien
3	1156	97.7	346	7	Q8MQ01	Q8MQ01 homo sapien
4	1156	97.7	346	7	Q8WLP5	Q8WLP5 homo sapien
5	1156	97.7	362	7	Q9TP68	Q9TP68 homo sapien
6	1156	97.7	442	7	Q9SHC0	Q9SHC0 homo sapien
7	1142	96.5	346	7	Q95IT2	Q95IT2 pan troglod
8	1142	96.5	362	6	Q7YR27	Q7YR27 pan troglod
9	937	79.2	362	7	Q9MXK1	Q9MXK1 pan troglod
10	931	78.7	273	7	Q8SNC9	Q8SNC9 homo sapien
11	931	78.7	274	7	Q19692	Q19692 homo sapien
12	931	78.7	362	7	P79612	P79612 homo sapien
13	931	78.7	362	7	Q78189	Q78189 homo sapien
14	930	78.6	362	4	Q29705	Q29705 homo sapien
15	927	78.4	354	7	Q95530	Q95530 pan troglod
16	927	78.4	354	7	Q9MM41	Q9MM41 macaca mula
17	927	78.4	359	7	Q29934	Q29934 homo sapien
18	927	78.4	362	7	Q9MXI2	Q9MXI2 pan troglod
19	926	78.3	362	7	Q9MXD1	Q9MXD1 pan troglod
20	925	78.2	341	7	Q19589	Q19589 homo sapien
21	925	78.2	362	7	Q86017	Q86017 homo sapien
22	924	78.1	362	7	Q9TFW6	Q9TFW6 homo sapien
23	923	78.0	298	7	Q9GJF1	Q9GJF1 homo sapien
24	923	78.0	362	7	Q9MXM2	Q9MXM2 pan troglod
25	923	78.0	362	7	Q7YQ80	Q7YQ80 homo sapien
26	920	77.8	362	7	Q861E8	Q861E8 homo sapien
27	920	77.8	362	7	Q9MXI0	Q9MXI0 pan troglod
28	920	77.8	362	7	Q9MXL8	Q9MXL8 pan troglod
29	919	77.7	338	7	Q95HL2	Q95HL2 homo sapien
30	918	77.6	354	7	Q95412	Q95412 hylobates 1
31	917	77.5	355	7	Q95529	Q95529 pan troglod
32	917	77.5	355	7	Q9MXJ8	Q9MXJ8 pan troglod
33	917	77.5	363	7	Q8MH3	Q8MH3 pan troglod
34	916	77.4	362	7	Q9MXG3	Q9MXG3 pan troglod
35	916	77.4	362	7	Q9MXK5	Q9MXK5 pan troglod
36	915	77.3	273	7	Q9TFL5	Q9TFL5 pan troglod
37	915	77.3	273	7	Q9GJ38	Q9GJ38 homo sapien
38	914	77.3	350	7	Q95IH9	Q95IH9 homo sapien
39	914	77.3	354	7	Q19691	Q19691 homo sapien
40	914	77.3	362	7	Q30933	Q30933 pan troglod
41	914	77.3	362	7	Q9MXK4	Q9MXK4 pan troglod
42	914	77.3	362	7	Q9GIX2	Q9GIX2 homo sapien
43	914	77.3	363	7	Q31602	Q31602 homo sapien
44	913	77.2	273	7	Q8HML6	Q8HML6 homo sapien
45	913	77.2	273	7	Q7YQ36	Q7YQ36 homo sapien

ALIGNMENTS

RESULT 1
Q861F0 PRELIMINARY; PRT; 324 AA.
ID Q861F0
AC Q861F0; (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Nonclassical MHC class I antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Liu Y., Zeng Y.;
RT "Nonclassical MHC class I HLA-F";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY216682; C:membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR PRODOM; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGL; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 FT NON_TER 1 324
 FT NON_TER 324 324
 SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Alignment Scores:
 Pred. No.: 2,27e-83 Length: 324
 Score: 1156.00 Matches: 213
 Percent Similarity: 99.07% Conservative: 0
 Best Local Similarity: 99.07% Mismatches: 2
 Query Match: 97.72% Indels: 0
 DB: 7 Gaps: 0

US-09-819-371-3 (1-645) x Q861F0 (1-324)

QY 1 ATGCGGTGAGTACGTAGACGACGCAATTCCTGGGTTCGACAGCGCGCGGATT 60
 Db 40 ILeAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 59
 QY 61 CCGAGGTGAGCGCGGGAGCGGTGGTGGAGCAAGAGCGCGCGGATTGGGAGTGG 120
 Db 60 ProArgMetGluProArgGluProTyrValGluGluGluGluGluGluGluGlu 79
 QY 121 ACCACGGGTACGCCAAGGCGACGACGACGACTGCGAGTGGCCCTGAGACCTGCTC 180
 Db 80 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 99
 QY 181 CGCGCTTACCAACAGACGAGGTGGTCTCCAGCCCTCCAGGGAATGAATGGCTCAGATC 240
 Db 100 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGluGlnGlyMetAsnGlyCysAsp 119
 QY 241 ATGGGGCCCGACGCGTGGCCACACCCATCTCTGACCATGAGGCCACCCCTGAGG 300
 Db 120 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 139
 QY 301 TACATCTCCCTGAACAGAGACTGGCTCTCGCGGGTATCACACGACGCGTACACGCGGCA 360
 Db 140 TyrIleSerLeuAsnGluAspLeuArgSerThrAlaAlaAspThrValAlaGlnIle 159
 QY 361 ACCACGCGCTTCTATGAGGCGAGGAATATGACAGAGGAGTTCAGACCTACTGAGGCG 420
 Db 160 ThrGlnArgPheTyrGluAlaGluGluGluGluGluGluGluGluGluGluGlu 179
 QY 421 GAGTGGCTGGAGTGGTCCGAGATCTTGGAGATGGGAGGAGAGCTACAGCGCGCA 480
 Db 180 GluCysLeuGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 199
 QY 481 GATCCTCCAAAGGACACGCTGGCCACACCCATCTCTGACCATGAGGCCACCCCTGAGG 540
 Db 200 AspProTyrAlaHisValAlaHisProIleSerAspHisGlnAlaThrLeuArg 219
 QY 541 TGCTGGCGCTGGGCTTACCTCGCGAGATCAGCTGACCTGGCGAGCGGATGGGAG 600
 Db 220 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 239
 QY 601 GAACAGACCCAGGACACAGACTTGTGGAGACCAAGGCGCTGCAGGG 645
 Db 240 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 254

RESULT 2
 Q861E9 PRELIMINARY; PRT; 324 AA.
 AC Q861E9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MHC class I antigen (Fragment).
 GN HLA-F.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Y., Xu L., Zeng Y., He X.;
 RT "A new polymorphism in non-classical MHC class I HLA-F";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY221102; AA034407.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR PRODOM; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGL; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 FT NON_TER 1 324
 FT NON_TER 324 324
 SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Alignment Scores:
 Pred. No.: 2,27e-83 Length: 324
 Score: 1156.00 Matches: 213
 Percent Similarity: 99.07% Conservative: 0
 Best Local Similarity: 99.07% Mismatches: 2
 Query Match: 97.72% Indels: 0
 DB: 7 Gaps: 0

US-09-819-371-3 (1-645) x Q861E9 (1-324)

QY 1 ATGCGGTGAGTACGTAGACGACGCAATTCCTGGGTTCGACAGCGCGCGGATT 60
 Db 40 ILeAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 59
 QY 61 CCGAGGTGAGCGCGGGAGCGGTGGTGGAGCAAGAGCGCGCGGATTGGGAGTGG 120
 Db 60 ProArgMetGluProArgGluProTyrValGluGluGluGluGluGluGluGlu 79
 QY 121 ACCACGGGTACGCCAAGGCGACGACGACGACTGCGAGTGGCCCTGAGGAACTGCTC 180
 Db 80 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeu 99
 QY 181 CGCGCTTACCAACAGACGAGGTGGTCTCCAGCCCTCCAGGGAATGAATGGCTCAGATC 240
 Db 100 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGluGlnGlyMetAsnGlyCysAsp 119
 QY 241 ATGGGGCCCGACGCGTGGCCACACCCATCTCTGACCATGAGGCCACCCCTGAGG 300
 Db 120 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 139
 QY 301 TACATCTCCCTGAACAGAGACTGGCTCTCGCGGGTATCACACGACGCGTACACGCGGCA 360
 Db 140 TyrIleSerLeuAsnGluAspLeuArgSerThrAlaAlaAspThrValAlaGlnIle 159
 QY 361 ACCACGCGCTTCTATGAGGCGAGGAATATGACAGAGGAGTTCAGACCTACTGAGGCG 420
 Db 160 ThrGlnArgPheTyrGluAlaGluGluGluGluGluGluGluGluGluGluGlu 179
 QY 421 GAGTGGCTGGAGTGGTCCGAGATCTTGGAGATGGGAGGAGAGCTACAGCGCGCA 480
 Db 180 GluCysLeuGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 199
 QY 481 GATCCTCCAAAGGACACGCTGGCCACACCCATCTCTGACCATGAGGCCACCCCTGAGG 540
 Db 200 AspProTyrAlaHisValAlaHisProIleSerAspHisGlnAlaThrLeuArg 219
 QY 541 TGCTGGCGCTGGGCTTACCTCGCGAGATCAGCTGACCTGGCGAGCGGATGGGAG 600
 Db 220 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 239
 QY 601 GAACAGACCCAGGACACAGACTTGTGGAGACCAAGGCGCTGCAGGG 645
 Db 240 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 254

QY 481 GATCTCTCAAGGACACGTTGTCACCCACCCATCTCTGACCATGAGGCCACCTGAGG 540
 Db 200 AspProProlysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 219
 QY 541 TGCTGGGCGCTGGCTTCTACCTCGCGAGATACCGTGAACCTGCGGCGGATGGGGAG 600
 Db 220 CysTrpAlaLeuGlyPheTyProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 239
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAGGCGCTGCGAGG 645
 Db 240 GluInThrGlnAspThrGluLeuValGluThrArgProAlaGly 254

RESULT 3

Q8MGQ1 PRELIMINARY; PRT; 346 AA.
 AC Q8MGQ1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MHC class Ib antigen.
 GN HLA-F.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
 RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation
 spanning the nonclassical class I genes."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 IMMUNE SYSTEM (BY SIMILARITY).
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN) (BY SIMILARITY).
 CC EMBL; AF523284; AAM74981.1; -.
 CC EMBL; AF523291; AAM74986.1; -.
 CC EMBL; AF523292; AAM74987.1; -.
 CC GO; GO:0016021; C: integral to membrane; IEA.
 CC GO; GO:0006955; P: immune response; IEA.
 CC InterPro; IPR001064; Crystallin.
 CC DR InterPro; IPR007110; IG-like.
 CC DR InterPro; IPR003597; IG_c1.
 CC DR InterPro; IPR003006; IG_MHC.
 CC DR InterPro; IPR001039; MHC_I.
 CC Pfam; PF00047; IG_1.
 CC Pfam; PF00129; MHC_I; 1.
 CC PRINTS; PR01638; MHCCLASS1.
 CC ProDom; PD000050; MHC_I; 1.
 CC SMART; SM00407; IGc1; 1.
 CC PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 CC PROSITE; PS00835; IG_LIKE; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 SQ SEQUENCE 346 AA; 39061 MW; D4782968A67B9B7D CRC64;

Alignment Scores:

Pred. No.: 2,298-83 Length: 346
 Score: 1156.00 Matches: 213
 Percent Similarity: 99.07% Conservative: 0
 Best Local Similarity: 99.07% Mismatches: 2
 Query Match: 97.72% Indels: 0
 DB: 7 Gaps: 0

US-09-819-371-3 (1-645) x Q8MGQ1 (1-346)

QY 1 ATCGCGGTGGAGTACGTAGACACACGCAATTCCTGCGGTTCGACAGCGCGCGCGATT 60
 Db 44 IleAlaValGluTyValAspAspThrGlnPheLeuArgPheAspSerAspAlaAla 63
 QY 61 CCGAGGATGGAGCCCGGGAGCGGTGGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 120

Db 64 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyTrpGluTrp 83
 QY 121 ACCACSGGTAGCCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGGAACCTGTCTC 180
 Db 84 ThrThrGlyTyAlaIysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
 QY 181 CCGCGCTACACACAGAGAGCGGTGGTCTCAACSCCTCCAGGAAATGATGGCTGGCAG 240
 Db 104 ArgArgTyAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
 QY 241 ATGGGCGCCGACGACGCGCTCTCCGCGGGTATACACAGACGCGTACGACGCGCAAGGAT 300
 Db 124 MetGlyProAspGlyArgLeuLeuArgGlyTyHisGlnHisAlaTyAspGlyLysAsp 143
 QY 301 TACATCTCCCTGAACAGAGACCTGCGCTCTGGACCGCGCGGACACACCGTGGCTCAGATC 360
 Db 144 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
 QY 361 ACCCAGCGCTTCTATGAGCAGAGGAATATGCAGAGGAGTTCCAGACCTTACCTGGAGGC 420
 Db 164 ThrGlnArgPheTyArgAlaGluGluTyAlaGluGluPheArgThrTyrlLeuGluGly 183
 QY 421 GAGTGCCTCGAGTTGCTCCGCGAGATCTTGGAGATGGGAGAGACGCTACAGCGCGCA 480
 Db 184 GluCysLeuGluLeuLeuArgArgTyrlLeuGluAsnGlyLysGluThrLeuGlnArgAla 203
 QY 481 GATCTCTCAAGGACACACGCTTCCACACCCATCTCTGACCATGAGGCCACCTGAGG 540
 Db 204 AspProProlysAlaHisValAlaHisHisProIleSerAspHisGluAlaThrLeuArg 223
 QY 541 TGCTGGGCGCTGGCTTCTACCTCGCGAGATCACGCTGACCTGCGCGGATGGGGAG 600
 Db 224 CysTrpAlaLeuGlyPheTyProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACGCGCTGAGAGCGCGCTGAGG 645
 Db 244 GluInThrGlnAspThrGluLeuValGluThrArgProAlaGly 258

RESULT 4
 Q8WLPS PRELIMINARY; PRT; 346 AA.
 ID Q8WLPS;
 AC Q8WLPS;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MHC class Ib antigen.
 GN HLA-F.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
 RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation
 spanning the nonclassical class I genes."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 IMMUNE SYSTEM (BY SIMILARITY).
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN) (BY SIMILARITY).
 CC EMBL; AF523284; AAM74981.1; -.
 CC EMBL; AF523291; AAM74986.1; -.
 CC EMBL; AF523292; AAM74987.1; -.
 CC GO; GO:0016021; C: integral to membrane; IEA.
 CC GO; GO:0006955; P: immune response; IEA.
 CC InterPro; IPR001064; Crystallin.
 CC DR InterPro; IPR007110; IG-like.
 CC DR InterPro; IPR003597; IG_c1.
 CC DR InterPro; IPR003006; IG_MHC.
 CC DR InterPro; IPR001039; MHC_I.
 CC Pfam; PF00047; IG_1.
 CC Pfam; PF00129; MHC_I; 1.
 CC PRINTS; PR01638; MHCCLASS1.
 CC ProDom; PD000050; MHC_I; 1.
 CC SMART; SM00407; IGc1; 1.
 CC PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 CC PROSITE; PS00835; IG_LIKE; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 SQ SEQUENCE 346 AA; 39061 MW; D4782968A67B9B7D CRC64;

DR EMBL; AF523293; AAM74988.1; -
DR EMBL; AF523294; AAM74989.1; -
DR EMBL; AF523295; AAM74990.1; -
DR EMBL; AF523296; AAM74991.1; -
DR EMBL; AF523297; AAM74992.1; -
DR EMBL; AY253269; AAO86773.1; -
DR EMBL; AY253270; AAO86774.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR PROSITE; PS000225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Alignment Scores:
Pred. No.: 2,29e-83 Length: 346
Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
Gaps: 0
DB: 7
US-09-819-371-3 (1-645) x Q8WLP5 (1-346)

Qy 1 ATCCCGCTGAGTACGTAGACACGCAATTCCTCGGTTCGACAGCGCGCGCGATT 60
Db 44 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaIle 63
Qy 61 CCAGAGTGGAGCGCGGAGCCGTGGTGGAGCAAGAGGGCGCGAGTATGGAGTGG 120
Db 64 ProArgMetGluProCArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr 83
Qy 121 ACCACGGGTACGACAGGCGCAAGCGACAGACTACCGAGTGGCCCTGAGAACCTGCTC 180
Db 84 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
Qy 181 CGCCGCTACACAGGAGCGCTGCTCACSCCTCCAGGGAATGAATGGCTGCGAC 240
Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
Qy 241 TGCTGGGCGCTGGGCTTACCTCGGAGATACGCTGACCTGGACCGGGATGGGAG 600
Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGCGCTGCGAGG 645

Db 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258
RESULT 5
Q8TP68 PRELIMINARY; PRT; 362 AA.
ID Q8TP68
AC Q8TP68
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE DJ37H4.9 (Major histocompatibility complex, class I, F (CDA12)).
GN HLA-F
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; AL022723; CAB46623.1; -
DR HSP; Q30201; 1A6Z.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40578 MW; 970D072C813A07E2 CRC64;

Alignment Scores:
Pred. No.: 2,3e-83 Length: 362
Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
Gaps: 0
DB: 7
US-09-819-371-3 (1-645) x Q8TP68 (1-362)

Qy 1 ATCCCGCTGAGTACGTAGACACGCAATTCCTCGGTTCGACAGCGCGCGCGATT 60
Db 44 IleAlaValGluTyrValAspAspThrGlnPheLeuArgPheAspSerAspAlaIle 63
Qy 61 CCAGAGTGGAGCGCGGAGCCGTGGTGGAGCAAGAGGGCGCGAGTATGGAGTGG 120
Db 64 ProArgMetGluProCArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluTyr 83
Qy 121 ACCACGGGTACGACAGGCGCAAGCGACAGACTACCGAGTGGCCCTGAGAACCTGCTC 180
Db 84 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
Qy 181 CGCCGCTACACAGGAGCGCTGCTCACSCCTCCAGGGAATGAATGGCTGCGAC 240
Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
Qy 241 TGCTGGGCGCTGGGCTTACCTCGGAGATACGCTGACCTGGACCGGGATGGGAG 600
Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
Qy 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGCGCTGCGAGG 645

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Db      124 MetGlyProAspGlyA-zgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
Qy      301 TACATCTCCCTGAACGAGGACTCGCTCTCTGAGACCGCGCGGACACACCGTGGCTCAGATC 360
Db      144 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
Qy      361 ACCAGCGCTCTATGAGGAGAGAGATATGACAGAGAGTTCCAGAGAGTTCCAGACTACCTGGAGGC 420
Db      164 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGluPheArgThrTyrLeuGluGly 183
Qy      421 GAGTGCCTGGAGTTGCTCCGAGATACCTTGAGAAATGGAGAGAGCGCTACAGCGGCA 480
Db      184 GluCysLeuGluLeuLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 203
Qy      481 GATCTTCAAAGGACACGTTGCCACACACCCCATCTCTGACCATGAGGCCACCTGAGG 540
Db      204 AspProProlysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 223
Qy      541 TGCTGGGCGCTTCTACCTCGGAGATACGCTGACCTGCAGCGGATGGGAG 600
Db      224 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 243
Qy      601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTGCAGG 645
Db      244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258

RESULT 6
Q95HCO PRELIMINARY; PRT; 442 AA.
AC
AD Q95HCO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to major histocompatibility complex, class I, F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Strausberg R.;
RL EMBL; BC009260; AA09260.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00230; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 442 AA; 50427 MW; 6459D3B5F4B5704A CRC64;

Alignment Scores:
Pred. No.: 2,35e-83 Length: 442
Score: 1156.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 7 Gaps: 0

US-09-819-371-3 (1-645) x Q95HCO (1-442)
Qy 1 ATCGCGGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGCGCGCGCGATT 60

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Db      44 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaIle 63
Qy      61 CCGAGATGAGACCGCGGAGCCGTGGGTGGAGCAAGAGCGCGCGAGTATTGGAGTGG 120
Db      64 ProArgMetGluProArgGluProTrpValGluGlnGluGlyProGlnTyrTrpGluTrp 83
Qy      121 ACCAGSGGTAGCCCAAGCCCAACGACACAGACTGACCGAGTGGCCCTGAGGAACCTGGCTC 180
Db      84 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspA-gvalAlaLeuArgAsnLeuLeu 103
Qy      181 CGCGCTTACAACACAGAGCGAGGCTGGGTCTCACSCCCTCCAGGGAAATGAATGGCTCGCAC 240
Db      104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
Qy      241 ATGGGCGCGACGAGCGCCCTCTCCGCGGTATCACACGACGCGTACGACGCGCAGGAT 300
Db      124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
Qy      301 TACATCTCCCTGAACGAGGACCTCGCTCTCGACCGCGCGGACACACCCCTGGCTCAGATC 360
Db      144 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
Qy      361 ACCAGCGCTTCTATGAGGACAGAGAAATATGACAGAGAGTTCCAGAGACTTACCTGGAGGC 420
Db      164 ThrGlnArgPheTyrGluAlaGluGlyTyrAlaGluGluPheArgThrTyrLeuGluGly 183
Qy      421 GAGTGCCTGGAGTTGCTCCGAGATACCTTGAGAAATGGAGAGAGCGCTACAGCGCGCA 480
Db      184 GluCysLeuGluLeuLeuLeuArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 203
Qy      481 GATCTTCAAAGGACACGTTGCCACACACCCCATCTCTGACCATGAGGCCACCTGAGG 540
Db      204 AspProProlysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 223
Qy      541 TGCTGGGCGCTTCTACCTCGGAGATACGCTGACCTGCAGCGGATGGGAG 600
Db      224 CysTrpAlaLeuGlyPheTyrProAlaGluLeuThrLeuThrTrpGlnArgAspGlyGlu 243
Qy      601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTGCAGG 645
Db      244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258

RESULT 7
Q95IT2 PRELIMINARY; PRT; 346 AA.
AC
AD Q95IT2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21291697; PubMed=11398964;
RA Adams E.J.; Parham P.;
RT "Genomic analysis of common chimpanzee major histocompatibility complex class I genes."
RL Immunogenetics 53:200-208(2001).
DR EMBL; AF338335; AAK77479.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.

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DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC I; 1.
DR SMART; SM00407; IGL; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 346 AA; 39009 MW; 0BCEFI2B7DB17B814 CRC64;
Alignment Scores:
Pred. No.: 2,95e-82 Length: 346
Score: 1142.00 Matches: 212
Percent Similarity: 98.60% Conservatives: 0
Best Local Similarity: 98.60% Mismatches: 3
Query Match: 96.53% Indels: 0
DB: 7 Gaps: 0
US-09-819-371-3 (1-645) x Q95IIT2 (1-346)
QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCCAGACGCGCGCGGATT 60
Db 44 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 63
QY 61 CCGAGGATGGAGCGCGGAGCCGCTGGGTGGAGCAAGAGGCGCGAGTATTGGAGTGG 120
Db 64 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluArg 83
QY 121 ACCACGGGTACGCCAAGCCCAACGACAGCTACCGAGTGGCCCTGAGAACCTGCTC 180
Db 84 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
QY 181 CGCGCTACACACGAGGAGCGTGGGTCTCACCCCTCCAGGGAATGAATGGCTGGAC 240
Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
QY 241 ATGGGGCCGACGCGCTCTCCGCGGTATCACACGACGCGTACGACGCGCAAGGAT 300
Db 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
QY 301 TACATCTCCCTGAAGGACCTCGCTCCGCGGTATCACACGACGCGTACGACGCGCA 360
Db 144 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
QY 361 ACCCAGCGCTTATGAGGACGAGGAATATGACGAGGAGTTCAGGACCTACCTGGAGGC 420
Db 164 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuGluGly 183
QY 421 GAGTGGCTGGAGTTCCTCCGAGATCTTGGAGAAATGGGAAGGAGACGCTACAGCGGCA 480
Db 184 GluCysLeuGluLeuLeuArgGlyTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 203
QY 481 GATCTCTCAAAGGCACACGCTTCCACCAACCCCATCTCTGACCATGAGCCACCTGAGG 540
Db 204 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 223
QY 541 TGCTGGGCGCTGGCTTACCTCGGAGATCACTGACCTGACCTGGCAGCGGATGGGAG 600
Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
QY 601 GRACAGACCCAGGACACAGCTTGGAGACCGAGCCCTGCAGGG 645
Db 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258
RESULT 8
Q7YR27
ID Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Class Ib.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22709134; PubMed=12799463;
RA Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA Yamagata T., Kishi J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamazaki M., Tashiro H., Iwamoto C., Umenara Y., Imanishi T.,
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT "Comparative sequencing of human and chimpanzee MHC class I regions
RT unveils insertions/deletions as the major path to genomic
RT divergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713 (2003).
DR EMBL; AB100087; BAC78191.1; -. BAS699D08181A1FF CRC64;
SQ SEQUENCE 362 AA; 40625 MW; BAS699D08181A1FF CRC64;
Alignment Scores:
Pred. No.: 2,96e-82 Length: 362
Score: 1142.00 Matches: 212
Percent Similarity: 98.60% Conservatives: 0
Best Local Similarity: 98.60% Mismatches: 3
Query Match: 96.53% Indels: 0
DB: 6 Gaps: 0
US-09-819-371-3 (1-645) x Q7YR27 (1-362)
QY 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCCAGACGCGCGCGGATT 60
Db 44 IleAlaValGluTyrValAspThrGlnPheLeuArgPheAspSerAspAlaAlaIle 63
QY 61 CCGAGGATGGAGCGCGGAGCCGCTGGGTGGAGCAAGAGGCGCGAGTATTGGAGTGG 120
Db 64 ProArgMetGluProArgGluProTyrValGluGlnGluGlyProGlnTyrTrpGluArg 83
QY 121 ACCACGGGTACGCCAAGCCCAACGACAGCTACCGAGTGGCCCTGAGAACCTGCTC 180
Db 84 ThrThrGlyTyrAlaLysAlaAsnAlaGlnThrAspArgValAlaLeuArgAsnLeuLeu 103
QY 181 CGCGCTACACACGAGGAGCGTGGGTCTCACCCCTCCAGGGAATGAATGGCTGGAC 240
Db 104 ArgArgTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnGlyMetAsnGlyCysAsp 123
QY 241 ATGGGGCCGACGCGCTCTCCGCGGTATCACACGACGCGTACGACGCGCAAGGAT 300
Db 124 MetGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnHisAlaTyrAspGlyLysAsp 143
QY 301 TACATCTCCCTGAAGGACCTCGCTCCGCGGTATCACACGACGCGTACGACGCGCA 360
Db 144 TyrIleSerLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrValAlaGlnIle 163
QY 361 ACCCAGCGCTTATGAGGACGAGGAATATGACGAGGAGTTCAGGACCTACCTGGAGGC 420
Db 164 ThrGlnArgPheTyrGluAlaGluTyrAlaGluGluPheArgThrTyrLeuGluGly 183
QY 421 GAGTGGCTGGAGTTCCTCCGAGATCTTGGAGAAATGGGAAGGAGACGCTACAGCGGCA 480
Db 184 GluCysLeuGluLeuLeuArgGlyTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 203
QY 481 GATCTCTCAAAGGCACACGCTTCCACCAACCCCATCTCTGACCATGAGCCACCTGAGG 540
Db 204 AspProProLysAlaHisValAlaHisProIleSerAspHisGluAlaThrLeuArg 223
QY 541 TGCTGGGCGCTGGCTTACCTCGGAGATCACTGACCTGACCTGGCAGCGGATGGGAG 600
Db 224 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 243
QY 601 GRACAGACCCAGGACACAGCTTGGAGACCGAGCCCTGCAGGG 645
Db 244 GluGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 258
RESULT 9
Q9MXK1

ID Q9MXK1 PRELIMINARY; PRT; 362 AA.
 AC Q9MXK1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE MHC class I antigen.
 GN PATR-B.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=20322475; PubMed=10866106;
 RA de Groot N.G., Otting N., Arguello R., Watkins D.I., Doxiadis G.G.M.,
 RA Madrigal J.A., Bontrop R.E.;
 RT "Major histocompatibility complex class I diversity in a West African
 chimpanzee population: implications for HIV research.";
 RL Immunogenetics 51:398-409(2000).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 CC IMMUNE SYSTEM (BY SIMILARITY).
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).
 DR EMBL; AF168410; RA72791.1; -;
 DR HSP; P03989; IHS.A.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 SQ SEQUENCE 362 AA; 40442 MW; 4E1A081945D3A4F3 CRC64;
 Alignment Scores:
 Pred. No.: 5,32e-66 Length: 362
 Score: 937.00 Matches: 174
 Percent Similarity: 86.09% Conservative: 11
 Best Local Similarity: 80.93% Mismatches: 30
 Query Match: 79.21% Indels: 0
 DB: 7 Gaps: 0
 US-09-819-371-3 (1-645) x Q9MXK1 (1-362)
 QY 1 ATCGCGGTGGAGTACGTAGACACAGCGCAATTCCTCGGTTCGACAGCGCGCGCGATT 60
 DB 47 IleAlaValAlGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaIle 66
 QY 61 CCGAGATGTGAGCGCGGAGCGGTGGTGGAGAGAGGCGCGCGAGTATGGAGTGG 120
 DB 67 ProArgMetGluProArgAlaProIleGlnGlnGlyProGluTyrTrpAspArg 86
 QY 121 ACCACGGGTACGCCAAGCCCAACGACAGACTGACCGAGTGGCCCTCAGGAACCTGCTC 180
 DB 87 AsnThrGlnGlyIleIleYsThrGlnAlaGlnThrAspArgGluAsnLeuArgThrLeuLeu 106
 QY 181 CCGCGCTACACAGCGAGCGGTGGTCTACSCCTCCAGGATGAATGGCTGGAC 240
 DB 107 ArgTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnSerMetTyrGlyCysAsp 126
 QY 241 ATGGGCGCGAGCGCGCTCTCCGCGGTATCACAGCGCGGTACGAGCGGCAAGGAT 300
 DB 127 MetGlyProAspGlyArgLeuLeuArgGlyTyrAspGlnTyrAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCTGACAGGAGACTGCGCTCCTGGACCGCGGGGACACCGTGGCTCAGATC 360

Db 147 TyrIleAlaLeuAsnLysAspLeuSerSerTyrThrAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCAGCGCTTCTATGAGCGAGAGGATATGACAGGAGTTCAGGACCTACCTGGAGGCG 420
 Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGlnLeuArgAlaTyrLeuGluGly 186
 QY 421 GAGTGGCTGGAGTTGCTCCGACAGATCTTGGAGAATGGGAAGGAGACGCTACAGCGCGCA 480
 Db 187 ThrCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
 QY 481 GATCCTCCAAAGGACACGCTTGGCCACCCCATCTCTGACCATGAGGCGCCCTGAGG 540
 Db 207 AspProLysThrHisValThrHisProIleSerAspHisGluAlaThrLeuArg 226
 QY 541 TGTGGCGCTCGGCTTACCTGGGAGATCACGCTGAGCTGACCTGAGCGCGGATGGGAG 600
 Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GACACAGCCAGACACAGAGCTTGGGAGACCGAGCGCTGCGAGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261
 RESULT 10
 Q8SNC9 PRELIMINARY; PRT; 273 AA.
 ID Q8SNC9
 AC Q8SNC9;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE MHC class I antigen (Fragment).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Garcia-Sanchez P., Vicario J.L., Alonso M., Balas A., Lillo R.;
 RT "Four new HLA class I alleles in Caucasoids.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 CC IMMUNE SYSTEM (BY SIMILARITY).
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).
 DR EMBL; AF480612; AAL87223.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 FT NON TER 273
 FT NON TER 273
 SQ SEQUENCE 273 AA; 31602 MW; 0C8731F012089A7E CRC64;
 Alignment Scores:
 Pred. No.: 1,54e-65 Length: 273
 Score: 931.00 Matches: 173
 Percent Similarity: 85.12% Conservative: 10
 Best Local Similarity: 80.47% Mismatches: 32
 Query Match: 78.70% Indels: 0
 DB: 7 Gaps: 0
 US-09-819-371-3 (1-645) x Q8SNC9 (1-273)

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QY 1 ATCCGCTGGAGTACGTAGCAGCAGCAATTCCTCGGTTTCGACAGCGCCGCGGATT 60
Db 22 ILeThrValGlyTyrValAspSerThrLeuPheValArgPheAspSerAspAlaAlaSer 41
QY 61 CCAGAGTGGAGCGCGGAGCCCTGGGTGGAGCAAGAGGGCGCGAGTATTCGGAGTGG 120
Db 42 ProArgGluGluProArgAlaProTPIleGluGlnGluGlyProGluTyrTrpAspArg 61
QY 121 ACCACSGGTACGCCAAGGCCAAGCCAGCAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 62 GluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGluAspLeuArgThrLeuLeu 81
QY 181 CGCCGCTACACACAGAGAGGCTGCTCCTGAGACCCCTCCAGGGAATGAATGGCTCGAC 240
Db 82 ArgTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnAsnMetTyrGlyCysAsp 101
QY 241 ATGGGGCGGACGACGCTCTCCGCGGGTATCACAGCAGCGGTACGACGGCAAGGAT 300
Db 102 ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp 121
QY 301 TACATCTCCCTGAACGAGGACCTCGCTCTCTGGACCGCGGACACCGTGGCTCAGATC 360
Db 122 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 141
QY 361 ACCCAGCGCTTCTATGAGGAGAGGAATATGACAGAGGATTCAGGACCTACCTGGAGGC 420
Db 142 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly 161
QY 421 GAGTGCCTGGAGTGTCTCCGAGATCTTGGAGATGGAGAGAGAGCGTACACGGCGCA 480
Db 162 GluCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 181
QY 481 GATCCTCCAAAGGCACAGCTTGTCCACACCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 182 AspProLysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 201
QY 541 TGCTGGGCCCTGGGCTTACCTCGGAGATCAGCTGACCTGGAGCGGAGTGGGGAG 600
Db 202 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 221
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGGCTGCGAGG 645
Db 222 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 236

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RESULT 11

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O19692
AC O19692; PRELIMINARY; PRT; 274 AA.
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HLA-B protein (Fragment).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87009855; PubMed=3489755;
RA Coppin H.L., McDevitt H.O.;
RT "Absence of polymorphism between HLA-B*27 genomic exon sequences
RT isolated from normal donors and ankylosing spondylitis patients.";
RL J. Immunol. 137:2168-2172(1986).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; M14013; AAA59643.1; -.
DR HSP; P03959; 1HSN.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.

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DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG; 1.
DR ProDom; PD00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 274 AA; 31659 MW; 0C9A7A49023B3219 CRC64;

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Alignment Scores:

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Pred. No.: 1,548-65 Length: 274
Score: 531.00 Matches: 173
Percent Similarity: 85.12% Conservative: 10
Best Local Similarity: 80.47% Mismatches: 32
Query Match: 78.70% Indels: 0
DB: 7 Gaps: 0

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US-09-819-371-3 (1-645) x O19692 (1-274)

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QY 1 ATCCGCTGGAGTACGTAGCAGCAGCAATTCCTCGGTTTCGACAGCGCCGCGGATT 60
Db 23 ILeThrValGlyTyrValAspSerThrLeuPheValArgPheAspSerAspAlaAlaSer 42
QY 61 CCAGAGTGGAGCGCGGAGCCCTGGGTGGAGCAAGAGGGCGCGAGTATTCGGAGTGG 120
Db 43 ProArgGluGluProArgAlaProTPIleGluGlnGluGlyProGluTyrTrpAspArg 62
QY 121 ACCCAGCGGTACGCCAAGGCCAAGCCAGCAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
Db 63 GluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGluAspLeuArgThrLeuLeu 82
QY 181 CGCCGCTACACACAGAGAGGCTGCTCCTCGGAGATTCAGGACCTACCTGGAGGC 240
Db 83 ArgTyrTyrAsnGlnSerGluAlaGlySerHisThrLeuGlnAsnMetTyrGlyCysAsp 102
QY 241 ATGGGGCGGACGACGCTCTCCGCGGGTATCACAGCAGCGGTACGACGGCAAGGAT 300
Db 103 ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp 122
QY 301 TACATCTCCCTGAACGAGGACCTGCTCCTCGGAGATTCAGGACCTACCTGGAGGC 360
Db 123 TyrIleAlaLeuAsnGluAspLeuSerSerTrpThrAlaAlaAspThrAlaAlaGlnIle 142
QY 361 ACCCAGCGCTTCTATGAGGAGAGGAATATGACAGAGGATTCAGGACCTACCTGGAGGC 420
Db 143 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly 162
QY 421 GAGTGCCTGGAGTGTCTCCGAGATCTTGGAGATGGAGAGAGAGCGTACGACGGCGCA 480
Db 163 GluCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 182
QY 481 GATCCTCCAAAGGCACACAGCTTGTCCACACCCATCTCTGACCATGAGGCCACCTGAGG 540
Db 183 AspProLysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 202
QY 541 TGCTGGGCCCTGGGCTTACCTCGGAGATCAGCTGACCTGGAGCGGAGTGGGGAG 600
Db 203 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 222
QY 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAAGGCTGCGAGG 645
Db 223 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 237

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RESULT 12

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P79612
ID P79612 PRELIMINARY; PRT; 362 AA.

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P79612;
 01-MAY-1997 (TrEMBLrel. 03, Created)
 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 HLA-B protein.
 HLA-B.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Blood;
 Hasegawa T., Sugahara Y., Moriyama Y., Nanzai H., Ogawa A., Tawara K.,
 Kondo S., Tokunaga K.,
 "Molecular characterization of a novel HLA-B*27 allele."
 Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 IMMUNE SYSTEM (BY SIMILARITY).
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN) (BY SIMILARITY).
 CC EMBL; D83043; BAA11753.1; -.
 DR HSPF; P03989; IJSA.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0006955; P: immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 SQ SEQUENCE 362 AA; 40441 MW; 3CA65547B65FDF84 CRC64;
 Alignment Scores:
 Pred. No.: 1,596-65 Length: 362
 Score: 931.00 Matches: 172
 Percent Similarity: 86.51% Conservatives: 14
 Best Local Similarity: 80.0% Mismatches: 29
 Query Match: 78.70% Indels: 0
 DB: Gaps: 0
 US-09-819-371-3 (1-645) x P79612 (1-362)
 QY 1 ATCCCGGTGAGTACGTAGACACGCAATTCTCGGGTTCGACAGCGCGCGCGATT 60
 Db 47 ILeThrValGlyTy-ValAspAspThrLeuPheValArgPheAspSerAspAlaAlaSer 66
 QY 61 CCGAGGATGGAGCGCGGAGCGGTGGTGGAGCAAGAGGCGCGCAGTATTGGGAGTGG 120
 Db 67 ProArgGluGluProArgAlaProIleGluGluGluGlyProGluTyTrpAspArg 86
 QY 121 ACCACGGGTACGCCAAGCCACACACAGACTGACGAGTGGCGCTGAGGAACCTGCTC 180
 Db 87 GluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGluSerLeuArgThrLeuLeu 106
 QY 181 CGCCGCTACACAGAGCGGCTGGTCTACSCCTCCAGGGAATGAATGGTGGAC 240
 Db 107 ArgTyTrpAsnGlnSerGluAlaGlySerHisThrLeuGlnSerMetTyrglyCysAsp 126
 QY 241 ATGGGGCGCGGAGCGGCTCTCCGCGGGTATCACCAGCAGCGGTACGACGCGCAAGGAT 300
 Db 127 ValGlyProAspGlyArgLeuLeuArgGlyHisAsnGlnTyAlaTyAspGlyLeuAsp 146
 QY 301 TCATCTCCCTGAACAGAGACCTGCTGCTGAGACCGCGCGGAGACCGCTGCTGATC 360
 Db 147 TyriIleAlaLeuAsnGluAspLeuArgSerTrpThrAlaAlaAspThrAlaAlaGlnIle 166

QY 361 ACCAGCGCTTCTATGAGGACAGGAATATGACAGAGGAGTTCCAGGACCTACTCGAGGSC 420
 Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyLeuGluGly 186
 QY 421 GAGTCTCTGAGTCTCGCAGATCTTGGAGATGGAGAGGACGCTACAGCGCGCA 480
 Db 187 GluCysValGluTrpLeuArgArgTyLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
 QY 481 GATCTCTCAAGGACACAGTCTCCACACACCCATCTCTGACCATGAGCCACCTGAGG 540
 Db 207 AspProTyLeuThrHisValThrHisProIleSerAspHisGluAlaThrLeuArg 226
 QY 541 TGTGGCGCTGGGCTTCTACCTCGGAGATCAGCTGACCTGGCAGCGGATGGGAG 600
 Db 227 CysTrpAlaLeuGlyPheTyProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GAACAGACCCAGGACACAGAGCTTGTGAGACGAGCGCTGCGAGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261
 RESULT 13
 078189 PRELIMINARY; PRT; 362 AA.
 AC 078189;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MHC class I antigen.
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98427840; PubMed=9756409;
 RA Seurynck K., Baxter-Lowe L.A.;
 RT "Novel polymorphism detected in exon 1 of HLA-B*2713."
 RL Tissue Antigens 52:187-189(1998).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 IMMUNE SYSTEM (BY SIMILARITY).
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN) (BY SIMILARITY).
 CC EMBL; AF026218; AAC42275.1; -.
 DR HSPF; P03989; IJSA.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0006955; P: immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 SQ SEQUENCE 362 AA; 40485 MW; BC00FC372955711D CRC64;
 Alignment Scores:
 Pred. No.: 1,596-65 Length: 362
 Score: 931.00 Matches: 173
 Percent Similarity: 85.12% Conservatives: 10
 Best Local Similarity: 80.47% Mismatches: 32
 Query Match: 78.70% Indels: 0
 DB: Gaps: 0
 US-09-819-371-3 (1-645) x 078189 (1-362)
 QY 1 ATCCCGGTGAGTACGTAGACACGCAATTCTCGGGTTCGACAGCGCGCGCGATT 60

Db 47 IleThrValGlyTyrValAspAspThrLeuPheValArgPheAspSerAspAlaAlaSer 66
 QY 61 CCAGAGTGGAGCGCGGAGCGGTGGGTGGAGCAAGAGCGCGCGAGTATTGGAGTGG 120
 Db 67 ProArgGluGluProArgAlaProTyrIleGluGlnGluGlyProGluTyrTrpAspArg 86
 QY 121 ACCACGGGTACGCCAAGCCCAACGACAGACTGAGCGAGTGGCCCTGAGGAACCTGCTC 180
 Db 87 GluThrGlnIleCysIysAlaIysAlaGlnThrAspArgGluAspLeuArgThrLeuLeu 106
 QY 181 CGCGCGTACACACAGAGCGAGCGGTGGTCTCACSCCCTCCAGGGAATGAATGGCTGCAC 240
 Db 107 ArgTyrTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnAsnMetTyrGlyCysAsp 126
 QY 241 ATGGGCGCCGACGAGCGCTCTCCGGGGTATCCACGACGCGTACACGCGCAAGGAT 300
 Db 127 ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCCTGACACGAGCGAGCGGTGGTCTCCAGCGCGCGGACACCGTGGCTCAGATC 360
 Db 147 TyrIleAlaLeuAsnGlnAspLeuSerTyrTrpThrAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCGAGCGCTTCTATGAGGCGAGGAGGAATATGACAGGAGTTCAGGACCTACCTGAGGCG 420
 Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
 QY 421 GAGTGGCTGGAGTGTCTCCGACATATCTGGAGAAATGGAGAGCGCTACAGCGCGCA 480
 Db 187 GluCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
 QY 481 GATCTCTCAAGGACACAGCTGTGCCACCCCATCTCTGACCATGAGCGCCACCTGAGG 540
 Db 207 AspProLysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 226
 QY 541 TGCTGGCGCTGGCTTACCTCGGAGATACGCTGACCTGCGAGCGGAGTGGGAG 600
 Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GAACAGACCCAGACACAGAGCTGTGGAGACGAGCGCTGCAGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 14
 Q29705
 ID Q29705 PRELIMINARY; PRT; 362 AA.
 AC Q29705;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE MHC class I antigen HLA-B precursor.
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Balas A., Santos S., Vicario J.L.;
 RT "Serological and molecular characterization of a novel HLA-B allele.";
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U31971; AAA98506.1; -;
 DR HSSP; P03989; 1HSA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR0031597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASS1.
 DR ProDom; PD000050; MHC_I; 1.

DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW SIGNAL.
 FT CHAIN 1 24 POTENTIAL.
 SQ SEQUENCE 362 AA; 40479 MW; 148856561595A505 CRC64;
 Alignment Scores:
 Pred. No.: 1.91e-65 Length: 362
 Score: 930.00 Matches: 172
 Percent Similarity: 85.58% Conservative: 12
 Best Local Similarity: 80.00% Mismatches: 31
 Query Match: 78.61% Indels: 0
 DB: 4 Gaps: 0

US-09-819-371-3 (1-645) x Q29705 (1-362)

QY 1 ATCCCGCTGGAGTACGTAGACGACACGCAATCTCGGTTCGACAGCGCGCGCGGATT 60
 Db 47 IleSerValGlyTyrValAspAspThrGlnPheValArgPheAspSerAspAlaAlaSer 66
 QY 61 CCAGGATGGAGCGCGGAGCGCGGTGGTGGAGCAAGAGCGCGCGAGTATTGGAGTGG 120
 Db 67 ProArgThrGluProArgAlaProTyrIleGluGlnGluGlyProGluTyrTrpAspArg 86
 QY 121 ACCACGGGTACGCCAAGCGCAACGACAGACTGACGAGTGGCCCTGAGGAACCTGCTC 180
 Db 87 GluThrGlnIleSerLysThrAsnThrGlnThrTyrArgGluAspLeuArgThrLeuLeu 106
 QY 181 CGCGCTACACACAGAGCGAGCGGTGGTCTCACSCCCTCCAGGGAATGAATGGCTGCAC 240
 Db 107 ArgTyrTyrAsnGlnSerGlnAlaGlySerHisThrLeuGlnAsnMetTyrGlyCysAsp 126
 QY 241 ATGGGCGCCGACGAGCGCTCTCCGGGGTATCCACGACGCGTACGAGCGCAAGGAT 300
 Db 127 ValGlyProAspGlyArgLeuLeuArgGlyTyrHisGlnAspAlaTyrAspGlyLysAsp 146
 QY 301 TACATCTCCCTGACACGAGGAGCGGTGGTCTCGGAGCGCGCGGACACCGTGGCTCAGATC 360
 Db 147 TyrIleAlaLeuAsnGlnAspLeuSerTyrTrpThrAlaAlaAspThrAlaAlaGlnIle 166
 QY 361 ACCGAGCGCTTCTATGAGGCGAGGAGGAATATGACAGGAGTTCAGGACCTACCTGAGGCG 420
 Db 167 ThrGlnArgLysTrpGluAlaAlaArgValAlaGluGlnLeuArgAlaTyrLeuGluGly 186
 QY 421 GAGTGGCTGGAGTGTCTCCGACATATCTGGAGAAATGGAGAGCGCTACAGCGCGCA 480
 Db 187 GluCysValGluTrpLeuArgArgTyrLeuGluAsnGlyLysGluThrLeuGlnArgAla 206
 QY 481 GATCTCTCAAGGACACAGCTGTGCCACCCCATCTCTGACCATGAGCGCCACCTGAGG 540
 Db 207 AspProLysThrHisValThrHisHisProIleSerAspHisGluAlaThrLeuArg 226
 QY 541 TGCTGGCGCTGGCTTACCTCGGAGATACGCTGACCTGCGAGCGGAGTGGGAG 600
 Db 227 CysTrpAlaLeuGlyPheTyrProAlaGluIleThrLeuThrTrpGlnArgAspGlyGlu 246
 QY 601 GAACAGACCCAGACACAGAGCTGTGGAGACGAGCGCTGCAGG 645
 Db 247 AspGlnThrGlnAspThrGluLeuValGluThrArgProAlaGly 261

RESULT 15
 Q29530
 ID Q29530 PRELIMINARY; PRT; 354 AA.
 AC Q29530;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Class I histocompatibility antigen (Fragment).
 GN HLA-B.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Teppie;
EX MEDLINE=94286544; PubMed=8016085;
RA McAdam S.N., Boyson J.E., Liu X., Garber T.L., Hughes A.L.,
RA Bontrop R.E., Watkins D.I.;
RT "A uniquely high level of recombination at the HLA-B locus";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; U05581; AAA50184.1; -;
DR PIR; I80170; I80170.
DR HSSP; P30685; IA9E.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR Pfam; PF00129; MHC_1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_1; 1.
DR SMART; SM00407; IGc1_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 354 AA; 39555 MW; 61942B24D173786F CRC64;

Search completed: June 18, 2004, 07:39:01
Job time : 69 secs

Alignment Scores:
Pred. No.: 354
Score: 927.00
Percent Similarity: 86.05%
Best Local Similarity: 80.00%
Query Match: 78.36%
Indels: 0
Gaps: 0

US-09-819-371-3 (1-645) x Q95530 (1-354)

QY 1 ATCCGCGTGGAGTAGACGACACGCAATTCTCGGTTTCGACAGCGCGCGGATT 60
DB 39 IleaValGlyTyrValAspThrGlnPheValArgPheAspSerAspAlaIle 58
QY 61 CCGAGGATGGAGCCCGGGAGCCGTGGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG 120
DB 59 ProArgMetGluProArgAlaProTrpIleGluGlnGluGlyProGluTyrTrpAspArg 78
QY 121 ACCACSGGTACGCCCAAGCCCAACACAGACTGACCGAGTGGCCCTGAGGAACCTGCTC 180
DB 79 GluThrGlnIleSerLysThrAsnAlaGlnThrTyrArgValGlyLeuArgAsnLeuArg 98
QY 181 CGCCGCTACACACAGCAGGAGCTGGGTCTCACSCCTCCAGGGAATGAATGGCTGGGAC 240
DB 99 GlyTyrTyrAsnGlnSerGluAlaGlySerHisThrTrpGlnThrMetTyrGlyCysAsp 118
QY 241 ATGGGGCCGAGCGGCGCTCTCCGCGGTATCACACGACGCGGTACGACGCAAGGAT 300
DB 119 ValGlyProAspGlyArgLeuLeuArgGlyTyrArgGlnPheAlaTyrAspGlyLysAsp 138
QY 301 TACATCTCCCTGAACGAGGACCTGGGCTCTCGACCGCGGGGACACCGTGCTGCAGATC 360
DB 139 TyrIleAlaLeuAsnLysAspLeuSerTrpThrAlaAspThrAlaAlaGlnIle 158
QY 361 ACCCAGCGCTTATGAGCAGAGGAATATGACAGAGAGTTCAGGACCTACTGGAGGCGC 420
DB 159 ThrGlnArgLysTrpGluAlaAlaAlaArgTrpAlaGluGlnLeuArgAlaTyrLeuGly 178
QY 421 GAGTGCTGGAGTGTGCTCCGAGATCTGGAGATGGAGAGACGCTACAGCGCGCA 480

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 18, 2004, 02:53:01 ; Search time 2411 Seconds
(without alignments)
7988.845 Million cell updates/sec

Title: US-09-819-371-3
Perfect score: 645
Sequence: 1 atgcgcgtgagtagtaga.....tggagaccaggcctgcagg 645

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues 55026578

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gas_hum:*
- 18: em_gas_inv:*
- 19: em_gas_pin:*
- 20: em_gas_vrt:*
- 21: em_gas_mam:*
- 22: em_gas_mus:*
- 23: em_gas_pro:*
- 24: em_gas_rod:*
- 25: em_gas_rod:*
- 26: em_gas_phg:*
- 27: em_gas_vrl:*
- 28: gb_ges1:*
- 29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640.2	99.3	926	13	BQ707312
2	637.6	98.9	875	13	BQ962778
3	635.4	98.5	949	12	BM561951
4	629.6	97.6	829	14	CD514705

5	626.6	97.1	886	13	BQ688194
6	625	96.9	928	13	BQ710481
7	615.4	95.4	941	13	BQ711764
8	607.4	94.2	892	13	BQ690438
9	602.6	93.4	931	13	BQ928296
10	592	91.8	1130	12	BM517072
11	572.8	88.8	745	12	BQ762711
12	569.2	88.2	718	12	BG679105
13	565	87.6	749	12	BG743996
14	528.8	82.0	550	10	BF110304
15	500.6	77.6	968	13	BQ709603
16	497.4	77.1	892	13	BQ849484
17	497.4	77.1	907	13	BQ931092
18	496.8	77.0	985	12	BM561722
19	496.8	77.0	1069	9	AL558822
20	496.8	77.0	1201	9	AL531206
21	496	76.9	506	10	BF477881
22	495.8	76.9	858	14	CD172147
23	492.2	76.3	666	12	BQ016533
24	491.6	76.2	1201	9	AL552699
25	491.4	76.2	1081	12	BQ051893
26	490.4	76.0	859	14	CD251094
27	490.4	76.0	875	14	CD251782
28	490.4	76.0	1020	14	CD515795
29	490.4	76.0	1201	9	AL545738
30	490	76.0	1030	13	BX438723
31	490	76.0	1201	13	BX403678
32	489.8	75.9	1106	12	BM553410
33	489.4	75.9	870	14	CD108051
34	489.2	75.8	817	10	BF683616
35	488.8	75.8	888	13	BQ878404
36	488.8	75.8	920	14	CD515151
37	488.8	75.8	939	9	AL524367
38	488.8	75.8	950	13	BQ893633
39	488.8	75.8	1102	9	AL542771
40	488.8	75.8	1131	12	BM477065
41	488.8	75.8	1201	9	AL537919
42	488.4	75.7	840	13	BQ933133
43	488	75.7	1201	9	AL545647
44	487.8	75.6	901	13	BQ227072
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ALIGNMENTS

RESULT 1
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LOCUS BQ707312 926 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT 8354575 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281285
5', mRNA sequence.
ACCESSION BQ707312 GI:21846211
VERSION BQ707312.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2473 row: n column: 06
High quality sequence stop: 628.

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BQ710481	AGENCOURT
BQ711764	AGENCOURT
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BQ928296	AGENCOURT
BM517072	AGENCOURT
BG672711	602734620
BG679105	602627060
BG743996	602722769
BF110304	7n36c07.x
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BQ849484	AGENCOURT
BQ931092	AGENCOURT
BM561722	AGENCOURT
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AL531206	AL531206
BF477881	7r06e05.x
CD172147	AGENCOURT
BQ016533	UI-H-D10-
AL552699	AL552699
BQ051893	AGENCOURT
CD251094	AGENCOURT
CD251782	AGENCOURT
CD515795	AGENCOURT
AL545738	AL545738
BX438723	BX438723
BX403678	BX403678
BM553410	AGENCOURT
CD108051	AGENCOURT
BF683616	602139839
BQ878404	AGENCOURT
CD515151	AGENCOURT
AL524367	AL524367
BQ893633	AGENCOURT
AL542771	AL542771
BM477065	AGENCOURT
AL537919	AL537919
BQ933133	AGENCOURT
AL545647	AL545647
BQ227072	AGENCOURT
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FEATURES	source	Location/Qualifiers
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		/db_xref="taxon:9606"
		/clone="IMAGE:6281285"
		/lab_host="DH10B (phage-resistant)"
		/clone_lib="NIH_MGC_113"
		/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN		
	Query Match	99.3%; Score 640.2; DB 13; Length 926;
	Best Local Similarity	99.5%; Pred. No. 3.4e-115;
	Matches 642; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1	ATCGCGGTGGAGTACGTAGACGACACGCAATTCCTCGGTTTCGACGCGCGCGCGGATT 60
Db	129	ATCGCGGTGGAGTACGTAGACGACACGCAATTCCTCGGTTTCGACGCGCGCGCGGATT 188
QY	61	CCGAGGATGGAGCCGCGCGAGCCGTGGTGGACCAAGAGGCGCGCAGTATTGGAGTGG 120
Db	189	CCGAGGATGGAGCCGCGCGAGCCGTGGTGGACCAAGAGGCGCGCAGTATTGGAGTGG 248
QY	121	ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTCAGGAACTCGTC 180
Db	249	ACCACGGGTACGCCAAGGCCAACGACAGACTGACCGAGTGGCCCTCAGGAACTCGTC 308
QY	181	CGCCCTACACACGACGAGGCTGGTCTCACSCCTCCAGGGAATGAATGGCTGGCAC 240
Db	309	CGCCCTACACACGAGCGAGCTGGTCTCACSCCTCCAGGGAATGAATGGCTGGCAC 368
QY	241	ATGGGGCCCGACGACGCGCTCTCCGCGGTATCACACGACGCGTACGACGGCAAGGAT 300
Db	369	ATGGGGCCCGACGACGCGCTCTCCGCGGTATCACACGACGCGTACGACGGCAAGGAT 428
QY	301	TACATCTCCCTGAACGAGGACTCGCTCTCTGACCGCGCGGACACCGTGGCTCAGATC 360
Db	429	TACATCTCCCTGAACGAGGACTCGCTCTCTGACCGCGCGGACACCGTGGCTCAGATC 488
QY	361	ACCACAGCGTCTTATGAGCGACAGGAATATGACAGAGGTTACGACCTTACCTGAGGGC 420
Db	489	ACCACAGCGTCTTATGAGCGACAGGAATATGACAGAGGTTACGACCTTACCTGAGGGC 548
QY	421	GAGTGCCTGGAGTTGCTCCGAGATATCTTGAGAAATGGGAGAGCGCTACAGCGCGCA 480
Db	549	GAGTGCCTGGAGTTGCTCCGAGATATCTTGAGAAATGGGAGAGCGCTACAGCGCGCA 608
QY	481	GATCTCTCAAAGGACACGTTGCCACACACCCATCTTGACCATGAGGCCACCTCAGG 540
Db	609	GATCTCTCAAAGGACACGTTGCCACACACCCATCTTGACCATGAGGCCACCTCAGG 668
QY	541	TGCTGGGCCCTGGGTTCTTACCTCGGAGATCAAGCTGACCTGGCAGCGGATCGGAG 600
Db	669	TGCTGGGCCCTGGGTTCTTACCTCGGAGATCAAGCTGACCTGGCAGCGGATCGGAG 728
QY	601	GGACAGACCCAGGACACAGACTTGTGGAGACGAGCGCTGCAGG 645
Db	729	GGACAGACCCAGGACACAGACTTGTGGAGACGAGCGCTGCAGG 773
RESULT 2		
BQ962778		
LOCUS	BQ962778	875 bp mRNA linear EST 21-AUG-2002
DEFINITION	AGENCOURT_8820719 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6380038	
ACCESSION	BQ962778	5', mRNA sequence.

BQ962778.1 GT:22378256
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2567 row: p column: 23
High quality sequence stop: 673.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 42"
/note="Organ: pancreas; Vector: pOTS7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH MGC library. |"

ORIGIN

Query Match	98.9%;	Score 637.6;	DB 13;	Length 875;
Best Local Similarity	99.2%;	Pred. No. 1.1e-114;		
Matches 640;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;
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DB	133	ATCGCGGTGGAGTACGTAGACACACGCAATTCCTGCGGTTCCACAGCGCCGCCGATT	192	
QY	61	CCGAGGATGGAGCCGCGGAGCCGTGGTGGAGCAAGAGGGGCCCGCAGTATTGGGAGTGG	120	
DB	193	CCGAGGATGGAGCCGCGGAGCCGTGGTGGAGCAAGAGGGGCCCGCAGTATTGGGAGTGG	252	
QY	121	ACCACSGGCTAGCCCAAGGCCAACGCACACAGATGTACCAGAGTGGCCCTCGAGGAACCTGC	180	
DB	253	ACCACAGGGTACGCCAAGGCCAACGCACACAGATGTACCAGAGTGGCCCTCGAGGAACCTGC	312	
QY	181	CGCGGCTACAACACAGAGCAGGCTGGGTCTCACSCCCTCCAGGGAATGAATGGCTCGCAC	240	
DB	313	CGCGGCTACAACACAGAGCAGGCTGGGTCTCACACCTCCAGGGAATGAATGGCTCGCAC	372	
QY	241	ATGGGCGCCGACGGAGCGCTCTCCGCGGGTATCACACGACGCGGTACGACGGCAGGAT	300	
DB	373	ATGGGCGCCGACGGAGCGCTCTCCGCGGGTATCACACGACGCGGTACGACGGCAGGAT	432	
QY	301	TACATCTCCCTGAAACGAGGACCTGCGCTCTCTGGACCGCGCGGACACCGTGGCTCAGATC	360	
DB	433	TACATCTCCCTGAAACGAGGACCTGCGCTCTCTGGACCGCGCGGACACCGTGGCTCAGATC	492	
QY	361	ACCCAGCGCTTCATGAGGCAGAGGAATATGCAGAGGATTCAGGACCTTACCTGGAGGGC	420	
DB	493	ACCCAGCGCTTCATGAGGCAGAGGAATATGCAGAGGATTCAGGACCTTACCTGGAGGGC	552	

RESULT 2	BQ962778	BQ962778	875 bp	mRNA	linear	EST 21-AUG-2002
LOCUS						
DEFINITION		AGENCOURT.8820719 NIH.MGC.42 Homo sapiens cDNA clone IMAGE:6380038				
ACCESSION		5', mRNA sequence.				
		BQ962778				

Db	433	TACATTCCTCTGAACGAGGACCTCTGCGCTCTCTGACCGCGCGGACACCGTGGCTCAGATC	492
Qy	361	ACCCAGCGCTTCATGAGCGAGAGGAATATGACAGGAGTTCAGGACCTTACCTGGAGGGC	420
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QY 421 GAGTGCCTGGAGTTGCTCCGAGATACCTTGAGAAATGGAGGAGAGCGCTACAGCGGCA 480
Db 553 GAGTGCCTGGAGTTGCTCCGAGATACCTTGAGAAATGGAGGAGAGCGCTACAGCGGCA 612
QY 481 GATCCTCCAAAGGACACAGTTGCTCCGAGATACCTTGAGAAATGGAGGAGAGCGCTACAGCGGCA 540
Db 613 GATCCTCCAAAGGACACAGTTGCTCCGAGATACCTTGAGAAATGGAGGAGAGCGCTACAGCGGCA 672
QY 541 TGCTGGGCTGGAGTTGCTCCGAGATACCTTGAGAAATGGAGGAGAGCGCTACAGCGGCA 600
Db 673 TGCTGGGCTGGAGTTGCTCCGAGATACCTTGAGAAATGGAGGAGAGCGCTACAGCGGCA 732
QY 601 GAAACAGACCCAGGACACAGAGTTGCTGGAGACCCAGGCTGAGGG 645
Db 733 GAACAGACCCAGGACACAGAGTTGCTGGAGACCCAGGCTGAGGG 777

RESULT 3
BM561951 949 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6593172 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5484505
DEFINITION 5', mRNA Sequence.
ACCESSION BM561951
VERSION BM561951.1 GI:18807627
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 949)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2013 row: 0 column: 02
High quality sequence stop: 682.
Location/Qualifiers
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/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH MGC 106"
/notes="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 98.5%; Score 635.4; DB 12; Length 949;
Best Local Similarity 99.1%; Pred. No. 3e-114;
Matches 639; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 156 ATCGCGCTGGAGTACGACACGCGATTCCTGGGTTGAGAGCGCCCGCGGATT 215
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Db 516 ACCAGCGCTTCTATGAGGACAGGAATATGACAGGAGGTTCAGGACCTACCTGGAGGGC 575
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VERSION CD514705.1 GI:31446423
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 829)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Location/Qualifiers
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FEATURES
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AUTHORS		1 (bases 1 to 886)	
TITLE		NIH-MGC http://mgs.nci.nih.gov/	
JOURNAL		National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT		Unpublished (1999)	
		Contact: Robert Strausberg, Ph.D.	
		Email: cgapbs@mail.nih.gov	
		Tissue Procurement: ATCC	
		cDNA Library Preparation: Rubin Laboratory	
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
		DNA Sequencing by: Agencourt Bioscience Corporation	
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		Directionally cloned into EcoRI/XhoI sites using the	
		following 5' adaptor: GGCACGAG(G). Library constructed by	
		Ling Hong in the laboratory of Gerald M. Rubin (University	
		of California, Berkeley) using ZAP-cDNA synthesis kit	
		(Stratagene) and Superscript II RT (Life Technologies).	
		Note: this is a NIH_MGC Library."	
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QY	361	ACCACAGCGCTTCTATGAGCGAGAGGAATATGACAGAGGAGTTTCAGGACCTACCTGAGGGGC	420
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QY	421	GAGTGCCTGGAGTTCCTCCGAGATACCTTGGAGATGGAAGAGACCGCTACAGCGCGCA	480
DB	559	GAGTGCCTGGAGTTCCTCCGAGATACCTTGGAGATGGAAGAGACCGCTACAGCGCGCA	618
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QY	61	CGAGGATGAGCGCGCGGAGCGTGGTGGAGCAAGAGGGCGCGCAGTATTGGAGTGG	120
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QY	121	ACCACGGGTACGCGCAAGCGCAACGACAGACTGACCGAGTGGCGCTTGGAGAACCTGCTC	180
DB	262	ACCACAGGTTACGCGCAAGCGCAACGACAGACTGACCGAGTGGCGCTTGGAGAACCTGCTC	321
QY	181	CGCGCTTACACGAGCGAGGCTGGTCTCACGCCCTCCAGGGAATGAATGGCTGCCAC	240
DB	322	CGCGCTTACACGAGCGAGGCTGGTCTCACGCCCTCCAGGGAATGAATGGCTGCCAC	381
QY	241	ATGGGGCGCGACGCGCGCTCTCTCGCGGGTATCACCGACGCGCTACGACGCGCAAGGAT	300
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QY	421	GAGTGCCTGGAGTTCCTCCGAGATACCTTGGAGATGGAAGAGAGCGCTACAGCGCGCA	480
DB	562	GAGTGCCTGGAGTTCCTCCGAGATACCTTGGAGATGGAAGAGAGCGCTACAGCGCGCA	621
QY	481	GATCTCTCAAGGACACGCTTGGCGGACCGCGGACCGCTTCTGACATGAGGCGCACCTGAGG	540
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QY	541	TGCTGGGCGCTTCTTACCTTCGCGAGATACCGTGGACCTTGGCGAGGATGGGGAG	600
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RESULT 5		886 bp	
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DEFINITION		AGENCOURT_8064678 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206180	
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ACCESSION		B0688194	
VERSION		B0688194.1	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 928)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Dr. Mark Watson
  cDNA Library Preparation: Rubin Laboratory
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
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      into EcoRI/XhoI sites using the following 5' adaptor:
      GGCACGAG(G). Library constructed by Ling Hong in the
      laboratory of Gerald M. Rubin (University of California,
      Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
      Superscript II RT (Life Technologies). Note: this is a
      NIH_MGC Library."

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      laboratory of Gerald M. Rubin (University of California,
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VERSION
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 941)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Dr. Mark Watson
  cDNA Library Preparation: Rubin Laboratory
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
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      GGCACGAG(G). Library constructed by Ling Hong in the
      laboratory of Gerald M. Rubin (University of California,
      Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
      Superscript II RT (Life Technologies). Note: this is a
      NIH_MGC Library."

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5' mRNA sequence.
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VERSION BQ926296.1 GI:22341327
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/BTP/Gazdar
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2604 row: e column: 14
High quality sequence stop: 638.
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
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GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

FEATURES
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Location/Qualifiers

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BM917072
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1130)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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Best Local Similarity 97.4%; Pred. No. 1e-105;

Query Match 93.4%; Score 602.6; DB 13; Length 931;
Best Local Similarity 97.8%; Pred. No. 7.9e-108;
Matches 631; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

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QY 61 CCGAGGATGGAGCCCGGGAGCCGTTGGGTGGAGCAAGAGGGCGCGCAGTATTGGGAGTGG 120
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QY 121 ACCAGSGGTACGCAAGCCAGCCAGCAGCTGACGAGTGGCGCTCGAGCACTGCTC 180
|||||
Db 264 ACCAGSGGTACGCAAGCCAGCCAGCAGCTGACGAGTGGCGCTCGAGCACTGCTC 323
|||||
QY 181 CGCCGCTACAACAGAGCGAGGCTGGGTCTCACSCCTCCAGGGAATGAATGGCTGCGAC 240
|||||
Db 324 CGCCGCTACAACAGAGCGAGGCTGGGTCTCACSCCTCCAGGGAATGAATGGCTGCGAC 383
|||||
QY 241 ATGGGGCCCGAGCGAGCGCTCTCCGCGGGTATACACGACGCGGTACGAGCGGAGGAT 300
|||||
Db 384 ATGGGGCCCGAGCGAGCGCTCTCCGCGGGTATACACGACGCGGTACGAGCGGAGGAT 443
|||||

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OM protein - protein search, using sw model

Run on: June 18, 2004, 08:50:11 ; Search time 71 seconds
(without alignments)
855.602 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 1173
Sequence: 1 IAVEYVDDTQFLRFDSDAAI.....QRDGEETQDTLVELTRPAG 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1986s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1164	99.2	215	4	AAG64619 Human can
2	1164	99.2	271	3	AAB433986 Human can
3	1164	99.2	274	4	AAG64618 Human can
4	1164	99.2	362	4	AAG64617 Human can
5	1164	99.2	362	4	ABB50296 HLA-Cw ov
6	1164	99.2	677	4	ABG26726 Novel hum
7	940	80.1	274	1	AAP80911 Consensus
8	927	79.0	362	1	AAP70155 Sequence
9	926	79.0	337	1	AAP70590 Sequence
10	922	78.6	369	4	AAB32882 Novel hum
11	922	78.6	374	4	AAG06772 Human pol
12	921	78.5	322	4	AAM23760 Human Bst
13	903	77.0	366	2	AAR12465 HLA-C exo
14	901	76.8	362	2	AAR03142 Sequence
15	900	76.7	362	7	ADBE64171 Human Pro
16	900	76.7	362	7	ADBE64175 Human Pro
17	900	76.7	374	4	AAR03144 Sequence
18	899	76.6	362	2	AAR03144 Sequence
19	899	76.6	366	2	AAY07033 Breast ca
20	893	76.1	366	2	AAR12466 HLA-C exo
21	886	75.5	362	2	AAR12464 HLA-B35 a
22	886	75.5	380	4	AAR12464 HLA-B35 a
23	882	75.2	362	2	AAR12463 HLA-Bw53
24	869	74.1	326	5	AAR79454 HLA-C rec
25	869	74.1	338	7	ADD46572 Human Pro

26	859.5	73.3	379	5	ABP70087 Human NOV
27	859.5	73.3	379	7	AD40254 Human NOV
28	857	73.1	365	3	AAV68272 Human leu
29	857	73.1	365	3	AAV52926 HLA-A2/A2
30	857	73.1	365	4	AAB58687 HLA-A2/A2
31	857	73.1	368	4	AAM24017 Human EST
32	856	73.0	365	3	AAV68268 Human leu
33	856	73.0	365	3	AAV52922 HLA-A2/A2
34	856	73.0	365	4	AAB58683 HLA-A2/A2
35	853	72.7	365	3	AAV58267 Human leu
36	853	72.7	365	3	AAV52921 HLA-A2/A2
37	853	72.7	365	4	AAB58682 HLA-A2/A2
38	852	72.6	274	3	AAV68275 Human leu
39	852	72.6	274	3	AAV68276 Human leu
40	852	72.6	274	3	AAV52930 HLA-A2/A2
41	852	72.6	274	3	AAV52929 HLA-A2/A2
42	852	72.6	274	4	AAB58690 HLA-A2/A2
43	852	72.6	274	4	AAB58691 HLA-A2/A2
44	852	72.6	364	5	ABP70088 Human NOV
45	851	72.5	365	3	AAV68271 Human leu

ALIGNMENTS

RESULT 1
AAG64619 standard; protein; 215 AA.
XX AC AAG64619;
DT 12-SEP-2001 (first entry)
XX DE Human cancer cell specific HLA-F antigen SEQ ID 6.
XX KW HLA-F antigen; cancer cell specific; human.
XX OS Homo sapiens.
XX PN JP2001095584-A.
XX PD 10-APR-2001.
XX PF 30-SEP-1999; 99JP-00279566.
XX PR 30-SEP-1999; 99JP-00279566.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA K.
XX DR WPI; 2001-360493/38.
XX DR N-PSDB; AAB45557.
XX FT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX PS Claim 1; Page 11-12; 12pp; Japanese.
XX CC This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention

XX Sequence 215 AA;

Query Match 99.2%; Score 1164; DB 4; Length 215;
Best Local Similarity 99.5%; Pred. No. 1.8e-107;
Matches 214; Conservative 1; Mismatches 0; Gaps 0;

QY 1 IAVEYVDDTQFLRFDSDAAIPRPFVWEQEGPQYWEITGYAKANAQTRVALRNL 60

Db 1 IAVEYVDDTQFLRFDSDAAIPRMEPRFPWQEGQYWEWTTGYAKANAQTDRLVALRNL 60
Qy 61 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGVGHQYHAMDGYIISLNEDLRSWTAADTVAQI 120
Db 61 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGVGHQYHAMDGYIISLNEDLRSWTAADTVAQI 120
Qy 121 TORFYAEABEYAEFRTYLEGECELELLRRYLENGKETLORADPPKAHVAHPISDHEATLR 180
Db 121 TORFYAEABEYAEFRTYLEGECELELLRRYLENGKETLORADPPKAHVAHPISDHEATLR 180
Qy 181 CWALGFYPAEITLTWQRDGEQTDTELVEITRPAG 215
Db 181 CWALGFYPAEITLTWQRDGEQTDTELVEITRPAG 215
RESULT 2
AAB43986
ID AAB43986 standard; protein; 271 AA.
AC AAB43986;
XX
XX
XX 08-FEB-2001 (first entry)
XX
XX Human cancer associated protein sequence SEQ ID NO:1431.
XX
XX Human: cancer associated gene; cancer antigen; detection; cancer;
XX diagnosis; cytostatic; proliferative; vulnary; immunomodulator;
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
XX dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
XX vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
XX immune disorder; haematopoietic cell disorder; autoimmune disorder;
XX allergic reaction; graft versus host disease; organ rejection;
XX haemostatic; thrombolytic; cardiovascular disorder; infection;
XX neurological disease; drug screening.
XX
XX Homo sapiens.
XX
XX WO200055350-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005892.
XX
XX 12-MAR-1999; 99US-0124270P.
XX (HUYA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587533/55.
XX N-PSDB; AAC78195.
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer.
XX
XX Claim 11; Page 2115-2116; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in
XX AAB43398 to AAB44239. The proteins can have activities based on the
XX tissues and cells the genes are expressed in. Example of activities
XX include: cytostatic; proliferative; vulnary; immunomodulator;
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
XX dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
XX nootropic; vasotropic; antipsoriatic and antiangiogenic. The
XX polynucleotides and polypeptides can be used for preventing, treating or
XX ameliorating medical conditions and diagnosing pathological conditions.
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from
XX the present invention may be used to treat immune disorders by activating
XX or inhibiting the proliferation, differentiation or mobilisation of
XX immune cells, to treat disorders of haematopoietic cells, autoimmune

CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies, to
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention
XX
XX Sequence 271 AA;
XX
XX Query Match 99.2%; Score 1164; DB 3; Length 271;
XX Best Local Similarity 99.5%; Pred. No. 2.4e-107;
XX Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IAVEYVDDTQFLRFDSDAAIPRMEPRFPWQEGQYWEWTTGYAKANAQTDRLVALRNL 60
Db 50 IAVEYVDDTQFLRFDSDAAIPRMEPRFPWQEGQYWEWTTGYAKANAQTDRLVALRNL 109
Qy 61 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGVGHQYHAMDGYIISLNEDLRSWTAADTVAQI 120
Db 110 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGVGHQYHAMDGYIISLNEDLRSWTAADTVAQI 169
Qy 121 TORFYAEABEYAEFRTYLEGECELELLRRYLENGKETLORADPPKAHVAHPISDHEATLR 180
Db 170 TORFYAEABEYAEFRTYLEGECELELLRRYLENGKETLORADPPKAHVAHPISDHEATLR 229
Qy 181 CWALGFYPAEITLTWQRDGEQTDTELVEITRPAG 215
Db 230 CWALGFYPAEITLTWQRDGEQTDTELVEITRPAG 264
RESULT 3
AAG64618
ID AAG64618 standard; protein; 274 AA.
XX
XX AAG64618;
XX
XX 12-SEP-2001 (first entry)
XX
XX Human cancer cell specific HLA-F antigen SEQ ID 5.
XX
XX HLA-F antigen; cancer cell specific; human.
XX
XX Homo sapiens.
XX
XX JF2001095584-A.
XX
XX 10-APR-2001.
XX
XX 30-SEP-1999; 99JP-00279566.
XX
XX 30-SEP-1999; 99JP-00279566.
XX (EGAW/) EGAWA K.
XX (MEDI-) MEDINET KK.
XX (KIMU/) KIMURA K.
XX
XX WPI; 2001-360493/38.
XX N-PSDB; AAH45556.
XX
XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX
XX Claim 2; Page 10-11; 12pp; Japanese.
XX
XX This invention relates to a cancer cell specific HLA-F antigen. The
XX invention includes DNA encoding the antigen, and a method for the
XX preparation of the cancer cell specific HLA-F antigen. The antigen may be
XX used in a method to diagnose cancer, in which the protein is used to
XX detect anti-HLA-F antibodies in bodily fluids of the patient. The present
XX sequence represents the cancer cell-specific HLA-F antigen of the
XX invention
XX
XX Sequence 274 AA;

Query Match 99.2%; Score 1164; DB 4; Length 274;
 Best Local Similarity 99.5%; Pred. No. 2.5e-107;
 Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVEYDDTQFLRFDSDAAIPRMPREPWEQPGQYWEWTTGYAKANAQTDRAVALRNL 60
 DB 23 IAVEYDDTQFLRFDSDAAIPRMPREPWEQPGQYWEWTTGYAKANAQTDRAVALRNL 82
 QY 61 RRYNQSAGSHTLQMGNGCDMPDGRLLRGYHQHAWDKDYISLNEDLSRWTAAADTVAQI 120
 DB 83 RRYNQSAGSHTLQMGNGCDMPDGRLLRGYHQHAWDKDYISLNEDLSRWTAAADTVAQI 142
 QY 121 TORFYAEYAEFFRYLEGECELELLRRYLENGKETLQRAADPPKHAHVAHPISDHEATLR 180
 DB 143 TORFYAEYAEFFRYLEGECELELLRRYLENGKETLQRAADPPKHAHVAHPISDHEATLR 202
 QY 181 CWALGFYPABIILTWORDEGEQTDTELVEVPAG 215
 DB 203 CWALGFYPABIILTWORDEGEQTDTELVEVPAG 237

RESULT 4
 AAG64617
 ID AAG64617 standard; protein; 362 AA.
 XX AAG64617;
 AC AAG64617;
 DT 12-SEP-2001 (first entry)
 DE Human cancer cell specific HLA-F antigen SEQ ID 4.
 KW HLA-F antigen; cancer cell specific; human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX JP2001095584-A.
 PN 10-APR-2001.
 PD 30-SEP-1999; 99JP-00279566.
 PF 30-SEP-1999; 99JP-00279566.
 PR (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 PA (KIMU/) KIMURA K.
 XX WPI; 2001-360493/38.
 DR N-PSDB; AAB45555.
 PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
 XX Disclosure; Page 9-10; 12pp; Japanese.

This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention

Sequence 362 AA;
 Query Match 99.2%; Score 1164; DB 4; Length 362;
 Best Local Similarity 99.5%; Pred. No. 3.6e-107;
 Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVEYDDTQFLRFDSDAAIPRMPREPWEQPGQYWEWTTGYAKANAQTDRAVALRNL 60
 DB 44 IAVEYDDTQFLRFDSDAAIPRMPREPWEQPGQYWEWTTGYAKANAQTDRAVALRNL 103

QY 61 RRYNQSAGSHTLQMGNGCDMPDGRLLRGYHQHAWDKDYISLNEDLSRWTAAADTVAQI 120
 DB 104 RRYNQSAGSHTLQMGNGCDMPDGRLLRGYHQHAWDKDYISLNEDLSRWTAAADTVAQI 163
 QY 121 TORFYAEYAEFFRYLEGECELELLRRYLENGKETLQRAADPPKHAHVAHPISDHEATLR 180
 DB 164 TORFYAEYAEFFRYLEGECELELLRRYLENGKETLQRAADPPKHAHVAHPISDHEATLR 223
 QY 181 CWALGFYPABIILTWORDEGEQTDTELVEVPAG 215
 DB 224 CWALGFYPABIILTWORDEGEQTDTELVEVPAG 258

RESULT 5
 ABB50296
 ID ABB50296 standard; protein; 362 AA.
 XX ABB50296;
 AC ABB50296;
 DT 08-FEB-2002 (first entry)
 DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.

Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine.

XX Homo sapiens.
 OS Homo sapiens.
 XX WO200175177-A2.
 PN 11-OCT-2001.
 PD 03-APR-2001; 2001WO-USO10947.
 PF 03-APR-2001; 2000US-0194336P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
 PI WPI; 2001-626450/72.
 PT N-PSDB; ABA83122.

Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker gene.
 Claim 23; Page 126-127; 140pp; English.

The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180, ABA83192 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179, ABA83182 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma, mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,

CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes or their encoded
CC proteins may be used as therapeutic targets for the treatment and
CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent
CC proteins encoded by ovarian tumour marker genes of the invention
XX
SQ Sequence 362 AA;

Query Match 99.2%; Score 1164; DB 4; Length 362;
Best Local Similarity 99.5%; Pred. No. 3.6e-107;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQDRVALRNLL 60
DB 44 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQDRVALRNLL 103
QY 61 RRYNQEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDGKDYISLNEDLSRWTAAADTVAQI 120
DB 104 RRYNQEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDGKDYISLNEDLSRWTAAADTVAQI 163
QY 121 TORFYAEYAEFFRTYLEGCELELLRRYLENGKETLQRAADPPKAVHAHPISDHEATLR 180
DB 164 TORFYAEYAEFFRTYLEGCELELLRRYLENGKETLQRAADPPKAVHAHPISDHEATLR 223
QY 181 CVALGFYPABEITLTWQDGEETQDTLVELTRPAG 215
DB 224 CVALGFYPABEITLTWQDGEETQDTLVELTRPAG 258

RESULT 6
ABG26726
ID ABG26726 standard; protein; 677 AA.
XX
AC ABG26726;
XX
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26717.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX

PF 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
DR N-PSDB; AAS90913.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 57085; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 677 AA;

Query Match 99.2%; Score 1164; DB 4; Length 677;
Best Local Similarity 99.5%; Pred. No. 8.4e-107;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQDRVALRNLL 60
DB 353 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQDRVALRNLL 412
QY 61 RRYNQEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDGKDYISLNEDLSRWTAAADTVAQI 120
DB 413 RRYNQEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDGKDYISLNEDLSRWTAAADTVAQI 472
QY 121 TORFYAEYAEFFRTYLEGCELELLRRYLENGKETLQRAADPPKAVHAHPISDHEATLR 180
DB 473 TORFYAEYAEFFRTYLEGCELELLRRYLENGKETLQRAADPPKAVHAHPISDHEATLR 532
QY 181 CVALGFYPABEITLTWQDGEETQDTLVELTRPAG 215
DB 533 CVALGFYPABEITLTWQDGEETQDTLVELTRPAG 567

RESULT 7
AAP80911
ID AAP80911 standard; protein; 274 AA.
XX
AC AAP80911;
XX
XX 25-MAR-2003 (revised)
DT 18-SEP-1990 (first entry)
XX
DE Consensus sequence of peptides which constitute the alpha-1, alpha-2 and
DE alpha-3 regions of a class I HLA molecule.
XX
KW HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH Region 1..90
FT Region /note= "alpha-1 region"
FT Region 91..180
FT Region /note= "alpha-2 region"
FT Region 181..272
FT Region /note= "alpha-3 region"
XX
XX WO8805784-A.
XX
PD 11-AUG-1988.

XX 27-JAN-1988; 88WO-US000245.
XX 30-JAN-1987; 87US-00008846.
XX 24-DEC-1987; 87US-00138547.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX Krensky AM, Farham P, Clayberger C;
XX WPI; 1988-235147/33.
XX New peptide corresp. to major histocompatibility antigen regions - used
XX for modulating cytotoxic T-lymphocyte activity in e.g. transplants or
XX auto-immune diseases.
XX Example 9; Fig 4; 60pp; English.
XX The consensus sequence is derived from a total of 23 HLA-A,B,C sequences.
XX The protein sequences in the three extracellular domains (alpha-1, alpha-
XX 2 and alpha-3) are shown. The example concerned the effect of peptides
XX from different HLA-A2 epitopes on cytotoxicity of target cells by CTL of
XX different specificities. (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
XX correct PA field.)
XX Sequence 274 AA;
Query Match 80.1%; Score 940; DB 1; Length 274;
Best Local Similarity 80.5%; Pred. No. 58-85;
Matches 173; Conservative 14; Mismatches 28; Indels 0; Gaps 0;
QY 1 IAVEYDDTQFLRFDSDAIPRMEPEPWVEQEGYQWWTGYAKANAQTDRVALRNL 60
DB 23 IAGYVDDTQFVRFDSDAIPRMEPEPWVEQEGYQWWTGYAKANAQTDRVALRNL 82
QY 61 RRYNQSEAGSHYQNGMCDMPDGRLLRGYHQAHDGKDYISLNEDLSRWTAAUTVAQI 120
DB 83 GYTNQSEAGSHYQRMGCDVGPGRLLRGYHQAHDGKDYISLNEDLSRWTAAUTVAQI 142
QY 121 TORFYEAEEVABEERTYLEGECLELLRRYLENGKETLQADPPKAVHHPISDHEATLR 180
DB 143 TQKWEARVAREQRAYLEGTCEVWLRYLENGKETLQADPPKTHVTHHPISDHEATLR 202
QY 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
DB 203 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 237
RESULT 8
AAP70155
ID AAP70155 standard; protein; 362 AA.
XX AAP70155;
XX AC AAP70155;
XX DT 25-MAR-2003 (revised)
XX DT 10-MAR-1993 (revised)
XX DT 03-APR-1991 (first entry)
XX Sequence encoded by genomic DNA encoding human histocompatibility antigen
XX HLA-B 27.
XX Ankylosing spondylitis; rheumatic disorder; diagnosis.
XX Homo sapiens.
XX EP226069-A.
XX 24-JUN-1987.
XX 21-NOV-1986; 86EP-00116139.
XX 30-NOV-1985; 85DE-00542024.

PR 21-DEC-1985; 85DE-03545576.
XX (BEHW) BEHRINGWERKE AG.
XX Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmulle G;
XX WPI; 1987-171469/25.
XX N-PSDB; AAN70225.
XX DNA coding for human histocompatibility antigen HLA-B 27 - useful for
XX diagnosis and antigen and antibody prodn.
XX Disclosure; Page 6; 13pp; German.
XX The DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human
XX genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27
XX antibodies in human serum. The antibodies may be used to determine HLA-B
XX 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp.
XX ankylosing spondylitis. (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 362 AA;
Query Match 79.0%; Score 927; DB 1; Length 362;
Best Local Similarity 80.0%; Pred. No. 1.4e-83;
Matches 172; Conservative 11; Mismatches 32; Indels 0; Gaps 0;
QY 1 IAVEYDDTQFLRFDSDAIPRMEPEPWVEQEGYQWWTGYAKANAQTDRVALRNL 60
DB 47 ITGVYDDTLFVRFDSDAIPRMEPEPWVEQEGYQWWTGYAKANAQTDRVALRNL 106
QY 61 RRYNQSEAGSHYQNGMCDMPDGRLLRGYHQAHDGKDYISLNEDLSRWTAAUTVAQI 120
DB 107 RYTNQSEAGSHYQNMVACDVGPGRLLRGYHQAHDGKDYISLNEDLSRWTAAUTVAQI 166
QY 121 TORFYEAEEVABEERTYLEGECLELLRRYLENGKETLQADPPKAVHHPISDHEATLR 180
DB 167 TQKWEARVAREQRAYLEGTCEVWLRYLENGKETLQADPPKTHVTHHPISDHEATLR 226
QY 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
DB 227 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 261
RESULT 9
AAP70590
ID AAP70590 standard; protein; 337 AA.
XX AAP70590;
XX AC AAP70590;
XX DT 10-APR-1991 (first entry)
XX Sequence of the human histocompatibility antigen HLA B27.
XX Rheumatic disorder; genetic screening; diagnosis; ankylosing spondylitis.
XX Homo sapiens.
XX DE3542024-A.
XX 04-JUN-1987.
XX 28-NOV-1985; 85DE-03542024.
XX 21-DEC-1985; 85DE-03545576.
XX (BEHW) BEHRINGWERKE AG.
XX Riethmulle G, Meo T, Weiss E, Szots H;
XX WPI; 1987-157893/23.
XX N-PSDB; AAN70935.
XX DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA,
XX PT

PT antigen or antibody.
XX
PS Disclosure; Page 5; 5pp; German.
XX
CC The DNA may be used as a hybridisation probe for detecting the HLA B27
CC gene, eg for assessing susceptibility to rheumatic disorders such as
CC ankylosis-spondylitis, or may be used to transform cells for prodn. of
CC HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human
CC serum, or to produce mono- or polyclonal HLA B27 antibodies for use in
CC immunoassay
XX
SQ Sequence 337 AA;
Query Match 79.0%; Score 926.5; DB 1; Length 337;
Best Local Similarity 80.5%; Pred. No. 1.5e-83;
Matches 173; Conservative 11; Mismatches 30; Indels 1; Gaps 1;
QY 1 IAVEYVDDTQFLRDSDAALPRMEPRPWPVQSGPOYWEWTTGYAKANAQTDRLVALRNLL 60
Db 23 ITVGYVDDTLFVRFDSDAASPREPRAPWIEQGPPEYWDRETQICKAKAQTDREDLRTILL 82
QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 120
Db 83 -RRNQSEAGSHTLQNMGYGCDVGPDLRLRGYHQAHDGKDYIALNEDLSWTAADTVAQI 141
QY 121 TORFYAEYVAEYFRPYLSEGCLELLRRYLENGKETLQADPPKAVHAHPISDHEATLR 180
Db 142 TORKEAARVAEQRLAYLEGCVEWMLRRYLENGKETLQADPPKAVHAHPISDHEATLR 201
QY 181 CWALGFYPAEITLTWQDGEQDTDELVETRPAG 215
Db 202 CWALGFYPAEITLTWQDGEQDTDELVETRPAG 236
RESULT 10
AAU32882
ID AAU32882 standard; protein; 369 AA.
AC AAU32882;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #3373.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WC200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
PS Claim 20; Page 683; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 369 AA;
Query Match 78.6%; Score 922; DB 4; Length 369;
Best Local Similarity 78.6%; Pred. No. 4.6e-83;
Matches 169; Conservative 18; Mismatches 28; Indels 0; Gaps 0;
QY 1 IAVEYVDDTQFLRDSDAALPRMEPRPWPVQSGPOYWEWTTGYAKANAQTDRLVALRNLL 60
Db 50 ISVGYVDDTQFVRFDSDAASPREPRAPWIEQGPPEYWDRETQICKAKAQTDREDLRTILL 109
QY 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 120
Db 110 GYNNQSEAGSHTLQSMYGCDDVGPDLRLRGYHQAHDGKDYIALNEDLSWTAADTVAQI 169
QY 121 TORFYAEYVAEYFRPYLSEGCLELLRRYLENGKETLQADPPKAVHAHPISDHEATLR 180
Db 170 TORKEAARVAEQRLAYLEGCVEWMLRRYLENGKETLQADPPKAVHAHPISDHEATLR 229
QY 181 CWALGFYPAEITLTWQDGEQDTDELVETRPAG 215
Db 230 CWALGFYPAEITLTWQDGEQDTDELVETRPAG 264
RESULT 11
AAO06772
ID AAO06772 standard; protein; 374 AA.
XX
AC AAO06772;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 20664.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI66703.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 20664; 1399pp + Sequence Listing; English.
PS
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA03910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 374 AA;

Query Match 78.6%; Score 922; DB 4; Length 374;
Best Local Similarity 80.5%; Pred. No. 4.7e-83;
Matches 173; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

QY 1 IAVEYDDTQFLRFDSDAAIPRMEPREPWEQEGPQYWEWTTGYAKANAQTDRAVLRNLL 60
DB 47 IAVGVDDTQFVRFDSDAASPRAPAPWIEQEGPEYWDRTNWKASQOTYRENRRL 106

QY 61 RRYNQSAGSHTLQGMNGCDMPDGRLLRGYHQHAWDKDYIISLNEDLSRWTAAQI 120
DB 107 RRYNQSAGSHTLQGMNGCDMPDGRLLRGYHQHAWDKDYIISLNEDLSRWTAAQI 166

QY 121 TORFYEAEYAEPRFTVLEGECLLRRLRYLENGKETLORADPPKAVHHPISDHEATLR 180
DB 167 TORKWEAREABQRLAYLEGLCVWRRLRYLENGKETLORADPPKTHVTHHPISDHEATLR 226

QY 181 CWALGFYPAEITLTWQDGEQDTQDTLVETRPAG 215
DB 227 CWALGFYPAEITLTWQDGEQDTQDTLVETRPAG 261

RESULT 12
AAM23760
ID AAM23760 standard; protein; 322 AA.
XX
AC AAM23760;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1285.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX

DR WPI; 2001-476164/51.
XX N-PSDB; AAH98419.
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 924-925; 1275pp; English.
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
SQ Sequence 322 AA;

Query Match 78.5%; Score 921; DB 4; Length 322;
Best Local Similarity 79.1%; Pred. No. 4.9e-83;
Matches 170; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 IAVEYDDTQFLRFDSDAAIPRMEPREPWEQEGPQYWEWTTGYAKANAQTDRAVLRNLL 60
DB 47 IAVGVDDTQFVRFDSDAASPRAPAPWIEQEGPEYWDRTNWKASQOTYRENRRL 106

QY 61 RRYNQSAGSHTLQGMNGCDMPDGRLLRGYHQHAWDKDYIISLNEDLSRWTAAQI 120
DB 107 RRYNQSAGSHTLQGMNGCDMPDGRLLRGYHQHAWDKDYIISLNEDLSRWTAAQI 166

QY 121 TORFYEAEYAEPRFTVLEGECLLRRLRYLENGKETLORADPPKAVHHPISDHEATLR 180
DB 167 TORKWEAREABQRLAYLEGLCVWRRLRYLENGKETLORADPPKTHVTHHPISDHEATLR 226

QY 181 CWALGFYPAEITLTWQDGEQDTQDTLVETRPAG 215
DB 227 CWALGFYPAEITLTWQDGEQDTQDTLVETRPAG 261

RESULT 13
AAR12465
ID AAR12465 standard; protein; 365 AA.
XX
AC AAR12465;
XX
DT 25-MAR-2003 (revised)
DT 29-AUG-1991 (first entry)
XX
DE HLA-C exon Cb-1.
XX
KW Human leukocyte antigen; probe; major histocompatibility complex; MHC;
KW class I.
XX
OS Homo sapiens.
XX
PN JP03112485-A.
XX
PD 14-MAY-1991.
XX
PF 22-SEP-1989; 89JP-00247695.
XX
PR 22-SEP-1989; 89JP-00247695.
XX
PA (OLYU) OLYMPUS OPTICAL CO LTD.
XX
XX WPI; 1991-182389/25.
DR N-PSDB; AAQ12116.
XX
PT HLA-C gene, DNA probe and transformant cells - for immunisation of
XX animals and monoclonal antibody development.
XX
PS Claim 3; Page 2; 13pp; Japanese.

XX Probes comprising part of the DNA sequence encoding the protein can be
CC used to identify Class I genes. The DNA can be expressed for immunisation
CC of animals and prodn. of monoclonal antibodies specific for the HLA-C
CC antigen. See also AAR12466 (same patent) and J03112486 and J03112487.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 366 AA;
Query Match 77.0%; Score 903; DB 2; Length 366;
Best Local Similarity 79.1%; Pred. No. 3.6e-81;
Matches 170; Conservative 14; Mismatches 31; Indels 0; Gaps 0;
QY 1 IAVEYDDTQFLRFDSDAALPRMEPRPWEQSGPQYWEWTTGYAKANAQTDRLVALNLL 60
Db 47 IAVGYVDDTQFVRFDSDAASPRPEPRAPWVEQSGPEYNDRETKYKRAQTDRLVSRLNR 106
QY 61 RRYNQSEAGSHTLQGMNGCDMPDGLRLRGYHQAHDGKDYISLNEDLSRWTAAADTVAQI 120
Db 107 GYTNQSEAGSHTLQWFGCDLGPDLRLRGYDQSAVDGKDYIALNEDLSRWTAAADTAAQI 166
QY 121 TORFYAEAEVAREPRTYLEGCELELLRRYLENGKETLQADPPKAVHAHPISDHEATLR 180
Db 167 TORKWEAAREAEORRAYLEGTCEVWELRRHLENGKETLQADPPKTHVTHHPVSDHEATLR 226
QY 181 CWALGFYPABITLTWQDGEEOQTDTLTVETRPAG 215
Db 227 CWALGFYPABITLTWQDGEDQTDTELTVETRPAG 261
RESULT 14
AAR03142
ID AAR03142 standard; protein; 362 AA.
AC AAR03142;
XX
DT 25-MAR-2003 (revised)
DT 19-MAR-1991 (first entry)
XX
DE Sequence of HLA-Bw52 antigen.
XX
KW Probe; HLA class I DNA; immunogen.
XX
OS Homo sapiens.
XX
PN EP354580-A.
XX
PD 14-FEB-1990.
XX
PF 10-AUG-1989; 89EP-00114857.
XX
PR 11-AUG-1988; 88JP-00200758.
XX
PR (OLYU) OLYMPUS OPTICAL CO LTD.
XX
PA Kano K, Takiguchi M;
XX
PI WPI; 1990-046289/07.
XX
DR New DNA for class I human leucocyte antigens - with derived probes and
XX transformed cells, used for DNA typing, as immunogens etc.
XX
XX Disclosure; Page 13; 23pp; English.
XX
CC The HLA class I DNA can be used as a source of probes for use in DNA typing.
CC transformed cells, which are useful as immunogens, can be obtained by
CC introducing these DNAs into eucaryotic cells. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 362 AA;
Query Match 76.8%; Score 901; DB 2; Length 362;
Best Local Similarity 77.7%; Pred. No. 5.6e-81;

Matches 167; Conservative 17; Mismatches 31; Indels 0; Gaps 0;
QY 1 IAVEYDDTQFLRFDSDAALPRMEPRPWEQSGPQYWEWTTGYAKANAQTDRLVALNLL 60
Db 47 IAVGYVDDTQFVRFDSDAASPRPEPRAPWVEQSGPEYNDRETKYKRAQTDRLVSRLNR 106
QY 61 RRYNQSEAGSHTLQGMNGCDMPDGLRLRGYHQAHDGKDYISLNEDLSRWTAAADTVAQI 120
Db 107 RRYNQSEAGSHTWQMYGCDVGPDLRLRGHNYAYDGKDYIALNEDLSRWTAAADTAAQI 166
QY 121 TORFYAEAEVAREPRTYLEGCELELLRRYLENGKETLQADPPKAVHAHPISDHEATLR 180
Db 167 TORKWEAAREAEORRAYLEGTCEVWELRRHLENGKETLQADPPKTHVTHHPVSDHEATLR 226
QY 181 CWALGFYPABITLTWQDGEEOQTDTLTVETRPAG 215
Db 227 CWALGFYPABITLTWQDGEDQTDTELTVETRPAG 261
RESULT 15
ADE64171
ID ADE64171 standard; protein; 362 AA.
XX
AC ADE64171;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P30474, SEQ ID NO 10123.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; P30474.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX	Sequence 362 AA;
SQ	
Query Match	76.7%; Score 900; DB 7; Length 362;
Best Local Similarity	77.7%; Pred. No. 7e-81; 33; Indels 0; Gaps 0;
Matches 167; Conservative 15; Mismatches 33; Indels 0; Gaps 0;	
QY	1 IAVEYVDDTQFLRFDSDAIPRMPEPVEQGPQYWEWTTGYAKANAQTDRLVALRNLL 60
DB	47 IAVGVDDTQFVRFDSDAASPTERAPWIEGEPYWDRTQIFKNTQYRESLRNL 106
QY	61 RRYNQEAGSHTLQWNGCDMGPDGRLRGYHGHAWDCKYISLNEDLRSWTAADTVAQI 120
DB	107 GYNGQEAGSHIIQRMYGCDLGPDGRLLRGHDQSAYDCKYIALNEDLSSWTAADTAAQI 166
QY	121 TORFYEAEYAEFEPTYLEGECLELRRYLENGKETLQRADPPKAAHVAHPISDEATLR 180
DB	167 TQKWEAAAEVAEQRAYLEGICVEWLRRLYLENGKETLQRADPPKTHVTHFPVSDHEATLR 226
QY	181 CWALGFYPAEITLTWQDGEQQTQDTLVETRPAG 215
DB	227 CWALGFYPAEITLTWQDGEDQTQDTLVETRPAG 261

Search completed: June 18, 2004, 10:50:13
Job time : 72 secs